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(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"			
(57) Abstract  The present invention provides open reading frames ORFX, encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.			

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## NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

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## BACKGROUND OF THE INVENTION

The invention relates generally to nucleic acids and polypeptides encoded thereby, and methods of using these nucleic acids and polypeptides.

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## SUMMARY OF THE INVENTION

The invention is based in part on the discovery of nucleic acids that include open reading frames encoding novel polypeptides, and on the polypeptides encoded thereby. The nucleic acids and polypeptides are collectively referred to herein as "ORFX".

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Accordingly, in one aspect, the invention provides an isolated nucleic acid molecule (SEQ ID NO:2 $n$ -1, wherein  $n$  is an integer between 1-3161), that encodes novel polypeptide, or a fragment, homolog, analog or derivative thereof. The nucleic acid can include, *e.g.*, a nucleic acid sequence encoding a polypeptide at least 85% identical to a polypeptide comprising the amino acid sequences of SEQ ID NO:2 $n$ , wherein  $n$  is an integer between 1-3161. The nucleic acid can be, *e.g.*, a genomic DNA fragment, or a cDNA molecule.

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Also included in the invention is a vector containing one or more of the nucleic acids described herein, and a cell containing the vectors or nucleic acids described herein.

The invention is also directed to host cells transformed with a recombinant expression vector comprising any of the nucleic acid molecules described above.

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In another aspect, the invention includes a pharmaceutical composition that includes an ORFX nucleic acid and a pharmaceutically acceptable carrier or diluent.

In a further aspect, the invention includes a substantially purified ORF polypeptide, *e.g.*, any of the ORFX polypeptides encoded by an ORFX nucleic acid, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition that includes a ORFX polypeptide and a pharmaceutically acceptable carrier or diluent.

5 In a still a further aspect, the invention provides an antibody that binds specifically to an ORFX polypeptide. The antibody can be, *e.g.*, a monoclonal or polyclonal antibody, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition including ORFX antibody and a pharmaceutically acceptable carrier or diluent. The invention is also directed to isolated antibodies that bind to an epitope on a  
10 polypeptide encoded by any of the nucleic acid molecules described above.

The invention also includes kits comprising any of the pharmaceutical compositions described above.

The invention further provides a method for producing an ORFX polypeptide by providing a cell containing a ORFX nucleic acid, *e.g.*, a vector that includes a ORFX nucleic  
15 acid, and culturing the cell under conditions sufficient to express the ORFX polypeptide encoded by the nucleic acid. The expressed ORFX polypeptide is then recovered from the cell. Preferably, the cell produces little or no endogenous ORFX polypeptide. The cell can be, *e.g.*, a prokaryotic cell or eukaryotic cell.

The invention is also directed to methods of identifying an ORFX polypeptide or nucleic  
20 acids in a sample by contacting the sample with a compound that specifically binds to the polypeptide or nucleic acid, and detecting complex formation, if present.

The invention further provides methods of identifying a compound that modulates the activity of a ORFX polypeptide by contacting ORFX polypeptide with a compound and determining whether the ORFX polypeptide activity is modified.

25 The invention is also directed to compounds that modulate ORFX polypeptide activity identified by contacting a ORFX polypeptide with the compound and determining whether the compound modifies activity of the ORFX polypeptide, binds to the ORFX polypeptide, or binds to a nucleic acid molecule encoding a ORFX polypeptide.

30 In a another aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a sample from the subject and measuring the amount of ORFX polypeptide in the subject sample.

The amount of ORFX polypeptide in the subject sample is then compared to the amount of ORFX polypeptide in a control sample. An alteration in the amount of ORFX polypeptide in the subject protein sample relative to the amount of ORFX polypeptide in the control protein sample indicates the subject has a tissue proliferation-associated condition. A control sample is preferably taken from a matched individual, *i.e.*, an individual of similar age, sex, or other general condition but who is not suspected of having a tissue proliferation-associated condition. Alternatively, the control sample may be taken from the subject at a time when the subject is not suspected of having a tissue proliferation-associated disorder. In some embodiments, the ORFX is detected using a ORFX antibody.

In a further aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a nucleic acid sample, *e.g.*, RNA or DNA, or both, from the subject and measuring the amount of the ORFX nucleic acid in the subject nucleic acid sample. The amount of ORFX nucleic acid sample in the subject nucleic acid is then compared to the amount of an ORFX nucleic acid in a control sample. An alteration in the amount of ORFX nucleic acid in the sample relative to the amount of ORFX in the control sample indicates the subject has a tissue proliferation-associated disorder.

In a still further aspect, the invention provides method of treating or preventing or delaying a ORFX-associated disorder. The method includes administering to a subject in which such treatment or prevention or delay is desired a ORFX nucleic acid, a ORFX polypeptide, or an ORFX antibody in an amount sufficient to treat, prevent, or delay a tissue proliferation-associated disorder in the subject.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

## DETAILED DESCRIPTION OF THE INVENTION

The invention provides novel polypeptides and nucleotides encoded thereby. The polynucleotides and their encoded polypeptides can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc.

Included in the invention are 3161 novel nucleic acid sequences and their encoded polypeptides. The sequences are collectively referred to as "ORFX nucleic acids" or ORFX polynucleotides" and the corresponding encoded polypeptide is referred to as a "ORFX polypeptide" or ORFX protein". For example, an ORFX nucleic acid according to the invention is a nucleic acid including an ORF1 nucleic acid, and an ORF polypeptide according to the invention is a polypeptide that includes the amino acid sequence of an ORF1 polypeptide. Unless indicated otherwise, "ORFX" is meant to refer to any of the ORF1-3161 sequences disclosed herein.

Table 1 provides a summary of the ORFX nucleic acids and their encoded polypeptides are summarized in Table 1. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention is provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 1 of Table 1, entitled "ORF #", denotes an ORF number assigned to a nucleic acid containing an open reading frame according to the invention.

Column 2 of Table 1, entitled "Internal Identification number (Nucleic Acid Sequence Identification Number, Polypeptide Sequence Identification Number), provides an internal identification number for the indicated ORF, along with sequence identification numbers (SEQ ID NOs.) corresponding to the indicated ORF. In general, for an ORF $n$  according to the invention (wherein  $n$  is any integer from 1 to 3161), a nucleic acid corresponding to the ORF is SEQ ID NO:2 $n$ -1, and an amino acid sequence encoded by the ORF is SEQ ID NO:2 $n$ . For example, a nucleic acid sequence corresponding to an ORF1 nucleic acid is SEQ ID NO:1, and a polypeptide sequence corresponding to an ORF1 polypeptide is SEQ ID NO:2. Similarly, a

nucleic acid sequence corresponding to an ORF4 nucleic acid is SEQ ID NO:7, and a polypeptide sequence corresponding to an ORF4 polypeptide is SEQ ID NO:8; a nucleic acid sequence corresponding to an ORF198 nucleic acid sequence is SEQ ID NO:395, and a polypeptide sequence corresponding to an ORF198 polypeptide is SEQ ID NO:396. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention are provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 2 of Table 1, entitled "Protein Similarity", lists previously described proteins that are related to polypeptides encoded by the ORFs. Genbank identifiers for the previously described proteins are provided. These can be retrieved from <http://www.ncbi.nlm.nih.gov/>.

To determine similarity to previously described proteins, polypeptides encoded by ORFX DNA sequences were tested using the Framesearch Algorithm against a nonredundant version of the GenPept Database from NCBI/Genbank. DNA sequences that had a score of '90' or above (Framesearch algorithm score, Edelman et. al. GCG Genetics) to a known protein were selected. Open reading frames were extended beyond the region of the protein matched using standard DNA translation and codon tables. Novel proteins that lacked a protein match were translated against the standard genetic codons and proteins with an ORF at least 80 amino acids and containing a Methionine start are included in the Table.

Column 3 of Table 3, entitled "Protein Domains", lists previously described protein domains, designated by pfam entries, that are present in polypeptides encoded by the ORFs. Also included in column 3 are proteins in which these domains are present. The pfam entries can be retrieved from <http://pfam.wustl.edu/>. DNA sequences were translated in all six frames and tested using the Hmmer Algorithm against the Pfam Database (References to the algorithm and Pfam database can be found at <http://pfam.wustl.edu/>). Translated DNA sequences that matched a protein domain entry in the Pfam database AND had a score of '7.5' were selected.

Column 4 of Table 3, entitled "Protein Classification", lists the type of classification assigned for the protein, based on its homology. Examples of proteins in the classification include the following proteins:

### **Amylases**

Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

### **5 Amyloid**

The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called amyloidosis, which affects the liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. 15 Amyloid deposition is also associated with type II diabetes mellitus.

### **Angiopoeitin**

Members of the angiopoeitin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an 20 essential step in tumor growth in order for the tumor to get the blood supply it needs to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

### **25 Apoptosis-related proteins**

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell

death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of anti-aging drugs.

## 5           **Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases**

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form  
10 of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

## **Colony-stimulating factor-related proteins**

Granulocyte/macrophage colony-stimulating factors are cytokines that act in  
15 hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

## **Complement-related proteins**

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a  
20 membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent  
25 cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I diabetes mellitus, meningitis neurological disorders such as nemaline myopathy, neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

### **Cytochrome**

The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

### **Kinesins**

Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

### **Cytokines, Interferon, Interleukin**

Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

### **G-protein coupled receptors**

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and dwarfism.



**Thioesterases**

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The key to the molecule type is as follows:

10	Abbrev:	Title:
	amylase	amylase protein
	amylaseinhib	amylase inhibitor
	amyloid	amyloid protein
15	apoptosis	apoptosis associated protein
	apoptosisinhib	apoptosis inhibitors
	apoptosisrecep	apoptosis receptors
	ATPase_associated	ATPase associated protein
	biotindp	biotin dependent enzyme/protein
20	cadherin	cadherin protein
	calcium_channel	calcium channel protein
	carboxylase	carboxylase protein
	cathepsin	cathepsin/carboxypeptidases
	cathepsininhib	cathepsin/carboxypeptidase inhibitor
25	chloride_channel	chloride channel protein
	collagen	collagen
	complement	complement protein
	complementrecept	complement receptor protein
	complementinhib	complement inhibitor
30	csf	colony stimulating factor
	csfrecept	colony stimulating factor receptor
	cyclin	cyclin protein
	cyto450	cytochrome p450 protein
	cytochrome	cytochrome related protein
35	deaminase	deaminase
	dehydrogenase	dehydrogenase
	desaturase	desaturase
	dna_rna_bind	DNA/RNA binding protein/factor
	dna_rna_inhib	DNA/RNA binding protein/factor inhibitor
40	dynein	dynein

	elastase	elastase
	elastaseinhib	elastase inhibitor
	eph	EPH family of tyrosine kinases
	esterase	esterase
5	esteraseinhib	esterase inhibitor
	fgf	fibroblast growth factor
	fgfreceptor	fibroblast growth factor receptor
	gaba	GABA receptor
	glucoamylase	glucoamylase
10	glucoronidase	glucoronidase
	glycoprotein	glycoprotein
	Guanylyl	guanylylate cyclase
	helicase	helicase
	histone	histone
15	HOM	homologous
	homeobox	homeobox protein
	hydrolase	hydrolase
	hydroxysteroid	hydroxysteroid associated protein
	hypoxanthine	hypoxanthine associated protein
20	immunoglob	immunoglobulin
	immunoglobrecept	immunoglobulin receptor
	interferon	interferon
	interleukin	interleukin
	interleukinrecept	interleukin receptor
25	isomerase	isomerase
	isomeraseinhibitor	isomerase inhibitor
	isomerasereceptor	isomerase receptor
	kinase	kinase
	kinaseinhibitor	kinase inhibitor
30	kinasereceptor	kinase receptor
	kinesin	kinesin
	laminin	laminin associated protein
	lipase	lipase
	metallothionein	metallothionein
35	MHC	major histocompatibility complex
	misc_channel	miscellaneous channel
	ngf	nerve growth factor
	nuci_recpt	nuclear receptor
	nuclease	nuclease
40	oncogene	oncogene associated protein
	oxidase	oxidase
	oxygenase	oxygenase
	peptidase	peptidase
	peroxidase	peroxidase
45	phosphatase	phosphatase
	phosphataseinhib	phosphatase inhibitor

	phosphorylase	phosphorylase
	PIR	PIR DATABASE (release 56, 29-OCT-1998)
5	polymerase	polymerase
	potassium_channel	potassium channel protein
	prostaglandin	prostaglandin
	protease	protease
	proteaseinhib	protease inhibitor
10	reductase	reductase
	ribosomalprot	ribosomal associated protein
	RTR	EMBLDATABASE translated entries not to be incorporated into SWISS-PROT (20-JUL-1998)
15	SIM	similar
	SPTR	EMBL DATABASE translated entries to be incorporated into SWISS-PROT (20-JUL-1998)
20	struct	structural associated protein
	sulfotransferase	sulfotransferase
	SWP	SWISS-PROT DATABASE (release 18-OCT-1998)
	SWPN	SWISS-PROT Update (release 11-NOV-98)
	synthase	synthase
25	tgf	transforming growth factor
	tgfreceptor	transforming growth factor receptor
	thioesterase	thioesterase
	thiolase	thiolase
	tm7	seven transmembrane domain G-protein coupled receptor
30	tnf	necrosis factor receptor
	traffic	tumor necrosis factor
	tnfreceptor	tumor trafficking associated protein
	TRN	EMBL DATABASE translated entries update (20-JUL-1998)
35	transcriptfactor	transcription factor
	transferase	transferase
	transport	transport protein
	tubulin	tubulin
40	ubiquitin	ubiquitin
	unclassified	Protein not categorized into one of the aforementioned protein families
	water channel	water channel protein

Column 5 of Table 1, entitled, "Cells or Tissues in Which Gene is Expressed", denotes tissues, represented by five digit numbers, in which RNA homologous to the ORF nucleic acid sequences is present. Tissues or cells corresponding to the numbers are provided in Table 2.

5 ORFX nucleic acids, and their encoded polypeptides, according to the invention are useful in a variety of applications and contexts. For example, various ORFX nucleic acids and polypeptides according to the invention are useful, *inter alia*, as novel members of the protein families indicated in Table 1, and/or according to the presence of domains and sequence relatedness to previously described proteins as summarized in Table 1.

10 ORFX nucleic acids and polypeptides according to the invention can also be used to identify cell types listed in Table 1 for an indicated ORFX according to the invention. Additional utilities for ORFX nucleic acids and polypeptides according to the invention are disclosed herein.

### ORFX Nucleic Acids

15 The novel nucleic acids of the invention include those that encode an ORFX or ORFX-like protein, or biologically active portions thereof. The nucleic acids include nucleic acids encoding polypeptides that include the amino acid sequence of one or more of SEQ ID NO:2*n*, wherein *n* = 1 to 3161. The encoded polypeptides can thus include, *e.g.*, the amino acid sequences of SEQ ID NO: 2, 4, 6, 8, 10, . . . , 6310, 6312, 6314, 6316, 6318, 6320, and/or 6322.

20 In some embodiments, a nucleic acid encoding a polypeptide having the amino acid sequence of one or more of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) includes the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof. Additionally, the invention includes mutant or variant nucleic acids of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof, any of whose bases may be changed from the disclosed sequence while still encoding a protein that maintains its ORFX-like activities and physiological functions. The invention further includes the complement of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), including fragments, derivatives,

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analogues and homolog thereof. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications.

Also included are nucleic acid fragments sufficient for use as hybridization probes to identify ORFX-encoding nucleic acids (*e.g.*, ORFX mRNA) and fragments for use as  
5 polymerase chain reaction (PCR) primers for the amplification or mutation of ORFX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is  
10 double-stranded DNA.

"Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, *e.g.*, 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually obtained from a natural or recombinant source, are highly specific and  
15 much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Examples of isolated nucleic  
20 acid molecules include, but are not limited to, recombinant DNA molecules contained in a vector, recombinant DNA molecules maintained in a heterologous host cell, partially or substantially purified nucleic acid molecules, and synthetic DNA or RNA molecules. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism  
25 from which the nucleic acid is derived. For example, in various embodiments, the isolated ORFX nucleic acid molecule can contain less than about 50 kb, 25 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular  
30 material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement of any of this nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n*=1 to 3161) as a hybridization probe, ORFX nucleic acid sequences can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, eds., MOLECULAR CLONING: A LABORATORY MANUAL 2<sup>nd</sup> Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to ORFX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement thereof. Oligonucleotides may be chemically synthesized and may be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion of this nucleotide sequence. A nucleic acid molecule that is complementary to the nucleotide sequence shown in

is one that is sufficiently complementary to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161),, thereby forming a stable duplex.

- 5           As used herein, the term “complementary” refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term “binding” means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, Von der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect.
- 10 Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

- Moreover, the nucleic acid molecule of the invention can comprise only a portion of the
- 15 nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), *e.g.*, a fragment that can be used as a probe or primer, or a fragment encoding a biologically active portion of ORFX. Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively,
- 20 and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but
- 25 differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type.

- Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or
- 30 analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the

invention, in various embodiments, by at least about 70%, 80%, 85%, 90%, 95%, 98%, or even 99% identity (with a preferred identity of 80-99%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below. An exemplary program is the Gap program (Wisconsin Sequence Analysis Package, Version 8 for UNIX, Genetics Computer Group, University Research Park, Madison, WI) using the default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2: 482-489, which is incorporated herein by reference in its entirety).

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of ORFX polypeptide. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for a ORFX polypeptide of species other than humans, including, but not limited to, mammals, and thus can include, *e.g.*, mouse, rat, rabbit, dog, cat cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human ORFX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) as well as a polypeptide having ORFX activity. Biological activities of the ORFX proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human ORFX polypeptide.

The nucleotide sequence determined from the cloning of the human ORFX gene allows for the generation of probes and primers designed for use in identifying the cell types disclosed and/or cloning ORFX homologues in other cell types, *e.g.*, from other tissues, as well as ORFX homologues from other mammals. The probe/primer typically comprises a substantially purified



oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 or more consecutive sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or an anti-sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161);  
5 or of a naturally occurring mutant of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

Probes based on the human ORFX nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.*, the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be  
10 used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a ORFX protein, such as by measuring a level of a ORFX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting ORFX mRNA levels or determining whether a genomic ORFX gene has been mutated or deleted.

"A polypeptide having a biologically active portion of ORFX" refers to polypeptides  
15 exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of ORFX" can be prepared by isolating a portion of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), that encodes a polypeptide having a ORFX biological activity (biological activities of the ORFX  
20 proteins are summarized in Table 1), expressing the encoded portion of ORFX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of ORFX. For example, a nucleic acid fragment encoding a biologically active portion of ORFX can optionally include a domain as shown in Table 1, column 4.

## 25 ORFX variants

The invention further encompasses nucleic acid molecules that differ from the disclosed ORFX nucleotide sequences due to degeneracy of the genetic code. These nucleic acids thus encode the same ORFX protein as that encoded by the nucleotide sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of  
30 the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

In addition to the human ORFX nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of ORFX may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the ORFX gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a ORFX protein, preferably a mammalian ORFX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the ORFX gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in ORFX that are the result of natural allelic variation and that do not alter the functional activity of ORFX are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding ORFX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the ORFX cDNAs of the invention can be isolated based on their homology to the human ORFX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500 or 750 nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding ORFX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. The  $T_m$  is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at  $T_m$ , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (*e.g.*, 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions is hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C. This hybridization is followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of any of SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161) corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161), or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are

hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well known in the art. See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981, *Proc Natl Acad Sci USA* 78: 6789-6792.

#### Conservative mutations

In addition to naturally-occurring allelic variants of the ORFX sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), thereby leading to changes in the amino acid sequence of the encoded ORFX protein, without altering the functional ability of the ORFX protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of ORFX without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are conserved among the ORFX proteins of the present invention, are predicted to be particularly unamenable to alteration.

Amino acid residues that are conserved among members of an ORFX family members are predicted to be less amenable to alteration. For example, an ORFX protein according to the present invention can contain at least one domain (*e.g.*, as shown in Table 1) that is a typically conserved region in an ORFX family member. As such, these conserved domains are not likely to be amenable to mutation. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved among members of the ORFX family) may not be as essential for activity and thus are more likely to be amenable to alteration.

Another aspect of the invention pertains to nucleic acid molecules encoding ORFX proteins that contain changes in amino acid residues that are not essential for activity. Such ORFX proteins differ in amino acid sequence from any of any of SEQ ID NO:2 $n$  (wherein  $n = 1$  to 3161), yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 75% homologous to the amino acid sequence of any of SEQ ID NO:2 $n$  (wherein  $n = 1$  to 3161). Preferably, the protein encoded by the nucleic acid is at least about 80% homologous to any of SEQ ID NO:2 $n$  (wherein  $n = 1$  to 3161), more preferably at least about 90%, 95%, 98%, and most preferably at least about 99% homologous to SEQ ID NO:2.

An isolated nucleic acid molecule encoding a ORFX protein homologous to the protein of any of SEQ ID NO:2 $n$  (wherein  $n = 1$  to 3161) can be created by introducing one or more nucleotide substitutions, additions or deletions into the corresponding nucleotide sequence, *i.e.* SEQ ID NO:2 $n$ -1 for the corresponding  $n$ , such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161) by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline,

phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in ORFX is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a ORFX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ORFX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

In one embodiment, a mutant ORFX protein can be assayed for (1) the ability to form protein:protein interactions with other ORFX proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant ORFX protein and a ORFX receptor; (3) the ability of a mutant ORFX protein to bind to an intracellular target protein or biologically active portion thereof; (*e.g.*, avidin proteins); (4) the ability to bind BRA protein; or (5) the ability to specifically bind an anti-ORFX protein antibody.

#### Antisense

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire ORFX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a ORFX protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) or antisense nucleic acids complementary to a ORFX nucleic acid sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid

residues (*e.g.*, the protein coding region of a human ORFX that corresponds to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161)). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding ORFX disclosed herein (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of ORFX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ORFX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ORFX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil,

3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a ORFX protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-O-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

#### **Ribozymes and PNA moieties**

Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are



carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme.

- 5 Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave ORFX mRNA transcripts to thereby inhibit translation of ORFX mRNA. A ribozyme having specificity for a ORFX-encoding
- 10 nucleic acid can be designed based upon the nucleotide sequence of a ORFX DNA disclosed herein (*i.e.*, SEQ ID NO:2*n*-1 (wherein  $n = 1$  to 3161)). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a ORFX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742.
- 15 Alternatively, ORFX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

- Alternatively, ORFX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the ORFX (*e.g.*, the ORFX promoter and/or
- 20 enhancers) to form triple helical structures that prevent transcription of the ORFX gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

- In various embodiments, the nucleic acids of ORFX can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of
- 25 the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has
- 30 been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide

synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of ORFX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of ORFX can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of ORFX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of ORFX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or

the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

### ORFX polypeptides

The novel protein of the invention includes the ORFX-like protein whose sequence is provided in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in FIG. 1 while still encoding a protein that maintains its ORFX-like activities and physiological functions, or a functional fragment thereof. For example, the invention includes the polypeptides encoded by the variant ORFX nucleic acids described above. In the mutant or variant protein, up to 20% or more of the residues may be so changed.

In general, an ORFX -like variant that preserves ORFX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above. Furthermore, without limiting the scope of the invention, positions of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) may be substituted such that a mutant or variant protein may include one or more substitutions

The invention also includes isolated ORFX proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-ORFX antibodies. In one embodiment, native ORFX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, ORFX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a ORFX

protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the ORFX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ORFX protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of ORFX protein having less than about 30% (by dry weight) of non-ORFX protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-ORFX protein, still more preferably less than about 10% of non-ORFX protein, and most preferably less than about 5% non-ORFX protein. When the ORFX protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein having less than about 30% (by dry weight) of chemical precursors or non-ORFX chemicals, more preferably less than about 20% chemical precursors or non-ORFX chemicals, still more preferably less than about 10% chemical precursors or non-ORFX chemicals, and most preferably less than about 5% chemical precursors or non-ORFX chemicals.

Biologically active portions of a ORFX protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the ORFX protein, *e.g.*, the amino acid sequence shown in SEQ ID NO:2 that include fewer amino acids than the full length ORFX proteins, and exhibit at least one activity of a ORFX protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the ORFX protein. A biologically active portion of a ORFX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

A biologically active portion of a ORFX protein of the present invention may contain at least one of the above-identified domains conserved between the FGF family of proteins. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native ORFX protein.

In an embodiment, the ORFX protein has an amino acid sequence shown in any of SEQ ID NO:2n (wherein n = 1 to 3161). In other embodiments, the ORFX protein is substantially homologous to any of SEQ ID NO:2n (wherein n = 1 to 3161) and retains the functional activity of the protein of any of SEQ ID NO:2n (wherein n = 1 to 3161), yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below.

Accordingly, in another embodiment, the ORFX protein is a protein that comprises an amino acid sequence at least about 45% homologous, and more preferably about 55, 65, 70, 75, 80, 85, 90, 95, 98 or even 99% homologous to the amino acid sequence of any of SEQ ID NO:2n (wherein n = 1 to 3161) and retains the functional activity of the ORFX proteins of the corresponding polypeptide having the sequence of SEQ ID NO:2n (wherein n = 1 to 3161).

#### **Determining homology between two or more sequences**

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in either of the sequences being compared for optimal alignment between the sequences). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, *Needleman and Wunsch 1970 J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a

degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region. The term "percentage of positive residues" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical and conservative amino acid substitutions, as defined above, occur in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of positive residues.

#### **Chimeric and fusion proteins**

The invention also provides ORFX chimeric or fusion proteins. As used herein, a ORFX "chimeric protein" or "fusion protein" includes a ORFX polypeptide operatively linked to a non-ORFX polypeptide. A "ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to ORFX, whereas a "non-ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the ORFX protein, *e.g.*, a protein that is different from the ORFX protein and that is derived from the same or a different organism. Within a ORFX fusion protein the ORFX polypeptide can correspond to all or a portion of a ORFX protein. In one embodiment, a ORFX fusion protein comprises at least one biologically active portion of a ORFX protein. In another embodiment, a ORFX fusion protein comprises at least two biologically active portions of a

ORFX protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the ORFX polypeptide and the non-ORFX polypeptide are fused in-frame to each other. The non-ORFX polypeptide can be fused to the N-terminus or C-terminus of the ORFX polypeptide.

5           For example, in one embodiment a ORFX fusion protein comprises a ORFX polypeptide operably linked to the extracellular domain of a second protein. Such fusion proteins can be further utilized in screening assays for compounds that modulate ORFX activity (such assays are described in detail below).

10           In another embodiment, the fusion protein is a GST-ORFX fusion protein in which the ORFX sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant ORFX.

15           In yet another embodiment, the fusion protein is a ORFX protein containing a heterologous signal sequence at its N-terminus. For example, the native ORFX signal sequence can be removed and replaced with a signal sequence from another protein. In certain host cells (e.g., mammalian host cells), expression and/or secretion of ORFX can be increased through use of a heterologous signal sequence.

20           In another embodiment, the fusion protein is a ORFX-immunoglobulin fusion protein in which the ORFX sequences comprising one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The ORFX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ORFX ligand and a ORFX protein on the surface of a cell, to thereby suppress ORFX-mediated signal transduction *in vivo*. In one nonlimiting example, a contemplated ORFX ligand of the invention is an ORFX receptor. The ORFX-immunoglobulin fusion proteins can be used to modulate the bioavailability of a ORFX cognate ligand. Inhibition of the ORFX ligand/ORFX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the ORFX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-ORFX antibodies in a subject, to purify ORFX ligands, and in screening assays to identify molecules that inhibit the interaction of  
30   ORFX with a ORFX ligand.

A ORFX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A ORFX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ORFX protein.

#### **ORFX agonists and antagonists**

The present invention also pertains to variants of the ORFX proteins that function as either ORFX agonists (mimetics) or as ORFX antagonists. Variants of the ORFX protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the ORFX protein. An agonist of the ORFX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the ORFX protein. An antagonist of the ORFX protein can inhibit one or more of the activities of the naturally occurring form of the ORFX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the ORFX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the ORFX proteins.

Variants of the ORFX protein that function as either ORFX agonists (mimetics) or as ORFX antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the ORFX protein for ORFX protein agonist or antagonist activity. In one



embodiment, a variegated library of ORFX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ORFX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential ORFX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of ORFX sequences therein. There are a variety of methods which can be used to produce libraries of potential ORFX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ORFX sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu Rev Biochem* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucl Acid Res* 11:477).

#### Polypeptide libraries

In addition, libraries of fragments of the ORFX protein coding sequence can be used to generate a variegated population of ORFX fragments for screening and subsequent selection of variants of a ORFX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a ORFX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the ORFX protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ORFX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,

transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify ORFX variants (Arkin and Yourvan (1992) PNAS 89:7811-7815; Delgrave *et al.* (1993) Protein Engineering 6:327-331).

### Anti-ORFX Antibodies

The invention further encompasses antibodies and antibody fragments, such as  $F_{ab}$  or  $(F_{ab})_2$ , that bind immunospecifically to any of the proteins of the invention.

An isolated ORFX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind ORFX using standard techniques for polyclonal and monoclonal antibody preparation. Full-length ORFX protein can be used. Alternatively, the invention provides antigenic peptide fragments of ORFX for use as immunogens. The antigenic peptide of ORFX comprises at least 4 amino acid residues of the amino acid sequence shown in any of SEQ ID NO:2*n* (wherein  $n = 1$  to 3161). The antigenic peptide encompasses an epitope of ORFX such that an antibody raised against the peptide forms a specific immune complex with ORFX. The antigenic peptide may comprise at least 6 aa residues, at least 8 aa residues, at least 10 aa residues, at least 15 aa residues, at least 20 aa residues, or at least 30 aa residues. In one embodiment of the invention, the antigenic peptide comprises a polypeptide comprising at least 6 contiguous amino acids of any of SEQ ID NO:2*n* (wherein  $n = 1$  to 3161).

In an embodiment of the invention, epitopes encompassed by the antigenic peptide are regions of ORFX that are located on the surface of the protein, *e.g.*, hydrophilic regions. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each incorporated herein by reference in their entirety.

As disclosed herein, an ORFX protein sequence of any of SEQ ID NO:2*n* (wherein  $n = 1$  to 3161), or derivatives, fragments, analogs or homologs thereof, may be utilized as immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and

immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as ORFX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain,  $F_{ab}$  and  $F_{(ab)_2}$  fragments, and an  $F_{ab}$  expression library. In a specific embodiment, antibodies to human ORFX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to a ORFX protein sequence of any of SEQ ID NO:2n (wherein  $n = 1$  to 3161) or derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed ORFX protein or a chemically synthesized ORFX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against ORFX can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of ORFX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular ORFX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular ORFX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND

CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND  
 5 CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations are incorporated herein by reference in their entirety

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a ORFX protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F<sub>ab</sub> expression libraries (see *e.g.*, Huse, *et al.*,  
 10 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F<sub>ab</sub> fragments with the desired specificity for a ORFX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Each of the above citations are incorporated herein by reference. Antibody fragments that contain the idiotypes to a ORFX protein may be produced by  
 15 techniques known in the art including, but not limited to: (i) an F<sub>(ab)<sup>2</sup></sub> fragment produced by pepsin digestion of an antibody molecule; (ii) an F<sub>ab</sub> fragment generated by reducing the disulfide bridges of an F<sub>(ab)<sup>2</sup></sub> fragment; (iii) an F<sub>ab</sub> fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F<sub>v</sub> fragments.

Additionally, recombinant anti-ORFX antibodies, such as chimeric and humanized  
 20 monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent  
 25 Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988), *J.*  
 30 *Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525;

Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060. Each of the above citations are incorporated herein by reference.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of a ORFX protein is facilitated by generation of hybridomas that bind to the fragment of a ORFX protein possessing such a domain. Antibodies that are specific for one or more domains within a ORFX protein, *e.g.*, the domain spanning the first fifty amino-terminal residues specific to ORFX when compared to FGF-9, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-ORFX antibodies may be used in methods known within the art relating to the localization and/or quantitation of a ORFX protein (*e.g.*, for use in measuring levels of the ORFX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for ORFX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds [hereinafter "Therapeutics"].

An anti-ORFX antibody (*e.g.*, monoclonal antibody) can be used to isolate ORFX by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-ORFX antibody can facilitate the purification of natural ORFX from cells and of recombinantly produced ORFX expressed in host cells. Moreover, an anti-ORFX antibody can be used to detect ORFX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the ORFX protein. Anti-ORFX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase,  $\beta$ -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or

phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .

### ORFX Recombinant Vectors and Host Cells

5 Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding ORFX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can  
10 be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are  
15 replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the  
20 invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the  
25 recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation  
30 system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements

(*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, ORFX proteins, mutant forms of ORFX, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of ORFX in prokaryotic or eukaryotic cells. For example, ORFX can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (1) to increase expression of recombinant protein; (2) to increase the solubility of the recombinant protein; and (3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

5 One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons  
10 for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the ORFX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*,  
15 (1987) *EMBO J* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (Invitrogen Corp, San Diego, Calif.).

Alternatively, ORFX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*,  
20 SF9 cells) include the pAc series (Smith *et al.* (1983) *Mol Cell Biol* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J*  
25 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells. See, *e.g.*, Chapters 16 and 17 of Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory,  
30 Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.



In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv Immunol* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the  $\alpha$ -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to ORFX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, "Antisense RNA as a molecular tool for genetic analysis," Reviews--Trends in Genetics, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant

host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, ORFX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding ORFX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) ORFX protein. Accordingly, the invention further provides methods for producing ORFX protein using the host cells of the invention. In one embodiment,

the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding ORFX has been introduced) in a suitable medium such that ORFX protein is produced. In another embodiment, the method further comprises isolating ORFX from the medium or the host cell.

## 5 Transgenic animals

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which ORFX-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous ORFX sequences  
10 have been introduced into their genome or homologous recombinant animals in which endogenous ORFX sequences have been altered. Such animals are useful for studying the function and/or activity of ORFX and for identifying and/or evaluating modulators of ORFX activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal  
15 includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous  
20 recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous ORFX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing ORFX-encoding  
25 nucleic acid into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The human ORFX DNA sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human ORFX gene, such as a mouse ORFX gene, can be isolated based on hybridization to  
30 the human ORFX cDNA (described further above) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of

expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the ORFX transgene to direct expression of ORFX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan 1986, In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the ORFX transgene in its genome and/or expression of ORFX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding ORFX can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a ORFX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the ORFX gene. The ORFX gene can be a human gene (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), but more preferably, is a non-human homologue of a human ORFX gene. For example, a mouse homologue of human ORFX gene of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be used to construct a homologous recombination vector suitable for altering an endogenous ORFX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous ORFX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ORFX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous ORFX protein). In the homologous recombination vector, the altered portion of the ORFX gene is flanked at its 5' and 3' ends by additional nucleic acid of the ORFX gene to allow for homologous recombination to occur between the exogenous ORFX gene carried by the vector and an endogenous ORFX gene in an embryonic stem cell. The additional flanking ORFX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See *e.g.*, Thomas *et al.* (1987) *Cell* 51:503 for a description of

homologous recombination vectors. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced ORFX gene has homologously recombined with the endogenous ORFX gene are selected (see e.g., Li *et al.* (1992) *Cell* 69:915).

The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. See e.g., Bradley 1987, In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Curr Opin Biotechnol* 2:823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, see, e.g., Lakso *et al.* (1992) *PNAS* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.* (1991) *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G<sub>0</sub> phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of

this female foster animal will be a clone of the animal from which the cell, *e.g.*, the somatic cell, is isolated.

### Pharmaceutical Compositions

The ORFX nucleic acid molecules, ORFX proteins, and anti-ORFX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a ORFX protein or anti-ORFX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use

as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder  
5 such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

10 For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated  
15 are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

20 The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible  
25 polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as  
30 pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811.



It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by any of a number of routes, *e.g.*, as described in U.S. Patent Nos. 5,703,055. Delivery can thus also include, *e.g.*, intravenous injection, local administration (see U.S. Pat. No. 5,328,470) or stereotactic injection (see *e.g.*, Chen *et al.* (1994) *PNAS* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

#### **Additional Uses and Methods of the Invention**

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: (a) screening assays; (b) detection assays (*e.g.*, chromosomal mapping, cell and tissue typing, forensic biology), (c) predictive medicine (*e.g.*, diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics); and (d) methods of treatment (*e.g.*, therapeutic and prophylactic).

The isolated nucleic acid molecules of the invention can be used to express ORFX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect ORFX mRNA (*e.g.*, in a biological sample) or a genetic lesion in a ORFX gene, and to modulate ORFX activity, as described further below. In addition, the ORFX proteins can be used to screen drugs or compounds that modulate the ORFX activity or expression as well as to treat disorders characterized by insufficient or excessive production of ORFX protein, for

example proliferative or differentiative disorders, or production of ORFX protein forms that have decreased or aberrant activity compared to ORFX wild type protein. In addition, the anti-ORFX antibodies of the invention can be used to detect and isolate ORFX proteins and modulate ORFX activity.

5           This invention further pertains to novel agents identified by the above described screening assays and uses thereof for treatments as described herein.

### Screening Assays

          The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides,  
10   peptidomimetics, small molecules or other drugs) that bind to ORFX proteins or have a stimulatory or inhibitory effect on, for example, ORFX expression or ORFX activity.

          In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a ORFX protein or polypeptide or biologically active portion thereof. The test compounds of the present invention can be obtained  
15   using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are  
20   applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des* 12:145).

          Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc Natl Acad Sci U.S.A.* 90:6909; Erb *et al.* (1994) *Proc Natl Acad Sci U.S.A.* 91:11422; Zuckermann *et al.* (1994) *J Med Chem* 37:2678; Cho *et al.* (1993)  
25   *Science* 261:1303; Carrell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2059; Carell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2061; and Gallop *et al.* (1994) *J Med Chem* 37:1233.

          Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), on chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner U.S. Pat. No. 5,223,409), spores (Ladner USP '409),  
30   plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and

Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirlla *et al.* (1990) *Proc Natl Acad Sci U.S.A.* 87:6378-6382; Felici (1991) *J Mol Biol* 222:301-310; Ladner above.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to a ORFX protein determined. The cell, for example, can of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the ORFX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the ORFX protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with  $^{125}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ , or  $^3\text{H}$ , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or a biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX or a biologically active portion thereof can be accomplished, for example, by determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule. As used herein, a "target molecule" is a molecule with which a ORFX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses a ORFX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule

associated with the internal surface of a cell membrane or a cytoplasmic molecule. A ORFX target molecule can be a non-ORFX molecule or a ORFX protein or polypeptide of the present invention. In one embodiment, a ORFX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.*, a signal generated by binding of a compound to a membrane-bound ORFX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with ORFX.

Determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular  $\text{Ca}^{2+}$ , diacylglycerol,  $\text{IP}_3$ , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising a ORFX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting a ORFX protein or biologically active portion thereof with a test compound and determining the ability of the test compound to bind to the ORFX protein or biologically active portion thereof. Binding of the test compound to the ORFX protein can be determined either directly or indirectly as described above. In one embodiment, the assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting ORFX protein or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or

biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX can be accomplished, for example, by determining the ability of the ORFX protein to bind to a ORFX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of ORFX can be accomplished by determining the ability of the ORFX protein further modulate a ORFX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the ORFX protein to preferentially bind to or modulate the activity of a ORFX target molecule.

The cell-free assays of the present invention are amenable to use of both the soluble form or the membrane-bound form of ORFX. In the case of cell-free assays comprising the membrane-bound form of ORFX, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of ORFX is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton<sup>®</sup> X-100, Triton<sup>®</sup> X-114, Thesit<sup>®</sup>, Isotridecypoly(ethylene glycol ether)<sub>n</sub>, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl)dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either ORFX or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to ORFX, or interaction of ORFX with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For

example, GST-ORFX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or ORFX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of ORFX binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either ORFX or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated ORFX or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with ORFX or target molecules, but which do not interfere with binding of the ORFX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or ORFX trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the ORFX or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the ORFX or target molecule.

In another embodiment, modulators of ORFX expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of ORFX mRNA or protein in the cell is determined. The level of expression of ORFX mRNA or protein in the presence of the candidate compound is compared to the level of expression of ORFX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of ORFX expression based on this comparison. For example, when expression of ORFX mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of ORFX mRNA or protein expression. Alternatively, when expression of ORFX mRNA or protein is less (statistically significantly less) in the presence of the candidate

compound than in its absence, the candidate compound is identified as an inhibitor of ORFX mRNA or protein expression. The level of ORFX mRNA or protein expression in the cells can be determined by methods described herein for detecting ORFX mRNA or protein.

In yet another aspect of the invention, the ORFX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, *e.g.*, U.S. Pat. No. 5,283,317; Zervos *et al.* (1993) *Cell* 72:223-232; Madura *et al.* (1993) *J Biol Chem* 268:12046-12054; Bartel *et al.* (1993) *Biotechniques* 14:920-924; Iwabuchi *et al.* (1993) *Oncogene* 8:1693-1696; and Brent WO94/10300), to identify other proteins that bind to or interact with ORFX ("ORFX-binding proteins" or "ORFX-bp") and modulate ORFX activity. Such ORFX-binding proteins are also likely to be involved in the propagation of signals by the ORFX proteins as, for example, upstream or downstream elements of the ORFX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for ORFX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a ORFX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with ORFX.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

#### Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a

minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample.

The ORFX sequences of the present invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Pat. No. 5,272,057).

Furthermore, the sequences of the present invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the ORFX sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The ORFX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), as described above, can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences are used, a more appropriate number of primers for positive individual identification would be 500-2,000.



### **Predictive Medicine**

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (e.g., blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (e.g., drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (e.g., the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (e.g., drugs, compounds) on the expression or activity of ORFX in clinical trials.

### **Use of Partial ORFX Sequences in Forensic Biology**

DNA-based identification techniques can also be used in forensic biology. Forensic biology is a scientific field employing genetic typing of biological evidence found at a crime scene as a means for positively identifying, for example, a perpetrator of a crime. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, or semen

found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide polynucleotide reagents, *e.g.*, PCR primers, targeted to specific loci in the human genome, that can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (*i.e.* another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NOs:\_\_\_ are particularly appropriate for this use as greater numbers of polymorphisms occur in the noncoding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the ORFX sequences or portions thereof, *e.g.*, fragments derived from the noncoding regions of one or more of SEQ ID NO:2*n*-1 (where *n* = 1 to 3161), having a length of at least 20 bases, preferably at least 30 bases.

The ORFX sequences described herein can further be used to provide polynucleotide reagents, *e.g.*, labeled or label-able probes that can be used, for example, in an *in situ* hybridization technique, to identify a specific tissue, *e.g.*, brain tissue, etc. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such ORFX probes can be used to identify tissue by species and/or by organ type.

In a similar fashion, these reagents, *e.g.*, ORFX primers or probes can be used to screen tissue culture for contamination (*i.e.* screen for the presence of a mixture of different types of cells in a culture).

### Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic

acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

5 Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

10 Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

These and other agents are described in further detail in the following sections.

#### **Diagnostic Assays**

15 Other conditions in which proliferation of cells plays a role include tumors, restenosis, psoriasis, Dupuytren's contracture, diabetic complications, Kaposi's sarcoma and rheumatoid arthritis.

An ORFX polypeptide may be used to identify an interacting polypeptide a sample or tissue. The method comprises contacting the sample or tissue with ORFX, allowing formation of a complex between the ORFX polypeptide and the interacting polypeptide, and detecting the complex, if present.

20 The proteins of the invention may be used to stimulate production of antibodies specifically binding the proteins. Such antibodies may be used in immunodiagnostic procedures to detect the occurrence of the protein in a sample. The proteins of the invention may be used to stimulate cell growth and cell proliferation in conditions in which such growth would be favorable. An example would be to counteract toxic side effects of chemotherapeutic agents on, for example, hematopoiesis and platelet formation, linings of the gastrointestinal tract, and hair follicles. They may also be used to stimulate new cell growth in neurological disorders including, for example, Alzheimer's disease. Alternatively, antagonistic treatments may be administered in which an antibody specifically binding the ORFX-like proteins of the invention

would abrogate the specific growth-inducing effects of the proteins. Such antibodies may be useful, for example, in the treatment of proliferative disorders including various tumors and benign hyperplasias.

Polynucleotides or oligonucleotides corresponding to any one portion of the ORFX  
5 nucleic acids of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) may be used to detect DNA containing a corresponding ORF gene, or detect the expression of a corresponding ORFX gene, or ORFX-like gene. For example, an ORFX nucleic acid expressed in a particular cell or tissue, as noted in Table 2, can be used to identify the presence of that particular cell type.

An exemplary method for detecting the presence or absence of ORFX in a biological  
10 sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes ORFX protein such that the presence of ORFX is detected in the biological sample. An agent for detecting ORFX mRNA or genomic DNA is a labeled  
15 nucleic acid probe capable of hybridizing to ORFX mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length ORFX nucleic acid, such as the nucleic acid of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to ORFX mRNA or genomic DNA, as described above. Other suitable probes for use in the diagnostic assays of the invention are described herein.

20 An agent for detecting ORFX protein is an antibody capable of binding to ORFX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')<sub>2</sub>) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or  
25 antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as  
30 tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect ORFX mRNA, protein, or genomic DNA in a biological sample *in vitro* as

well as *in vivo*. For example, *in vitro* techniques for detection of ORFX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of ORFX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of ORFX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of ORFX protein include introducing into a subject a labeled anti-ORFX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting ORFX protein, mRNA, or genomic DNA, such that the presence of ORFX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of ORFX protein, mRNA or genomic DNA in the control sample with the presence of ORFX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of ORFX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting ORFX protein or mRNA in a biological sample; means for determining the amount of ORFX in the sample; and means for comparing the amount of ORFX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect ORFX protein or nucleic acid.

### Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity in, *e.g.*, proliferative or differentiative disorders such as hyperplasias, tumors, restenosis, psoriasis, Dupuytren's

contracture, diabetic complications, or rheumatoid arthritis, etc.; and glia-associated disorders such as cerebral lesions, diabetic neuropathies, cerebral edema, senile dementia, Alzheimer's disease, etc. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the present invention provides a method for  
5 identifying a disease or disorder associated with aberrant ORFX expression or activity in which a test sample is obtained from a subject and ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. As used herein, a "test sample" refers to a biological sample obtained  
10 from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder  
15 associated with aberrant ORFX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder, such as a proliferative disorder, differentiative disorder, glia-associated disorders, etc. Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant ORFX expression or activity in which a test sample  
20 is obtained and ORFX protein or nucleic acid is detected (*e.g.*, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant ORFX expression or activity.)

The methods of the invention can also be used to detect genetic lesions in a ORFX gene, thereby determining if a subject with the lesioned gene is at risk for, or suffers from, a  
25 proliferative disorder, differentiative disorder, glia-associated disorder, etc. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding a ORFX-protein, or the mis-expression of the ORFX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of (1) a deletion  
30 of one or more nucleotides from a ORFX gene; (2) an addition of one or more nucleotides to a ORFX gene; (3) a substitution of one or more nucleotides of a ORFX gene, (4) a chromosomal

rearrangement of a ORFX gene; (5) an alteration in the level of a messenger RNA transcript of a ORFX gene, (6) aberrant modification of a ORFX gene, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a ORFX gene, (8) a non-wild type level of a ORFX-protein, (9) allelic loss of a ORFX gene, and (10) inappropriate post-translational modification of a ORFX-protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in a ORFX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, e.g., U.S. Pat. Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, e.g., Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the ORFX-gene (see Abravaya *et al.* (1995) *Nucl Acids Res* 23:675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (e.g., genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to a ORFX gene under conditions such that hybridization and amplification of the ORFX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990, *Proc Natl Acad Sci USA* 87:1874-1878), transcriptional amplification system (Kwoh, *et al.*, 1989, *Proc Natl Acad Sci USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *BioTechnology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in a ORFX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared.

5 Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Pat. No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

10 In other embodiments, genetic mutations in ORFX can be identified by hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin *et al.* (1996) *Human Mutation* 7: 244-255; Kozal *et al.* (1996) *Nature Medicine* 2: 753-759). For example, genetic mutations in ORFX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.* above. Briefly, a first hybridization array of probes can be used to scan through  
15 long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one  
20 complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the ORFX gene and detect mutations by comparing the sequence of the sample ORFX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert (1977) *PNAS*  
25 74:560 or Sanger (1977) *PNAS* 74:5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Naeve *et al.*, (1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, *e.g.*, PCT International Publ. No. WO 94/16101; Cohen *et al.* (1996) *Adv Chromatogr* 36:127-162; and Griffin *et al.* (1993) *Appl Biochem Biotechnol* 38:147-159).

30 Other methods for detecting mutations in the ORFX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA



heteroduplexes (Myers *et al.* (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type ORFX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton *et al* (1988) *Proc Natl Acad Sci USA* 85:4397; Saleeba *et al* (1992) *Methods Enzymol* 217:286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in ORFX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a ORFX sequence, *e.g.*, a wild-type ORFX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Pat. No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in ORFX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.* (1989) *Proc Natl Acad Sci USA*: 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments of sample and control ORFX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting

alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA, rather than DNA, in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. See, e.g., Keen *et al.* (1991) *Trends Genet* 7:5.

In yet another embodiment the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). See, e.g., Myers *et al.* (1985) *Nature* 313:495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. See, e.g., Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. See, e.g., Saiki *et al.* (1986) *Nature* 324:163; Saiki *et al.* (1989) *Proc Natl Acad. Sci USA* 86:6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs *et al.* (1989) *Nucleic Acids Res* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. See, e.g., Gasparini *et al.* (1992) *Mol Cell Probes* 6:1. It is anticipated that in certain embodiments amplification may also be performed using Taq ligase

for amplification. See, *e.g.*, Barany (1991) *Proc Natl Acad Sci USA* 88:189. In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

5       The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a ORFX gene.

10       Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which ORFX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

#### **Pharmacogenomics**

15       Agents, or modulators that have a stimulatory or inhibitory effect on ORFX activity (*e.g.*, ORFX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (*e.g.*, neurological, cancer-related or gestational disorders) associated with aberrant ORFX activity. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be  
20       considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate  
25       dosages and therapeutic regimens. Accordingly, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

30       Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996, *Clin Exp Pharmacol Physiol*, 23:983-985 and Linder, 1997, *Clin Chem*, 43:254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic

conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a ORFX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

### Monitoring Clinical Efficacy

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied in basic drug screening and in clinical trials. For example, the effectiveness of an agent  
5 determined by a screening assay as described herein to increase ORFX gene expression, protein levels, or upregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting decreased ORFX gene expression, protein levels, or downregulated ORFX activity.

Alternatively, the effectiveness of an agent determined by a screening assay to decrease ORFX gene expression, protein levels, or downregulate ORFX activity, can be monitored in clinical  
10 trials of subjects exhibiting increased ORFX gene expression, protein levels, or upregulated ORFX activity. In such clinical trials, the expression or activity of ORFX and, preferably, other genes that have been implicated in, for example, a proliferative or neurological disorder, can be used as a "read out" or marker of the responsiveness of a particular cell.

For example, genes, including ORFX, that are modulated in cells by treatment with an  
15 agent (*e.g.*, compound, drug or small molecule) that modulates ORFX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of ORFX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by  
20 Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of ORFX or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the  
25 agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, nucleic acid, peptidomimetic, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a  
30 subject prior to administration of the agent; (ii) detecting the level of expression of a ORFX protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more

post-administration samples from the subject; (iv) detecting the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the pre-administration sample with the ORFX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of ORFX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of ORFX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

#### Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant ORFX expression or activity.

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, (i) a ORFX polypeptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to a ORFX peptide; (iii) nucleic acids encoding a ORFX peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to a ORFX peptide) that are utilized to "knockout" endogenous function of a ORFX peptide by homologous recombination (see, *e.g.*, Capecchi, 1989, *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between a ORFX peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized

include, but are not limited to, a ORFX peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of a ORFX peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, etc.).

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant ORFX expression or activity, by administering to the subject an agent that modulates ORFX expression or at least one ORFX activity. Subjects at risk for a disease that is caused or contributed to by aberrant ORFX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the ORFX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of ORFX aberrancy, for example, a ORFX agonist or ORFX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

Another aspect of the invention pertains to methods of modulating ORFX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of ORFX protein activity associated with the cell. An agent that modulates ORFX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of a ORFX protein, a peptide, a ORFX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more ORFX protein activity. Examples of such stimulatory agents include active ORFX protein and a nucleic acid molecule encoding ORFX that has been introduced into the cell. In another embodiment, the agent inhibits one or more ORFX protein activity. Examples of such inhibitory agents include antisense ORFX nucleic acid molecules and anti-ORFX antibodies. These modulatory methods can be performed *in vitro*

(*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of a ORFX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, upregulates or downregulates) ORFX expression or activity. In another embodiment, the method involves administering a ORFX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant ORFX expression or activity.

### **Determination of the Biological Effect of a Therapeutic**

In various embodiments of the present invention, suitable *in vitro* or *in vivo* assays are utilized to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

### **Malignancies**

Some ORFX polypeptides are expressed in cancerous cells (*see, e.g.*, Tables 1 and 2). Accordingly, the corresponding ORF protein is involved in the regulation of cell proliferation. Accordingly, Therapeutics of the present invention may be useful in the therapeutic or prophylactic treatment of diseases or disorders that are associated with cell hyperproliferation and/or loss of control of cell proliferation (*e.g.*, cancers, malignancies and tumors). For a review of such hyperproliferation disorders, *see e.g.*, Fishman, *et al.*, 1985. MEDICINE, 2nd ed., J.B. Lippincott Co., Philadelphia, PA.

Therapeutics of the present invention may be assayed by any method known within the art for efficacy in treating or preventing malignancies and related disorders. Such assays include,



but are not limited to, *in vitro* assays utilizing transformed cells or cells derived from the patient's tumor, as well as *in vivo* assays using animal models of cancer or malignancies. Potentially effective Therapeutics are those that, for example, inhibit the proliferation of tumor-derived or transformed cells in culture or cause a regression of tumors in animal models, in comparison to the controls.

In the practice of the present invention, once a malignancy or cancer has been shown to be amenable to treatment by modulating (*i.e.*, inhibiting, antagonizing or agonizing) activity, that cancer or malignancy may subsequently be treated or prevented by the administration of a Therapeutic that serves to modulate protein function.

#### **Premalignant conditions**

The Therapeutics of the present invention that are effective in the therapeutic or prophylactic treatment of cancer or malignancies may also be administered for the treatment of pre-malignant conditions and/or to prevent the progression of a pre-malignancy to a neoplastic or malignant state. Such prophylactic or therapeutic use is indicated in conditions known or suspected of preceding progression to neoplasia or cancer, in particular, where non-neoplastic cell growth consisting of hyperplasia, metaplasia or, most particularly, dysplasia has occurred. For a review of such abnormal cell growth see *e.g.*, Robbins & Angell, 1976. BASIC PATHOLOGY, 2nd ed., W.B. Saunders Co., Philadelphia, PA.

Hyperplasia is a form of controlled cell proliferation involving an increase in cell number in a tissue or organ, without significant alteration in its structure or function. For example, it has been demonstrated that endometrial hyperplasia often precedes endometrial cancer. Metaplasia is a form of controlled cell growth in which one type of mature or fully differentiated cell substitutes for another type of mature cell. Metaplasia may occur in epithelial or connective tissue cells. Dysplasia is generally considered a precursor of cancer, and is found mainly in the epithelia. Dysplasia is the most disorderly form of non-neoplastic cell growth, and involves a loss in individual cell uniformity and in the architectural orientation of cells. Dysplasia characteristically occurs where there exists chronic irritation or inflammation, and is often found in the cervix, respiratory passages, oral cavity, and gall bladder.

Alternatively, or in addition to the presence of abnormal cell growth characterized as hyperplasia, metaplasia, or dysplasia, the presence of one or more characteristics of a transformed or malignant phenotype displayed either *in vivo* or *in vitro* within a cell sample derived from a patient, is indicative of the desirability of prophylactic/therapeutic administration of a Therapeutic that possesses the ability to modulate activity of An aforementioned protein. Characteristics of a transformed phenotype include, but are not limited to: (i) morphological changes; (ii) looser substratum attachment; (iii) loss of cell-to-cell contact inhibition; (iv) loss of anchorage dependence; (v) protease release; (vi) increased sugar transport; (vii) decreased serum requirement; (viii) expression of fetal antigens, (ix) disappearance of the 250 kDal cell-surface protein, and the like. See *e.g.*, Richards, *et al.*, 1986. MOLECULAR PATHOLOGY, W.B. Saunders Co., Philadelphia, PA.

In a specific embodiment of the present invention, a patient that exhibits one or more of the following predisposing factors for malignancy is treated by administration of an effective amount of a Therapeutic: (i) a chromosomal translocation associated with a malignancy (*e.g.*, the Philadelphia chromosome (*bcr/abl*) for chronic myelogenous leukemia and t(14;18) for follicular lymphoma, etc.); (ii) familial polyposis or Gardner's syndrome (possible forerunners of colon cancer); (iii) monoclonal gammopathy of undetermined significance (a possible precursor of multiple myeloma) and (iv) a first degree kinship with persons having a cancer or pre-cancerous disease showing a Mendelian (genetic) inheritance pattern (*e.g.*, familial polyposis of the colon, Gardner's syndrome, hereditary exostosis, polyendocrine adenomatosis, Peutz-Jeghers syndrome, neurofibromatosis of Von Recklinghausen, medullary thyroid carcinoma with amyloid production and pheochromocytoma, retinoblastoma, carotid body tumor, cutaneous melanocarcinoma, intraocular melanocarcinoma, xeroderma pigmentosum, ataxia telangiectasia, Chediak-Higashi syndrome, albinism, Fanconi's aplastic anemia and Bloom's syndrome).

In another embodiment, a Therapeutic of the present invention is administered to a human patient to prevent the progression to breast, colon, lung, pancreatic, or uterine cancer, or melanoma or sarcoma.

### Hyperproliferative and dysproliferative disorders

In one embodiment of the present invention, a Therapeutic is administered in the therapeutic or prophylactic treatment of hyperproliferative or benign dysproliferative disorders. The efficacy in treating or preventing hyperproliferative diseases or disorders of a Therapeutic of the present invention may be assayed by any method known within the art. Such assays include *in vitro* cell proliferation assays, *in vitro* or *in vivo* assays using animal models of hyperproliferative diseases or disorders, or the like. Potentially effective Therapeutics may, for example, promote cell proliferation in culture or cause growth or cell proliferation in animal models in comparison to controls.

Specific embodiments of the present invention are directed to the treatment or prevention of cirrhosis of the liver (a condition in which scarring has overtaken normal liver regeneration processes); treatment of keloid (hypertrophic scar) formation causing disfiguring of the skin in which the scarring process interferes with normal renewal; psoriasis (a common skin condition characterized by excessive proliferation of the skin and delay in proper cell fate determination); benign tumors; fibrocystic conditions and tissue hypertrophy (*e.g.*, benign prostatic hypertrophy).

### Neurodegenerative disorders

Some ORFX proteins are found in cell types have been implicated in the deregulation of cellular maturation and apoptosis, which are both characteristic of neurodegenerative disease. Accordingly, Therapeutics of the invention, particularly but not limited to those that modulate (or supply) activity of an aforementioned protein, may be effective in treating or preventing neurodegenerative disease. Therapeutics of the present invention that modulate the activity of an aforementioned protein involved in neurodegenerative disorders can be assayed by any method known in the art for efficacy in treating or preventing such neurodegenerative diseases and disorders. Such assays include *in vitro* assays for regulated cell maturation or inhibition of apoptosis or *in vivo* assays using animal models of neurodegenerative diseases or disorders, or any of the assays described below. Potentially effective Therapeutics, for example but not by way of limitation, promote regulated cell maturation and prevent cell apoptosis in culture, or reduce neurodegeneration in animal models in comparison to controls.

Once a neurodegenerative disease or disorder has been shown to be amenable to treatment by modulation activity, that neurodegenerative disease or disorder can be treated or prevented by administration of a Therapeutic that modulates activity. Such diseases include all degenerative disorders involved with aging, especially osteoarthritis and neurodegenerative disorders.

#### **Disorders related to organ transplantation**

Some ORFX can be associated with disorders related to organ transplantation, in particular but not limited to organ rejection. Therapeutics of the invention, particularly those that modulate (or supply) activity, may be effective in treating or preventing diseases or disorders related to organ transplantation. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity of an aforementioned protein) can be assayed by any method known in the art for efficacy in treating or preventing such diseases and disorders related to organ transplantation. Such assays include *in vitro* assays for using cell culture models as described below, or *in vivo* assays using animal models of diseases and disorders related to organ transplantation, see *e.g.*, below. Potentially effective Therapeutics, for example but not by way of limitation, reduce immune rejection responses in animal models in comparison to controls.

Accordingly, once diseases and disorders related to organ transplantation are shown to be amenable to treatment by modulation of activity, such diseases or disorders can be treated or prevented by administration of a Therapeutic that modulates activity.

#### **Cardiovascular Disease**

GENX has been implicated in cardiovascular disorders, including in atherosclerotic plaque formation. Diseases such as cardiovascular disease, including cerebral thrombosis or hemorrhage, ischemic heart or renal disease, peripheral vascular disease, or thrombosis of other major vessel, and other diseases, including diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage disease, systemic lupus erythematosus, homocysteinemia, and familial protein or lipid processing diseases, and the like, are either directly or indirectly associated with atherosclerosis. Accordingly, Therapeutics of the invention, particularly those that modulate (or supply) activity or formation may be effective in treating or preventing

atherosclerosis-associated diseases or disorders. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity) can be assayed by any method known in the art, including those described below, for efficacy in treating or preventing such diseases and disorders.

5           A vast array of animal and cell culture models exist for processes involved in atherosclerosis. A limited and non-exclusive list of animal models includes knockout mice for premature atherosclerosis (Kurabayashi and Yazaki, 1996, *Int. Angiol.* 15: 187-194), transgenic mouse models of atherosclerosis (Kappel *et al.*, 1994, *FASEB J.* 8: 583-592), antisense oligonucleotide treatment of animal models (Callow, 1995, *Curr. Opin. Cardiol.* 10: 569-576),  
10 transgenic rabbit models for atherosclerosis (Taylor, 1997, *Ann. N.Y. Acad. Sci.* 811: 146-152), hypercholesterolemic animal models (Rosenfeld, 1996, *Diabetes Res. Clin. Pract.* 30 Suppl.: 1-11), hyperlipidemic mice (Paigen *et al.*, 1994, *Curr. Opin. Lipidol.* 5: 258-264), and inhibition of lipoxygenase in animals (Sigal *et al.*, 1994, *Ann. N.Y. Acad. Sci.* 714: 211-224). In addition, *in vitro* cell models include but are not limited to monocytes exposed to low density lipoprotein  
15 (Frostegard *et al.*, 1996, *Atherosclerosis* 121: 93-103), cloned vascular smooth muscle cells (Suttles *et al.*, 1995, *Exp. Cell Res.* 218: 331-338), endothelial cell-derived chemoattractant exposed T cells (Katz *et al.*, 1994, *J. Leukoc. Biol.* 55: 567-573), cultured human aortic endothelial cells (Farber *et al.*, 1992, *Am. J. Physiol.* 262: H1088-1085), and foam cell cultures (Libby *et al.*, 1996, *Curr Opin Lipidol* 7: 330-335). Potentially effective Therapeutics, for  
20 example but not by way of limitation, reduce foam cell formation in cell culture models, or reduce atherosclerotic plaque formation in hypercholesterolemic mouse models of atherosclerosis in comparison to controls.

Accordingly, once an atherosclerosis-associated disease or disorder has been shown to be amenable to treatment by modulation of activity or formation, that disease or disorder can be  
25 treated or prevented by administration of a Therapeutic that modulates activity.

#### **Cytokine and Cell Proliferation/Differentiation Activity**

A GENX protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered

to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D,  
5 DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+ ), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-cell or thymocyte proliferation include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan *et al.*, Greene Publishing  
10 Associates and Wiley-Interscience (Chapter 3 and Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bertagnoli *et al.*, *J Immunol* 145:1706-1712, 1990; Bertagnoli *et al.*, *Cell Immunol* 133:327-341, 1991; Bertagnoli, *et al.*, *J Immunol* 149:3778-3783, 1992; Bowman *et al.*, *J Immunol* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or  
15 thymocytes include, without limitation, those described by Kruisbeek and Shevach, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1, pp. 3.12.1-14, John Wiley and Sons, Toronto 1994; and by Schreiber, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan eds. Vol 1 pp. 6.8.1-8, John Wiley and Sons, Toronto 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells  
20 include, without limitation, those described by Bottomly *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto 1991; deVries *et al.*, *J Exp Med* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 336:690-692, 1988; Greenberger *et al.*, *Proc Natl Acad Sci U.S.A.* 80:2931-2938, 1983; Nordan, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.6.1-5, John Wiley and Sons,  
25 Toronto 1991; Smith *et al.*, *Proc Natl Acad Sci U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, *et al.* In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto 1991; Ciarletta, *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto 1991.

30 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and

cytokine production) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds., Greene Publishing Associates and Wiley-Interscience (Chapter 3Chapter 6, Chapter 7); Weinberger *et al.*, *Proc Natl Acad Sci USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur J Immun* 11:405-411, 1981; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988.

### Immune Stimulating or Suppressing Activity

A GENX protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by vital (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by vital, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* species., malaria species. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response.

The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or energy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon re-exposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to energize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the



immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc Natl Acad Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and auto-antibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of auto-antibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the

patient. Another method of enhancing anti-vital immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells.

In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor

specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without  
5 limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981;  
10 Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bowman *et al.*, *J Virology* 61:1992-1998; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Brown *et al.*, *J Immunol* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which  
15 will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J Immunol* 144:3028-3033, 1990; and Mond and Brunswick In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, (eds.) Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins  
20 that generate predominantly Th1 and CTL responses) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *J Immunol* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by  
25 dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery *et al.*, *J Immunol* 134:536-544, 1995; Inaba *et al.*, *J Exp Med* 173:549-559, 1991; Macatonia *et al.*, *J Immunol* 154:5071-5079, 1995; Porgador *et al.*, *J Exp Med* 182:255-260, 1995; Nair *et al.*, *J Virol* 67:4062-4069, 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al.*, *J Exp Med* 169:1255-1264, 1989; Bhardwaj *et al.*, *J Clin Investig* 94:797-807, 1994; and Inaba *et al.*, *J Exp Med* 172:631-640, 1990.  
30

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J Immunol* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Internat J Oncol* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell Immunol* 155: 111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc Nat Acad Sci USA* 88:7548-7551, 1991.

#### **Hematopoiesis Regulating Activity**

A GENX protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.*, in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

5        Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson *et al.* *Cellular Biology* 15:141-151, 1995; Keller *et al.*, *Mol. Cell.*  
10 *Biol.* 13:473-486, 1993; McClanahan *et al.*, *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama *et al.*,  
15 *Proc Natl Acad Sci USA* 89:5907-5911, 1992; McNiece and Briddeli, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben *et al.*, *Exp Hematol* 22:353-359, 1994; Ploemacher, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Spoonceret *et al.*, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp.  
20 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Sutherland, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

#### **Tissue Growth Activity**

A GENX protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for  
25 wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation  
30 employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation

induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein

may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, EPIDERMAL WOUND HEALING, pp. 71-112 (Maibach and Rovee, eds.), Year Book Medical

Publishers, Inc., Chicago, as modified by Eaglstein and Menz, *J. Invest. Dermatol* 71:382-84 (1978).

#### **Activin/Inhibin Activity**

A GENX protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-b group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale *et al.*, *Endocrinology* 91:562-572, 1972; Ling *et al.*, *Nature* 321:779-782, 1986; Vale *et al.*, *Nature* 321:776-779, 1986; Mason *et al.*, *Nature* 318:659-663, 1985; Forage *et al.*, *Proc Natl Acad Sci USA* 83:3091-3095, 1986.

#### **Chemotactic/Chemokinetic Activity**

A protein of the present invention may have chemotactic or chemokinetic activity (*e.g.*, act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example,



attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

- 5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by following methods:

- 10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Coligan *et al.*,  
15 eds. (Chapter 6.12, MEASUREMENT OF ALPHA AND BETA CHEMOKINES 6.12.1-6.12.28); Taub *et al. J Clin Invest* 95:1370-1376, 1995; Lind *et al. APMIS* 103:140-146, 1995; Muller *et al., Eur J Immunol* 25: 1744-1748; Gruber *et al. J Immunol* 152:5860-5867, 1994; Johnston *et al., J Immunol* 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

- 20 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for  
25 treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

- Assay for hemostatic and thrombolytic activity include, without limitation, those  
30 described in: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.*

45:413-419, 1987; Humphrey *et al.*, *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

### **Receptor/Ligand Activity**

A protein of the present invention may also demonstrate activity as receptors, receptor  
5 ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and  
ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and  
their ligands, receptor phosphatases and their ligands, receptors involved in cell—cell  
interactions and their ligands (including without limitation, cellular adhesion molecules (such as  
selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation,  
10 antigen recognition and development of cellular and humoral immune responses). Receptors and  
ligands are also useful for screening of potential peptide or small molecule inhibitors of the  
relevant receptor/ligand interaction. A protein of the present invention (including, without  
limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of  
receptor/ligand interactions.

15 The activity of a protein of the invention may, among other means, be measured by the  
following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:  
CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan, *et al.*, Greene Publishing Associates and  
Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions  
20 7.28.1-7.28.22), Takai *et al.*, *Proc Natl Acad Sci USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp.*  
*Med.* 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160 1989; Stoltenborg *et al.*,  
*J Immunol Methods* 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995.

### **Anti-Inflammatory Activity**

Proteins of the present invention may also exhibit anti-inflammatory activity. The  
25 anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the  
inflammatory response, by inhibiting or promoting cell—cell interactions (such as, for example,  
cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory  
process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production  
of other factors which more directly inhibit or promote an inflammatory response. Proteins  
30 exhibiting such activities can be used to treat inflammatory conditions including chronic or acute

conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

### **Tumor Inhibition Activity**

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

### **Other Activities**

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ- or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting

deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Neural disorders in general include Parkinson's disease, Alzheimer's disease, Huntington's disease, multiple sclerosis, amyotrophic lateral sclerosis (ALS), peripheral neuropathy, tumors of the nervous system, exposure to neurotoxins, acute brain injury, peripheral nerve trauma or injury, and other neuropathies, epilepsy, and/or tremors.

## EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that particular novel compositions and methods involving nucleic acids, polypeptides, antibodies, detection and treatment have been described. Although these particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made as a matter of routine for a person of ordinary skill in the art to the invention without departing from the spirit and scope of the invention as defined by the claims. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

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Table 1

ORF#	Internal Identification Number	Protein similarity	Protein domain	Protein Classification	Cells or Tissues in which Gene is Expressed
1	13076366 (1, 2)	Novel Protein sim. GBank gi14691395[emb]CAB41562.1] - (AL049727) putative large secreted protein [Streptomyces coelicolor]		UNCLASSIFIED	264636
2	80248091 (3, 4)	Novel Protein sim. GBank gi2829506[sp]P71559[SUCC. MYCTU - SUCCINYL-COA SYNTHETASE BETA CHAIN (SCS-BETA)]	Contains protein domain (PF00349) - CoA-ligases	UNCLASSIFIED	264907, 264600, 264602, 264762, 264769, 264689, 264638, 264567
3	80415924 (5, 6)			UNCLASSIFIED	264910, 264604, 264634, 264605, 264636, 264691, 264907, 264692, 264629
4	82018837 (7, 8)			UNCLASSIFIED	264908, 264909, 264760, 264628, 264635
5	79970035 (9, 10)			UNCLASSIFIED	22279002, 264563
6	79842462 (11, 12)		Contains protein domain (PF00127) - Copper binding proteins, plastocyanin/azurin family	UNCLASSIFIED	264908
7	85515576 (13, 14)	Novel Protein sim. GBank gi14415926[gb]AAD20157] - (AC006282) unknown protein (Arabidopsis thaliana)		UNCLASSIFIED	20281099, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 265009, 264910, 264595, 264596, 264758, 264603, 264604, 264780, 264762, 264683, 264766, 264767, 264689, 35695917, 264690, 264692, 264693, 33657109, 264628, 264629, 35696423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566, 264486
8	56924278 (15, 16)	Novel Protein sim. GBank gi1585562[sp]Q06458[NIRB_KLEPN - NITRITE REDUCTASE (NAD(PH) LARGE SUBUNIT		reductase	264907
9	79394457 (17, 18)			UNCLASSIFIED	265007, 265019, 263972
10	79556459 (19, 20)			UNCLASSIFIED	264906
11	20414027 (21, 22)			UNCLASSIFIED	264605
12	94141210 (23, 24)	Novel Protein sim. GBank gi13878145[emb]CAA9987.1] - (Z75543) similar to potassium channel protein [Caenorhabditis elegans]		misc_channel	264259, 265007, 83373044
13	20750551 (25, 26)			UNCLASSIFIED	264556, 264557, 264564
14	95105114 (27, 28)	Novel Protein sim. GBank gi2832781[emb]CAA12845] - (AJ225805) inward potassium channel alpha subunit [Egeria densa]	Contains protein domain (PF00023) - Ank repeat	potassium_channel	35696286, 35696052, 264510, 35695917, 264691, 264628, 35696423, 264555, 264558, 264559, 83373044
15	20456307 (29, 30)	Novel Protein sim. GBank gi1170791[sp]Q10234[RT05_SCHPO - PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S5	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	264604
16	20760356 (31, 32)				264555

17	20292744 (33, 34)	Novel Protein sim. GBank gi 174884 sp P44391 URE1_HAEIN - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) - Urease	264600	
18	80246804 (35, 36)	Novel Protein sim. GBank gi 2281102 (AC002333) - SF16 isolog [Arabidopsis thaliana]		28331827, 284555, 284557, 284638, 284558	
19	80076624 (37, 38)	Novel Protein sim. GBank gi 2506112 sp P43672 UUP_ECOLI - ABC TRANSPORTER ATP-BINDING PROTEIN UUP	UNCLASSIFIED	22278998, 284907, 284910, 284600, 284693	
20	20724558 (39, 40)	Novel Protein sim. GBank gi 1730203 sp P50442 GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)	transport	264602	
21	80417554 (41, 42)	Novel Protein sim. GBank gi 1730203 sp P50442 GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)	UNCLASSIFIED	22278995, 284908, 285008, 285010, 285011, 284602, 284605, 284766, 284688, 21908784, 284691, 18108376, 284636, 18108387, 284486	
22	11705858 (43, 44)	Novel Protein sim. GBank gi 1877329 emb CAB07077  - (Z92771) fadE25 [Mycobacterium tuberculosis]		264685	
23	80419178 (45, 46)	Novel Protein sim. GBank gi 1877329 emb CAB07077  - (Z92771) fadE25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - dehydrogenase	264488, 284907, 284909, 284600, 284602, 284603, 284605, 284766, 284682, 284766, 32833986, 284636, 284486	
24	20291697 (47, 48)	Novel Protein sim. GBank gi 1730203 sp P50442 GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)		264600	
25	80253774 (49, 50)	Novel Protein sim. GBank gi 1730203 sp P50442 GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)		264593	
26	80255394 (51, 52)	Novel Protein sim. GBank gi 1730203 sp P50442 GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)	UNCLASSIFIED	22278996, 56182435, 285018, 284566	
27	80235795 (53, 54)	Novel Protein sim. GBank gi 4808369 emb CAB42783.1  - (AL049841) putative 30S ribosomal protein S14 [Streptomyces coelicolor]	Contains protein domain (PF00253) - ribosomal prot	18108370, 35696423, 284635, 284555	
28	79483581 (55, 56)	Novel Protein sim. GBank gi 3122280 sp O08333 K6PF_STRGO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)	UNCLASSIFIED	264638	
29	82448765 (57, 58)	Novel Protein sim. GBank gi 3122280 sp O08333 K6PF_STRGO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)	Contains protein domain (PF00365) - Phosphofructokinase	264601, 284762, 284766, 284768, 284636	
30	79199333 (59, 60)	Novel Protein sim. GBank gi 3560504 (AF027770) - unknown [Mycobacterium smegmatis]	UNCLASSIFIED	264908, 285019, 284687, 21906764, 21906766	
31	18848158 (61, 62)	Novel Protein sim. GBank gi 3560504 (AF027770) - unknown [Mycobacterium smegmatis]	UNCLASSIFIED	284534	
32	82449495 (63, 64)	Novel Protein sim. GBank gi 2129003 pir G64507 - hypothetical protein MJ1665 - Methanococcus jannaschii	UNCLASSIFIED	284689	
33	79582628 (65, 66)	Novel Protein sim. GBank gi 2129003 pir G64507 - hypothetical protein MJ1665 - Methanococcus jannaschii	UNCLASSIFIED	284687	
34	87467657 (67, 68)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	60432289, 284600, 284602, 284760, 18108357, 284769, 285020, 284691	
35	95005170 (69, 70)	Novel Protein sim. GBank gi 3287739 sp P73538 BIOB_SYN3 - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)	UNCLASSIFIED	284600, 284687, 284558, 284639	
36	18642042 (71, 72)	Novel Protein sim. GBank gi 3287739 sp P73538 BIOB_SYN3 - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)	synthase	284566	
37	20369215 (73, 74)	Novel Protein sim. GBank gi 2313134 gb AA007128.1  - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26895]	dehydrogenase	284603	

38	20466334 (75, 76)	Novel Protein sim. GBank gij3805970[emb]CAA06231] - (AJ004833) periplasmic nitrate reductase, large subunit [Rhodospseudomonas sp.]			reductase	264605	
39	94300715 (77, 78)	Novel Protein sim. GBank gij1929449 (L63543) - endodermin [Xenopus laevis]		Contains protein domain (PF00207) - Alpha-2-macroglobulin family	complement	264905, 264906, 264907, 66712502, 264908, 264909, 264511, 265009, 264910, 55812038, 264758, 265011, 264762, 264682, 264763, 264764, 264766, 265022, 264693, 264628, 264631, 264634, 264635, 264555, 264638, 18108381, 264558, 18108385, 264482	
40	20635625 (78, 80)				UNCLASSIFIED	264592	
41	80023287 (81, 82)	Novel Protein sim. GBank gij854055[emb]CAA58337] - (X63413) U88 [Human herpesvirus 6]				264591, 35695917	
42	20724566 (83, 84)				UNCLASSIFIED	264602	
43	20467069 (85, 86)	Novel Protein sim. GBank gij3820584 (AF086791) - carbamoylphosphate synthetase large subunit [Zymomonas mobilis]			synthase	264605	
44	13085207 (87, 88)	Novel Protein sim. GBank gij2494764[sp]Q50729[GUA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)]		Contains protein domain (PF00958) - GMP synthase C terminal domain	synthase	264769, 264636	
45	39384711 (89, 90)	Novel Protein sim. GBank gij1881738 (U89688) - myosin-I binding protein Acan125 [Acanthamoeba castellanii]			UNCLASSIFIED	264769, 264510, 264508	
46	95003398 (91, 92)				ngf	264566	
47	11696624 (93, 94)				UNCLASSIFIED	264689	
48	79407218 (95, 96)					18108385, 264635, 264828	
49	21658844 (97, 98)				UNCLASSIFIED	264603	
50	80503896 (99, 100)					264508, 264603, 264769, 264689, 264636, 264558, 264486	
51	80255569 (101, 102)	Novel Protein sim. GBank gij3411177 (AF076240) - MocC [Rhizobium leguminosarum bv. viciae]			UNCLASSIFIED	264593, 18108387	
52	78208528 (103, 104)	Novel Protein sim. GBank gij3914992[sp]Q26264[SM41_HEMPU - 41 KD SPICULE MATRIX PROTEIN PRECURSOR (HSM41) (HPSMC)]			struct	264634	
53	36996970 (105, 106)	Novel Protein sim. GBank gij3880411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]			UNCLASSIFIED	264762	
54	78570897 (107, 108)				UNCLASSIFIED	264630, 264909, 264768	
55	80202703 (109, 110)	Novel Protein sim. GBank gij1633572 (U52084) - Herpesvirus salmuri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]				29331824, 264102, 265018, 18108376	
56	8758408 (111, 112)	Novel Protein sim. GBank gij4321580[gb]AAD15785] - (AF050114) alginate lyase [Pseudomonas sp. W7]				264604	
57	11223386 (113, 114)			Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264557	

58	91227508 (115, 116)	(Novel Protein sim. GBank gl 5616074 gb AAD45618.1 AF06194 - (AF061943) protease-derived STE20-like kinase PSK (Homo sapiens)	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	56182575, 264259, 60432049, 35696052, 66712502, 264909, 265008, 265010, 265011, 264681, 29148784, 35695917, 60170615, 264691, 264692, 264693, 18108374, 35696423, 56182323, 60432113 264600, 264689, 264638
59	80077371 (117, 118)	(Novel Protein sim. GBank gl 1172920 sp P45830 RFE_MYCLE - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYL TRANSFERASE	Contains protein domain (PF00953) - transferase Glycosyl transferase	
60	12958341 (119, 120)			264689
61	80426808 (121, 122)	(Novel Protein sim. GBank gl 1710216 (U78260) - unknown [Homo sapiens]	glycoprotein	264766
62	13504968 (123, 124)			264630
63	16474553 (125, 126)		UNCLASSIFIED	265019
64	20724578 (127, 128)	(Novel Protein sim. GBank gl 420945 pir JA47041 - transposase homolog (insertion element [SAE1] - Alcaligenes eutrophus	UNCLASSIFIED	264602
65	79326308 (129, 130)	(Novel Protein sim. GBank gl 3122312 sp O08134 KPYK_MYCTU - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - kinase Pyruvate kinase	264563
66	46854384 (131, 132)	(Novel Protein sim. GBank gl 3928723 emb CAA22218  - (AL034355) putative ABC transporter [Streptomyces coelicolor]	transport	22278996, 264558
67	78952543 (133, 134)	(Novel Protein sim. GBank gl 231985 sp P30234 DHA_MYCTU - ALANINE DEHYDROGENASE [40 KD ANTIGEN])	dehydrogenase	265021
68	79817382 (135, 136)			264909
69	79841764 (137, 138)		UNCLASSIFIED	264908
70	79817329 (139, 140)			264908, 264908
71	65897456 (141, 142)		UNCLASSIFIED	264602, 265021
72	87734977 (143, 144)	(Novel Protein sim. GBank gl 4415926 gb AAD20157  - (AC008282) unknown protein [Arabidopsis thaliana])	UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264511, 265008, 264910, 264758, 87168474, 264682, 264766, 264686, 264689, 35695917, 265021, 60170615, 264691, 33657023, 264692, 264693, 264629, 264631, 264639, 22279000
73	80025241 (145, 146)		UNCLASSIFIED	60424178, 264508, 264908, 265007, 264603, 264687, 264689, 264692, 18108387
74	20377410 (147, 148)		UNCLASSIFIED	264605
75	11819032 (149, 150)	(Novel Protein sim. GBank gl 2853098 emb CAA16914  - (AL021787) vacuolar protein sorting [Schizosaccharomyces pombe])	UNCLASSIFIED	264689
76	95105303 (151, 152)	(Novel Protein sim. GBank gl 4468811 emb CAB38212  - (AL035601) putative protein [Arabidopsis thaliana])	UNCLASSIFIED	83373044, 264906, 264557
77	10144718 (153, 154)	(Novel Protein sim. GBank gl 854085 emb CAA56337  - (X63413) U88 [Human herpesvirus 6])	UNCLASSIFIED	264563
78	8758258 (155, 156)		UNCLASSIFIED	264604



79	94140180 (157, 158)	Novel Protein sim. GBank gij5689453[dj]BAA83010.1] - (AB028881) KIAA1058 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain		3569286, 2227898, 29331822, 29331824, 29331825, 29331827, 284905, 264906, 264907, 66712502, 264908, 264909, 265008, 265009, 264910, 60170831, 55812038, 33109954, 265017, 265018, 264288, 264768, 56181582, 21906765, 21906769, 29148784, 265020, 264690, 264691, 264692, 264693, 60431528, 35696423, 264631, 264632, 264634, 264636, 264639, 83373044, 264564, 264566, 264567
80	82314840 (159, 160)			UNCLASSIFIED	284759, 264601, 265006, 264910, 264604, 264605, 264634, 264635, 264805, 264762, 264637, 264592, 264628, 264807, 264691, 264908, 264587, 264909, 264766
81	20467247 (161, 162)	Novel Protein sim. GBank gij1723442[sp]Q10258[YD2A_SCHPO - HYPOTHETICAL 69.0 KD PROTEIN C56F8.10 IN CHROMOSOME 1]		reductase	264605
82	16331388 (163, 164)	Novel Protein sim. GBank gij2895866 (AF045770) - methylmalonate semi-aldehyde dehydrogenase [Onyza sativa]		dehydrogenase	264567
83	94741180 (165, 166)	Novel Protein sim. GBank gij3402673 (AC004697) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 264508, 264509, 264905, 264908, 264909, 264511, 264591, 264593, 264594, 264595, 264596, 264758, 264603, 264760, 264681, 18108351, 264762, 264682, 264784, 264684, 264766, 264686, 264632, 264637, 264557, 264638, 264639, 18108385, 264566
84	80355375 (167, 168)	Novel Protein sim. GBank gij1173364[sp]P45380[SAT1_RAT - SULFATE ANION TRANSPORTER 1 (CANALICULAR SULFATE TRANSPORTER) (SULFATE/CARBONATE ANTI-PORTER)]		transport	264508, 264906, 264907, 264908, 264909, 264910, 264760, 264763, 264764, 264768, 264768, 264769, 35695855, 264636, 264637
85	80499600 (169, 170)	Novel Protein sim. GBank gij2120998[p]rj[S70682 - glycosyltransferase homolog - Bordetella pertussis]		transferase	264605, 264762, 264687, 264769, 18108374, 264636, 264486
86	39559043 (171, 172)	Novel Protein sim. GBank gij3256023[emb]CAA17228.1] - (AL021897) hypothetical protein RV1112 [Mycobacterium tuberculosis]			264910
87	13856808 (173, 174)			UNCLASSIFIED	264093

88	95344718 (175, 176)	Novel Protein sim. GBank glij559703[dbj BAA07552] - (D38549) ha1025 is new [Homo sapiens]		52644507, 52646365, 18108398, 65274572, 56182575, 56994075, 35696286, 22278987, 22278998, 22278999, 264092, 264093, 264094, 264095, 264259, 29331822, 29331824, 56182181, 66714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 264105, 264508, 264905, 264906, 264907, 264908, 29331830, 66712502, 52644045, 56182435, 265007, 265009, 264910, 60170831, 264592, 60431735, 60433356, 33657402, 264757, 60433438, 55812038, 264758, 21906754, 52646317, 33109954, 52644296, 87168474, 265011, 87168559, 264601, 265017, 265018, 264604, 265019, 264448, 264368, 264288, 264766, 52644229, 21906786, 21906787, 21906768, 21908769, 55811957, 35695917, 265020, 265021, 265022, 60170615, 52644150, 33657023, 65274620, 33657109, 27486261, 27486264, 33657349, 35695763, 264628, 263972, 18108374, 55810764, 35696423, 55811576, 65274791, 35695855, 60431850, 264636, 52644332, 56182323, 60170394, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22279000, 22279002, 264482, 264564, 264486
88	80077389 (177, 178)	Novel Protein sim. GBank glij170383[sp P46352 RIPX_BACSU - PROBABLE INTEGRASE/RECOMBINASE RIPX		264600
90	82115988 (179, 180)	Novel Protein sim. GBank glij2498891[sp P76403 YEGQ_ECOLI - PUTATIVE PROTEASE IN BAER-OGK INTERGENIC REGION	UNCLASSIFIED protease	264760 265006
91	78906950 (181, 182)	Novel Protein sim. GBank glij3367754[embj CAA20078] - (AL031155) hypothetical protein SC3A7.16c [Streptomyces coelicolor]	UNCLASSIFIED	264691
92	78554871 (183, 184)	Novel Protein sim. GBank glij2895085 (AF011337) - putative E1-E2 ATPase [Mus musculus]	ATPase_associated	264907, 264908, 264910, 265009, 264605, 264769
93	80496778 (185, 186)	Novel Protein sim. GBank glij1171919[sp P46920 OPUA_BACSU - GLYCINE BETAINES TRANSPORT ATP-BINDING PROTEIN OPUAA	Contains protein domain (PF00571) - CBS domain	264908
94	78646649 (187, 188)			
95	11080238 (189, 190)			264594

96	94322125 (191, 192)	Novel Protein sim. GBank gl 4589560 db BAA76802.1  - (AB023175) KIAA0958 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 264259, 29331822, 29331826, 35696052, 29146499, 264509, 264906, 264907, 264908, 264909, 265007, 265008, 264910, 265009, 264593, 265010, 265017, 264604, 265019, 18108351, 264288, 264766, 264768, 264769, 21908765, 21908767, 21908769, 265020, 264892, 33657182, 35695763, 264828, 264628, 18108379, 264631, 264636, 18108381, 264559, 18108382, 83373044, 22279002, 264508
97	79605200 (193, 194)	Novel Protein sim. GBank gl 4583559 emb CAB40388.1  - (AJ005255) OxyR [Erwinia chrysanthemi]		UNCLASSIFIED	
98	79427000 (195, 196)	Novel Protein sim. GBank gl 1001693 db BAA10430  - (D84002) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	264909
99	20466524 (197, 198)	Novel Protein sim. GBank gl 1169479 sp P43925 EFG_HAEIN - ELONGATION FACTOR G (EF-G)		UNCLASSIFIED	264605
100	79640113 (199, 200)	Novel Protein sim. GBank gl 480897 pir J537465 - gene msg1 protein - mouse		UNCLASSIFIED	264693
101	80203298 (201, 202)	Novel Protein sim. GBank gl 2894166 emb CAA11773.1  - (AJ223898) PCZA361.18 [Amycolatopsis orientalis]		UNCLASSIFIED	265020, 264102, 263972
102	20467259 (203, 204)	Novel Protein sim. GBank gl 1731040 sp P54509 YQH_H_BACSU - HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	synthase	264605
103	20466368 (205, 206)	Novel Protein sim. GBank gl 854065 emb CAA56337  - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264605
104	80247572 (207, 208)	Novel Protein sim. GBank gl 1685117 U70770 - furrowed [Drosophila melanogaster]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	UNCLASSIFIED	264591, 264595, 264602
105	79605208 (209, 210)	Novel Protein sim. GBank gl 1705505 sp P54729 BS4_MOUSE - BS4 PROTEIN	Contains protein domain (PF00627) - UBA domain	complement	264508
106	28382058 (211, 212)	Novel Protein sim. GBank gl 4887229 gb AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]		UNCLASSIFIED	264511, 265009
107	80057791 (213, 214)	Novel Protein sim. GBank gl 263577 emb CAB15264  - (Z99120) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis]		ATPase-associated	28331824, 264591, 21906754, 265019
108	80237938 (215, 216)	Novel Protein sim. GBank gl 233078 emb CAB11265  - (Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]	Contains protein domain (PF00005) - ABC transporter	transport	18108374, 35695917, 22278996, 264113, 264600, 264602, 264603, 265017, 284910, 264906, 264636, 264766
109	95184148 (217, 218)	Novel Protein sim. GBank gl 233078 emb CAB11265  - (Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	264758, 264603, 264630, 264636, 264637
110	79582823 (219, 220)				264687
111	39565458 (221, 222)				264584
112	79656038 (223, 224)			UNCLASSIFIED	264908
113	17959439 (225, 226)			UNCLASSIFIED	265007
114	80502101 (227, 228)			UNCLASSIFIED	264769

115	80251003 (229, 230)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	52645156, 52845080, 33656970, 264592, 21908754, 27486264, 18108379, 35698423, 264635, 52844332, 18108382
116	81288889 (231, 232)				264805, 264906, 264907, 264908, 264909, 264910, 264758, 265010, 264763, 264682, 264764, 264766, 264685, 264686, 264768, 264769, 33657023, 264683, 33857108, 264628, 18108374, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 56528488, 264585, 264566
117	79836695 (233, 234)		Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	264639, 264693
118	80222170 (235, 236)				283974
119	91013071 (237, 238)	Novel Protein sim. GBank gi 732528 (U22327) - alpha2(IV) collagen [Caenorhabditis elegans]		UNCLASSIFIED	22278996, 29331824, 60432289, 265007, 60433438, 264603, 264605, 18108351, 264769, 264689, 265020, 264534, 27486281, 264558, 83373044, 18108385, 264584
120	8756481 (238, 240)	Novel Protein sim. GBank gi 2131219 pir IS0157 - cyclin-dependent kinase chain SRB10 - yeast (Saccharomyces cerevisiae)		kinase	264603
121	80026153 (241, 242)				264585
122	20457620 (243, 244)	Novel Protein sim. GBank gi 2052147 emb CAB08137  (Z94752) ksgA [Mycobacterium tuberculosis]	Contains protein domain (PF00398) - Ribosomal RNA adenine dimethylases	transferase	264605
123	8758278 (245, 246)				264604
124	79104017 (247, 248)	Novel Protein sim. GBank gi 2833385 sp Q43134 UGST_SORBI - GRANULE-BOUND GLYCOPROTEIN (STARCH) SYNTHASE PRECURSOR		synthase	18108394, 18108397, 265008, 265007, 265008, 265010, 265011, 18108355, 18108379, 18108380, 18108384
125	87787886 (249, 250)	Novel Protein sim. GBank gi 475542 (U08255) - glutamate receptor delta-1 subunit [Rattus norvegicus]	Contains protein domain (PF000060) - Ligand-gated ion channel	misc_channel	264508, 264906, 265009, 264596, 22279002
126	56701283 (251, 252)	Novel Protein sim. GBank gi 5102785 emb CAB45200.1  (AL079308) putative transcriptional regulator [Streptomyces coelicolor]			264511
127	20467267 (253, 254)				264605
128	80248473 (255, 256)	Novel Protein sim. GBank gi 130120 sp P23820 PHOB_PSEAE - PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB	Contains protein domain (PF00072) - Response regulator receiver domain	UNCLASSIFIED - phosphatase	264907, 264909, 264910, 264600, 264601, 264603, 264605, 18108351, 264693, 264557
129	95280543 (257, 258)	Novel Protein sim. GBank gi 2506493 sp P38036 YGC8_ECOLI - HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	35698423, 35695855, 264600, 264602, 264603, 264604, 264605, 264508, 264906, 264584, 264628, 264682, 264585, 264683
130	80085563 (259, 260)	Novel Protein sim. GBank gi 854065 emb CAA58337  (X83413) U88 [Human herpesvirus 6]			264634
131	94995022 (261, 262)	Novel Protein sim. GBank gi 107603 pir IS54860 - ABC transporter PstC-2 chain - Mycobacterium tuberculosis	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	18108376, 264769, 29331826, 264689, 22278996, 265021, 264600, 264511, 264601, 264602, 264605, 264905, 264636

132	10887692 (263, 264)	Novel Protein sim. GBank gij1877340[emb]CAB07088] - (Z92771) accA3 [Mycobacterium tuberculosis]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)		264636 264905, 264689
133	94630883 (265, 266)	Novel Protein sim. GBank gij458583[emb]CAB40932.1] - (AL049630) putative NADH dehydrogenase [Streptomyces coelicolor]		dehydrogenase	264905, 264605, 265021
134	79834660 (267, 268)	Novel Protein sim. GBank gij1460074[emb]CAB01049] - (Z77250) hypothetical protein Rvz566 [Mycobacterium tuberculosis]			264634
135	18885057 (269, 270)	Novel Protein sim. GBank gij212589[emb]CAA73511] - (Y13070) folypolyglutamate synthase [Streptomyces coelicolor]		synthase	264508
136	79846083 (271, 272)				
137	79819770 (273, 274)				264683, 264685, 264686, 264691, 264692, 264693
138	79835971 (275, 276)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	18108374, 18108385, 33657109, 33657182, 265010, 22278988, 265008, 265007, 265008, 265009, 264693
139	8688076 (277, 278)	Novel Protein sim. GBank gij5688912[emb]CAB52075.1] - (AL109732) putative mutase [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01817) - Chorismate mutase	dehydrogenase	22278986, 265007, 264910, 60433356, 265010, 264602, 264605, 264768, 264688, 264769, 264693, 32833986, 18108374, 18108387
140	79825759 (279, 280)			UNCLASSIFIED	264908
141	20700094 (281, 282)				264600
142	80028104 (283, 284)	Novel Protein sim. GBank gij3581916[emb]CAA20855] - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]		nuclease	264602, 265017
143	11072274 (285, 286)				
144	95009102 (287, 288)	Novel Protein sim. GBank gij3334127[sp]P87303[BAC2_MOUSE - TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2)]		UNCLASSIFIED	264600
145	80027058 (289, 290)	Novel Protein sim. GBank gij3757569[emb]CAA21315] - (AL031863) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method score=66.31; 1-evidence_end [Drosophila melanogaster]		UNCLASSIFIED	263978, 264600, 264910, 264632, 264508, 264563, 264564, 264591, 264556, 264908, 264629, 264639
146	13085662 (291, 292)	Novel Protein sim. GBank gij140807[sp]P24536[Y121_BURCE - INSERTION ELEMENT IS402 HYPOTHETICAL 24 KD PROTEIN]	Contains protein domain (PF01675) - Transposase		22278986, 264602
147	94320366 (293, 294)	Novel Protein sim. GBank gij2827608[emb]CAA16663] - (AL021646) uvrD2 [Mycobacterium tuberculosis]		helicase	264905, 264906, 264909, 264510, 265009, 60433356, 264600, 264601, 264604, 264605, 264687, 264769, 18108385, 65274791, 18108387
148	80248804 (295, 296)	Novel Protein sim. GBank gij2916947[emb]CAA17585] - (AL021999) hypothetical protein Rv0886 [Mycobacterium tuberculosis]		transport	265009, 265010, 264600, 264602, 264603, 264604, 264605, 264693, 33657109, 264636

149	80249373 (297, 298)	Novel Protein sim. GBank gi11723073 sp Q11040 Y081_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.01 Novel Protein sim. GBank gi13724125 emb CAA11905  - (AJ224340) maltosephosphorylase [Lactobacillus sanfrancisco]	Contains protein domain (PF000005) - ABC transporter	transport	265010, 264600, 264601, 264603, 264604, 27486265, 264636
150	20284748 (289, 300)	Novel Protein sim. GBank gi12497952 sp P55667 Y4TM_RHISN - HYPOTHETICAL HYDROLASE/PEPTIDASE Y4TM			264600
151	20726308 (301, 302)	Novel Protein sim. GBank gi128312 sp P07651 DEOB_ECOLI - PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE)	Contains protein domain (PF01676) - Metalloenzyme superfamily	UNCLASSIFIED	264602
152	95002877 (303, 304)	Novel Protein sim. GBank gi12497952 sp P55667 Y4TM_RHISN - HYPOTHETICAL HYDROLASE/PEPTIDASE Y4TM	peptidase		264602
153	80256685 (305, 306)	Novel Protein sim. GBank gi1323021 sp Q90508 VT1_FUNHE - VITELLOGENIN I PRECURSOR (VTG I) (CONTAINS: LIPOVITELIN 1 (LV1); PHOSVITIN (PV); LIPOVITELIN 2 (LV2))	UNCLASSIFIED		264593
154	82305966 (307, 308)	Novel Protein sim. GBank gi1419697 pir JN0443 - transcription initiation factor sigma homolog hrdB - Streptomyces aureofaciens	Contains protein domain (PF00140) - Sigma-70 factor		264810, 264762, 264691, 264634
155	20428859 (309, 310)	Novel Protein sim. GBank gi1628710 pir S41739 - hypothetical protein - Escherichia coli			264605
156	39564742 (311, 312)	Novel Protein sim. GBank gi13695013 (AF052586) - CtaA [Pseudomonas aeruginosa]	UNCLASSIFIED		264565
157	10358887 (313, 314)	Novel Protein sim. GBank gi1073072 pir C55543 - cnaU protein - Pseudomonas syringae pv. syringae	Contains protein domain (PF00142) - 4Fe-4S iron sulfur cluster binding proteins, NifH/rnC family	hydrolase	264691
158	78761938 (315, 316)	Novel Protein sim. GBank gi1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	UNCLASSIFIED		264905
159	78890376 (317, 318)	Novel Protein sim. GBank gi1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	265008
160	11075119 (319, 320)	Novel Protein sim. GBank gi1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00327) - ribosomal prot		264605
161	80055007 (321, 322)	Novel Protein sim. GBank gi15304869 emb CAB46028.1  - (AL031685) dJ963K23.2 (novel protein) [Homo sapiens]			22278996, 264600, 264803, 35695917, 32833986, 35698423, 264636
162	80016371 (323, 324)	Novel Protein sim. GBank gi15304869 emb CAB46028.1  - (AL031685) dJ963K23.2 (novel protein) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukin	264112, 264532, 22279002
163	11892308 (325, 326)	Novel Protein sim. GBank gi12661691 emb CAA15795  - (AL009204) putative protease [Streptomyces coelicolor]	UNCLASSIFIED		264639
164	80077902 (327, 328)	Novel Protein sim. GBank gi14416478 gb AAD20378  - (AF125999) transposase [Mycobacterium avium]	UNCLASSIFIED		264905, 264907, 264600
165	10856087 (329, 330)	Novel Protein sim. GBank gi14416478 gb AAD20378  - (AF125999) transposase [Mycobacterium avium]			264691
166	88095003 (331, 332)	Novel Protein sim. GBank gi176177 pir Q0ECFT - hypothetical 38.8K protein (fst 5' region) - Escherichia coli	UNCLASSIFIED		264605, 264486
167	16395460 (333, 334)	Novel Protein sim. GBank gi176177 pir Q0ECFT - hypothetical 38.8K protein (fst 5' region) - Escherichia coli	UNCLASSIFIED		265010
168	80079362 (335, 336)	Novel Protein sim. GBank gi176177 pir Q0ECFT - hypothetical 38.8K protein (fst 5' region) - Escherichia coli			264600
169	80239581 (337, 338)	Novel Protein sim. GBank gi176177 pir Q0ECFT - hypothetical 38.8K protein (fst 5' region) - Escherichia coli			264556, 264557, 264558, 264559

170	79612364 (339, 340)	Novel Protein sim. GBank	Contains protein domain (PF01810) - LysE type translocator	264906
171	95293073 (341, 342)	gll140888[sp]P27847[YIGK_ECOLI - HYPOTHETICAL 15.4 KD PROTEIN IN RECQ-PLDB INTERGENIC REGION (F138)]		264595, 264604
172	37797007 (343, 344)	Novel Protein sim. GBank gll4210905[gb]AAD12048.1] - (AF045609) AglG [Sinorhizobium meliloti]	Contains protein domain (PF00528) - transport Binding-protein-dependent transport systems inner membrane component	264769
173	57529660 (345, 346)	Novel Protein sim. GBank gll132854[sp]P02387[RL2_ECOLI] - 50S RIBOSOMAL PROTEIN L2	Contains protein domain (PF00181) - Ribosomal Proteins L2	264769
174	95293078 (347, 348)	Novel Protein sim. GBank gll1881350[db]BAA19371] - (AB001489) PROBABLE TRANSPORT PROTEIN, SIMILAR TO ANTIBIOTIC TRANSPORT-ASSOCIATED PROTEIN ACTII IN STREPTOMYCES COELICOLOR. [Bacillus subtilis]	transport	264510, 264593, 264602, 264603, 264605, 264762, 264693
175	79756270 (349, 350)	Novel Protein sim. GBank gll2072722[emb]CAB08328] - (Z95121) manA [Mycobacterium tuberculosis]	isomerase	264565
176	80066886 (351, 352)	Novel Protein sim. GBank gll1055198 (U40187) - similar to PIR-A41724 chicken LD (limb deformity) gene product and to formin; also P-rich region similar to collagen [Caenorhabditis elegans]	UNCLASSIFIED	264907, 264910, 264681, 264558
177	86684852 (353, 354)	Novel Protein sim. GBank gll23267[3]emb[CAB10952] - (Z98268) hypothetical protein Rv1695 [Mycobacterium tuberculosis]	Contains protein domain (PF01513) - Domain of unknown function	264768, 60424179, 264687, 264688, 264769, 29331826, 60432289, 18108376, 264689, 18108387, 32833986, 22278986, 265020, 264600, 264601, 264602, 264603, 264604, 264605, 264635, 264762, 264636, 264906, 264564, 264637, 264638, 264486, 60433356, 264766
178	79559526 (355, 356)	Novel Protein sim. GBank gll1906596 (U81788) - kinesin-73 [Drosophila melanogaster]	struc1	264693, 33657109, 264635
179	20263112 (357, 358)	Novel Protein sim. GBank	UNCLASSIFIED	264563
180	80488958 (359, 360)	gll1169387[sp]P45256[DNAB_HAEIN - REPLICATIVE DNA HELICASE]	helicase	264769
181	79585369 (361, 362)	Novel Protein sim. GBank gll3170615 (AF059485) - DOC4 [Mus musculus]	UNCLASSIFIED	21908787, 264635, 264639, 18108384
182	80577899 (363, 364)			
183	11614017 (365, 366)	Novel Protein sim. GBank gll1076627[pir]S54172 - Inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco	UNCLASSIFIED	264259, 35686052, 56182435, 264511, 265018, 33657109, 264555, 264568, 264690
184	10174167 (367, 368)	Novel Protein sim. GBank gll4371280[gb]AAD18138] - (AC006260) hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	264510

185	21660822 (368, 370)	Novel Protein sim. GBank gij3008178[embjCAA18398.1] - (AL022304) putative mma transport regulator [Schizosaccharomyces pombe]		UNCLASSIFIED	264604
186	80070329 (371, 372)	Novel Protein sim. GBank gij289802[spP94408]YCLF_BACSU - HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERKA INTERGENIC REGION		transport	264595
187	80186611 (373, 374)	Novel Protein sim. GBank gij3150260[embjCAA18179] - (AL023834) cyclin [Schizosaccharomyces pombe]		UNCLASSIFIED	264369
188	20464942 (375, 376)	Novel Protein sim. GBank gij2145853[pirjS72938 - hix protein - Mycobacterium leprae		kinase	264605
189	82338215 (377, 378)	Novel Protein sim. GBank gij1881244[dbjBAA19271] - (AB001488) SIMILAR TO PYRUVATE OXIDASE AND ACETOLACTATE SYNTHASE. [Bacillus subtilis]		UNCLASSIFIED	35696052, 264602, 264605, 264762, 264689, 35695917, 18108370, 18108372, 264638, 264585
190	80088821 (379, 380)	Novel Protein sim. GBank gij120226[spP28725]FKBP_STRCH - FK506-BINDING PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PIASE) (ROTAMASE)	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	synthase	264583
191	88095012 (381, 382)	Novel Protein sim. GBank gij1705461[spP53656]BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7-8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	264508, 264604, 264605, 264769, 264555
192	18333379 (383, 384)	Novel Protein sim. GBank gij4980892[gbjAAD35474.1]AE00171 - (AE001718) ABC transporter, ATP-binding protein [Thermotoga maritima]			264567
193	78910127 (385, 386)	Novel Protein sim. GBank gij1705461[spP53656]BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7-8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)			264808, 264693
194	20464949 (387, 388)	Novel Protein sim. GBank gij1705461[spP53656]BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7-8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)			264605
195	13518389 (389, 390)	Novel Protein sim. GBank gij1705461[spP53656]BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7-8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)		transport	264636
196	95005569 (391, 392)	Novel Protein sim. GBank gij1705461[spP53656]BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7-8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	Contains protein domain (PF00202) - gaba Aminotransferases class-III pyridoxal phosphate		264600, 264689, 264638
197	80248665 (393, 394)	Novel Protein sim. GBank gij3122305[spIQ2778]K8PF_SCHMA - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)	Contains protein domain (PF00365) - Phosphofructokinase	kinase	264602, 264682, 264682, 18108374
198	78163635 (395, 396)	Novel Protein sim. GBank gij1781203[embjCAB06110] - (Z83859) gnd [Mycobacterium tuberculosis]			264636
199	78890715 (397, 398)	Novel Protein sim. GBank gij1781203[embjCAB06110] - (Z83859) gnd [Mycobacterium tuberculosis]	Contains protein domain (PF00393) - 6-phosphogluconate dehydrogenases		265008
200	78413849 (399, 400)	Novel Protein sim. GBank gij2642222 (AF030885) - telomere-associated recQ-like helicase [Usiliago maydis]		UNCLASSIFIED	264595, 264596
201	86945824 (401, 402)	Novel Protein sim. GBank gij2884379[embjCAA74911.1] - (Y14573) ring finger protein [Hordeum vulgare]		UNCLASSIFIED	29331826, 265007, 264512, 33857402, 264596, 265017, 18108351, 264682, 264683, 264767, 264628, 55810764, 264634, 264635, 58182323, 60432113, 22279000



202	79588046 (403, 404)	Novel Protein sim. GBank gl 231772 sp P30598 CHS1_USTMA - CHITIN SYNTHASE 1 (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 1)	Contains protein domain (PF01644) - synthase Chitin synthase	264600	
203	79843827 (405, 406)	Novel Protein sim. GBank gl 1504042 dbj BAA13220  - (D86984) similar to yeast adenylate cyclase (S56776) (Homo sapiens)		22278995, 28331822, 28331825, 28331827, 264908, 21900754, 264683, 21806766, 21906769, 35698423, 264558	
204	79855188 (407, 408)		UNCLASSIFIED	264809	
205	10090563 (409, 410)	Novel Protein sim. GBank gl 2633808 emb CAB13310  - (Z89111) similar to hypothetical proteins [Bacillus subtilis]	transport	264809	
206	8758473 (411, 412)		UNCLASSIFIED	264604	
207	20754522 (413, 414)	Novel Protein sim. GBank gl 2134381 pir S60678 - polybromo 1 protein - chicken	UNCLASSIFIED	264556	
208	20289261 (415, 416)			264605	
209	80071069 (417, 418)	Novel Protein sim. GBank gl 2501040 sp O05814 SYP_MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE--TRNA LIGASE) (PRORS)		264605, 264689	
210	80168800 (419, 420)			264805, 264907, 264909, 264766, 264687, 264691, 264629, 18108374, 264638	
211	80034539 (421, 422)			263978	
212	82442474 (423, 424)	Novel Protein sim. GBank gl 5031809 ref NP_005536.1 p1SLR - immunoglobulin superfamily containing leucine-rich repeat	UNCLASSIFIED	264508, 264905, 264906, 264907, 264908, 264600, 264762, 264534, 264632, 264634, 264635, 264639, 264486	
213	80249562 (425, 426)	Novel Protein sim. GBank gl 3123359 sp O33123 LEU2_MYCLE - 3- ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)	Contains protein domain (PF00330) - aconitase family (aconitate hydratase)	22278996, 264508, 264800, 264602, 264603, 264605, 33657023, 264565, 264486	
214	80079381 (427, 428)	Novel Protein sim. GBank gl 116236 sp P19421 CH60_COXBU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (HEAT SHOCK PROTEIN B)	Contains protein domain (PF00116) - TCP-1/cpn60 chaperonin family	264600, 264693	
215	14973283 (429, 430)				
216	80177718 (431, 432)	Novel Protein sim. GBank gl 3417287 (AC002310) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	264629	
217	79603634 (433, 434)	Novel Protein sim. GBank gl 2506924 sp P49754 VP41_HUMAN - VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG (S53)	dna_rna_bind	264448	
218	80258475 (435, 436)	Novel Protein sim. GBank gl 173288 sp P38106 IRSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN		264508	
219	20438797 (437, 438)	Novel Protein sim. GBank gl 1781097 emb CAB06231  - (Z83864) gl B [Mycobacterium tuberculosis]	mapolymerase	264594	
220	13489572 (439, 440)	Novel Protein sim. GBank gl 2884703 (AF052427) - unknown [Trypanosoma cruzi]	synthase	264604	
221	11287498 (441, 442)	Novel Protein sim. GBank gl 4587313 dbj BAA76709.1  - (AB025248) alpha-1,2-mannosidase [Bacillus sp. M-90]	nucleosinhib	264689	
			UNCLASSIFIED	264555	

222	79862802 (443, 444)	Novel Protein sim. GBank gi1877268[emb]CAB07049] - (Z92770) hypothetical protein Rv0143c [Mycobacterium tuberculosis]		UNCLASSIFIED	284605, 264769, 35696423
223	83033869 (445, 446)			UNCLASSIFIED	284908, 284907, 284603
224	79557820 (447, 448)				284684, 284693
225	79559541 (449, 450)	Novel Protein sim. GBank gi2274851[dbj]BAA21515] - (D64159) 3-7 gene product [Homo sapiens]		UNCLASSIFIED	284692
226	79172397 (451, 452)	Novel Protein sim. GBank gi868245 (U29488) - C56C10.7 gene product [Caenorhabditis elegans]		UNCLASSIFIED	22278998, 284112, 33657023, 263981
227	81777196 (453, 454)			UNCLASSIFIED	35695917, 284636, 284907
228	79872285 (455, 456)				284768, 284907, 284908, 284692, 284593, 284639
229	79838288 (457, 458)				284908, 284910
230	11013209 (459, 460)			UNCLASSIFIED	284631
231	20622207 (461, 462)	Novel Protein sim. GBank gi1835114[emb]CAA71733] - (Y10744) homoserine O-acetyltransferase [Leptospira meyeri]			284906, 284600, 284603, 284692
232	80055035 (463, 464)			UNCLASSIFIED	284600, 284603, 284605, 284687, 284769
233	80063054 (465, 466)	Novel Protein sim. GBank gi2642340 (AF032870) - imidazole propionate hydrolase [Pseudomonas putida]	Contains protein domain (PF00449) - Urease		284604
234	7523988 (467, 468)	Novel Protein sim. GBank gi3510505 (AF030881) - polypeptide [Fugu rubripes]		UNCLASSIFIED	284369
235	80203671 (469, 470)	Novel Protein sim. GBank gi2104609[emb]CAB08805] - (Z95398) PckA [Mycobacterium leprae]		UNCLASSIFIED	284106
236	78940001 (471, 472)			carboxylase	284905
237	11755273 (473, 474)				284681
238	79461401 (475, 476)			UNCLASSIFIED	284639
239	82435190 (477, 478)	Novel Protein sim. GBank gi2495617[sp]Q57252[YDIJ_HAEIN - HYPOTHETICAL PROTEIN HI1163]	Contains protein domain (PF00037) - 4Fe-4S ferredoxins and related iron-sulfur cluster binding domains.		284908, 285010, 284603, 284762, 284682, 284636, 284638, 284486
240	21635575 (479, 480)	Novel Protein sim. GBank gi3183458[sp]P75796[YLIA_ECOLI - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YLIA]	transport		284259, 284769
241	80377307 (481, 482)	Novel Protein sim. GBank gi3875920[emb]CAB04111] - (Z81503) predicted using GeneFinder, similar to collagen; cDNA EST EMBL:D65450 comes from this gene; cDNA EST EMBL:D6888 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	284908, 284909, 284764, 284639
242	82148454 (483, 484)			UNCLASSIFIED	284489, 284907, 284908, 284511, 284760, 284764, 284692, 284635, 284637
243	79633207 (485, 486)				284908
244	80248682 (487, 488)	Novel Protein sim. GBank gi2624302[emb]CAA15575] - (AL008967) ald [Mycobacterium tuberculosis]		UNCLASSIFIED	284600, 284602, 284605, 284769, 284689
245	79863543 (489, 490)	Novel Protein sim. GBank gi2820625 (AF044499) - vgrE protein [Escherichia coli]		UNCLASSIFIED	284907, 284758
246	79162828 (491, 492)	Novel Protein sim. GBank gi5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01106) - NiU-like domain		284637, 18108381, 18108387, 284565

247	79873185 (493, 494)	Novel Protein sim. GBank gll1839006[emb CA806848] - (Z85982) argB [Mycobacterium tuberculosis]		kinase	264909, 264691, 35686423, 18108387
248	80488983 (495, 496)	Novel Protein sim. GBank gll1168574[sp P42484 ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	35686286, 264907, 264511, 264602, 264788, 264688, 265021, 35685855, 18108385
249	79764845 (497, 498)			UNCLASSIFIED	264907, 264910, 265011, 264762, 264638
250	78619980 (499, 500)				21908788, 264692
251	84359489 (501, 502)			UNCLASSIFIED	52645158, 28331822, 28331824, 52644045, 285018, 21906785, 21908788, 265020, 27486281, 27486285, 35695763, 18108376, 284558, 264559, 264585
252	79737758 (503, 504)	Novel Protein sim. GBank gll3327166[db BAA31651] - (AB014576) KIAA0678 protein [Homo sapiens]			284685, 264687, 264632
253	20443124 (505, 506)	Novel Protein sim. GBank gll3038880[emb CAA18513] - (AL022374) putative ATP-dependent DNA helicase [Streptomyces coelicolor]		helicase	264604
254	80027421 (507, 508)	Novel Protein sim. GBank gll3915488[sp O34981 YJMB_BACSU - HYPOTHETICAL SYMPORTER IN COTT-RAPA INTERGENIC REGION		UNCLASSIFIED	264508, 264806, 264602, 264687, 265021, 264486
255	11388315 (509, 510)	Novel Protein sim. GBank gll1665720[db BAA04134] - (D17312) diarrheal toxin [Bacillus cereus]		UNCLASSIFIED	264593
256	80028158 (511, 512)	Novel Protein sim. GBank gll465787[sp P34422 YL31_CAEEL - HYPOTHETICAL 86.0 KD PROTEIN F4489.1 IN CHROMOSOME III	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	264602, 264682
257	20289282 (513, 514)	Novel Protein sim. GBank gll1172039[sp P42315 SCOA_BACSU - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE SUBUNIT A (SUCCINYL COA:3-OXOACID COA-TRANSFERASE) (OXCT A)	Contains protein domain (PF01144) - Coenzyme A transferase	transferase	264605
258	20459464 (515, 516)	Novel Protein sim. GBank gll3127836[emb CAA18902] - (AL023496) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264604
259	78910152 (517, 518)			collagen	264681, 264688, 264692
260	20378437 (519, 520)			UNCLASSIFIED	264692, 264556
261	20285983 (521, 522)	Novel Protein sim. GBank gll123761[sp P24221 HUTH_STRGR - HISTIDINE AMMONIA-LYASE (HISTIDASE)	Contains protein domain (PF00221) - Phenylalanine and histidine ammonia lyases	UNCLASSIFIED	264600
262	80189317 (523, 524)			UNCLASSIFIED	285017, 264369
263	88095045 (525, 526)	Novel Protein sim. GBank gll3924708[emb CAA84646] - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL: T02089 comes from this gene; cDNA EST EMBL: D76135 comes from this gene; cDNA EST EMBL: D73147 comes from this gene; cDNA EST EMB...		UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264909, 264512, 264910, 264758, 264596, 264604, 265019, 264605, 264760, 18108351, 264763, 264764, 264288, 264768, 264789, 264691, 264692, 264693, 264628, 264634, 264635, 264555, 264638, 264638, 264639
264	67370826 (527, 528)	Novel Protein sim. GBank gll3043734[db BAA25531] - (AB011177) KIAA0605 protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	protease	264259, 264908, 21908754, 265018, 265019, 265020

265	95355646 (528, 530)	Novel Protein sim. GBank gij4589624[dbj BAA76834.1] - (AB023207) KIAA0980 protein [Homo sapiens]		kinase	264488, 35686286, 29331824, 56182181, 35696052, 264508, 264905, 264908, 264907, 66712502, 264908, 264809, 264511, 264512, 264910, 264592, 264595, 264758, 264586, 55811386, 264600, 265017, 264603, 264604, 264605, 264760, 18108351, 264762, 264681, 264764, 264288, 264768, 264768, 264769, 21908765, 21908767, 21908769, 265020, 264691, 33657023, 33657109, 33657182, 264628, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 83373044, 56526488, 87168518, 264584, 264586, 264488
266	79588075 (531, 532)			UNCLASSIFIED	264800
267	11382222 (533, 534)			UNCLASSIFIED	264828
268	79809568 (535, 536)			UNCLASSIFIED	264687, 264769, 264689
269	80025810 (537, 538)			UNCLASSIFIED	264602
270	84361144 (539, 540)	Novel Protein sim. GBank gij4507387[ref NP_003182.1 pTARS - threonyl-tRNA synthetase		UNCLASSIFIED	264693
271	79552301 (541, 542)			UNCLASSIFIED	264909, 264693
272	8674778 (543, 544)	Novel Protein sim. GBank gij4980738[gb AAD35331.1 AE00170 - (AE001707) glucose-1-phosphate adenylyltransferase [Thermotoga maritima]		synthase	264908
273	12840694 (545, 546)	Novel Protein sim. GBank gij1168224[sp P44569 5NTD_HAEIN - PROBABLE 5'-NUCLEOTIDASE PRECURSOR		UNCLASSIFIED	264688
274	39524246 (547, 548)				264564
275	82787041 (549, 550)	Novel Protein sim. GBank gij3253159 (AF005355) - translation initiation factor eIF2C [Oryctolagus cuniculus]		UNCLASSIFIED	264807, 264908, 264909, 264766, 264788, 264691, 264632, 264636
276	86671073 (551, 552)	Novel Protein sim. GBank gij134920[sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			265008, 60432229
277	80078735 (553, 554)	Novel Protein sim. GBank gij128021[sp P20964 OBG_BACSU - SPO0B-ASSOCIATED GTP-BINDING PROTEIN		ribosomal prot	264600, 18108387
278	12966947 (555, 556)			UNCLASSIFIED	264689
279	95292719 (557, 558)	Novel Protein sim. GBank gij79839[pir IS03812 - vvrB protein - Micrococcus luteus		nuclease	264508, 264604, 21906764, 264638, 264557, 264404
280	5603617 (559, 560)				264259
281	80249588 (561, 562)	Novel Protein sim. GBank gij3123180[sp Q18964 YLN2_CAEEL - HYPOTHETICAL 48.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II			18108392, 264634, 264555, 264556, 264557, 264558
282	18598682 (563, 564)			UNCLASSIFIED	265019
283	20814211 (565, 566)			UNCLASSIFIED	264555

284	91212160 (567, 568)	Novel Protein sim. GBank gll2428094 (U58632) - acetyl xylan esterase; AxeA (Thermotoga neapolitana)	Contains protein domain (PF00300) - Phosphoglycerate mutase family	UNCLASSIFIED	35696052, 28331828, 264508, 264905, 264600, 264602, 264605, 264682, 264764, 56181562, 21806764, 18108376, 264636, 264558, 18108387
285	8757940 (569, 570)	Novel Protein sim. GBank gll2072674[emb]CAB08305] - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	264603
286	80503235 (571, 572)	Novel Protein sim. GBank gll765323[bsb]157676 - (S74439) silk fibroin heavy chain (C-terminal) [Bombyx mori]; silkworms, Peptide Partial, 633 aa [Bombyx mori]		ATPase-associated	35696052, 264769, 264638
287	12745521 (573, 574)	Novel Protein sim. GBank gll1870009[emb]CAB06860] - (Z92539) hypothetical protein Rv1019 [Mycobacterium tuberculosis]		UNCLASSIFIED	264689
288	20756502 (575, 576)	Novel Protein sim. GBank gll1870009[emb]CAB06860] - (Z92539) hypothetical protein Rv1019 [Mycobacterium tuberculosis]		collagen	264557
289	80043804 (577, 578)	Novel Protein sim. GBank gll1870009[emb]CAB06860] - (Z92539) hypothetical protein Rv1019 [Mycobacterium tuberculosis]	Contains protein domain (PF00440) - Bacterial regulatory proteins, telR family		264593, 264600
290	80430175 (579, 580)	Novel Protein sim. GBank gll2506684[sp]P40120[YDCG ECOLI - 59.4 PROTEIN IN TRG-RIML INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264768
291	20747431 (581, 582)	Novel Protein sim. GBank gll1870009[emb]CAB06860] - (Z92539) hypothetical protein Rv1019 [Mycobacterium tuberculosis]		UNCLASSIFIED	264601
292	80052555 (583, 584)	Novel Protein sim. GBank gll1870009[emb]CAB06860] - (Z92539) hypothetical protein Rv1019 [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
293	80062519 (585, 586)	Novel Protein sim. GBank gll1718085[sp]P53528[UVRD_MYCLE - PUTATIVE DNA HELICASE II HOMOLOG		UNCLASSIFIED	264908, 264605, 264687, 264688, 264692
294	79830303 (587, 588)	Novel Protein sim. GBank gll117422[sp]P10040[CRB_DROME - CRUMBS PROTEIN PRECURSOR (95F)	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696052, 264906, 265011, 264628, 55811576
295	79444180 (589, 590)	Novel Protein sim. GBank gll1181619[db]BAA11565] - (D82384) a variant of TSC-22 [Gallus gallus]			52644507, 28331822, 264592, 265020, 264639
296	79607076 (591, 592)	Novel Protein sim. GBank gll3649789[db]BAA33403] - (AB012226) SecA [Vibrio alginolyticus]		synthase	264508
297	79631297 (593, 594)	Novel Protein sim. GBank gll5689967[emb]CAB52004.1] - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264905, 264687, 264638
298	80418898 (595, 596)			UNCLASSIFIED	264905, 264691, 264639, 264766

299	95293298 (597, 598)	Novel Protein sim. GBank gij220837[idj]BAA01477] - (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	264488, 263994, 56994075, 22278987, 22278998, 22278999, 20281099, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264906, 264907, 264908, 52644045, 264909, 264511, 265008, 264910, 264595, 264596, 264758, 33657084, 87168559, 265018, 265019, 264764, 264288, 264766, 264687, 58181582, 264769, 21908765, 21908768, 21908769, 33657023, 264092, 33657109, 27408261, 18108370, 264628, 264629, 55811576, 35695855, 264631, 264634, 264635, 264638, 264639, 63373044, 18108387, 87168518, 22278000, 22279002, 264585, 264586, 264587
300	20711340 (599, 600)		UNCLASSIFIED	264602
301	13511332 (601, 602)	Novel Protein sim. GBank gij145922 (M20981) - Iron diclitate transport protein precursor [Escherichia coli]	transport	264687
302	9875260 (603, 604)	Novel Protein sim. GBank gij1174661[sp]P44594[GTG] - HAEIN - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)		264908
303	79574895 (605, 606)			264689
304	20711344 (607, 608)	Novel Protein sim. GBank gij67985[pil]HJNVAV - helicase (EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus	helicase	264602
305	80412520 (609, 610)	Novel Protein sim. GBank gij728867[sp]P40602[APG] ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		264763
306	8515876 (611, 612)	Novel Protein sim. GBank gij1657554[gb]AAB18082.1] - (U73857) hypothetical protein [Escherichia coli]	UNCLASSIFIED	263978
307	80222901 (613, 614)		UNCLASSIFIED	265010, 21908768, 265020, 18108374, 263977
308	80064305 (615, 616)	Novel Protein sim. GBank gij1710812[sp]Q10793[RNH2] MYCTU - PROBABLE RIBONUCLEASE HII (RNASE HII)	Contains protein domain (PF01351) - Ribonuclease HII	264910, 264600, 264605, 264687, 264689, 264638, 18108387
309	80504138 (617, 618)	Novel Protein sim. GBank gij5420387[emb]CAB46678.1] - (A243459) proteophosphoglycan [Leishmania major]		264769
310	80053616 (619, 620)			264603
311	11090659 (621, 622)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]	synthase	264602
312	80054347 (623, 624)		UNCLASSIFIED	264566
313	80046168 (625, 626)			264603, 264567

314	87645112 (627, 628)	Novel Protein sim. GBank gij3561583 (AF092175) - ikaros [Danio rerio]	Contains protein domain (PF00320) - GATA zinc finger	dna_rna_bind	264259, 60432289, 29331828, 264905, 264906, 264908, 264909, 265008, 264910, 60432229, 33657402, 60433438, 33109854, 265011, 265017, 264603, 265018, 264288, 264766, 264692, 35695763, 264628, 264829, 264639, 60170394, 22279002, 264566
315	82356091 (629, 630)	Novel Protein sim. GBank gij1652620[dj]BAA17540] - (D90907) pyridine nucleotide transhydrogenase beta subunit [Synechocystis sp.]			264508, 264600, 264762, 264687, 264768, 52644229, 264769, 264689, 264635, 264636, 264638, 264486
316	78911071 (631, 632)	Novel Protein sim. GBank gij118244]spjP24176]DAPE, ECOLI - SUCCINYL-DIAMINOPIMELATE DESUCCINYLAISE (SDAP)	UNCLASSIFIED	UNCLASSIFIED	264693
317	20466944 (633, 634)	Novel Protein sim. GBank gij4680229]gibjAAD27583.1]AF11927 - (AF118274) DNB-5 [Homo sapiens]	Contains protein domain (PF00526) - Dictyostellum (slime mold) repeats	transport	264805
318	94141836 (635, 636)	Novel Protein sim. GBank gij17289360 (637, 638)		transport	264908, 264909, 264910, 264593, 264594, 264760, 264288, 264768, 264769, 21906769, 264691, 264693, 264628, 65274791, 264635, 264636, 264638, 83373044, 22279002, 264566
319	17289360 (637, 638)	Novel Protein sim. GBank gij1149693]embjCAA60220] - (X86499) rbsC [Clostridium perfringens]		synthase	265018
320	13527675 (639, 640)	Novel Protein sim. GBank gij2811033]spjO05314]GLGC, MYCTU - GLUCOSE-1-PHOSPHATE ADENYLTRANSFERASE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLAISE)			264687
321	94134387 (641, 642)	Novel Protein sim. GBank gij1680716 (U68234) - all-trans-retinoic acid 4-hydroxylase [Danio rerio]		cyto450	264509, 264906, 264907, 264908, 265009, 264596, 264764, 264628, 264634, 264635, 264638, 264639, 83373044, 264567
322	66489053 (643, 644)	Novel Protein sim. GBank gij1160355 (U33058) - UNC-89 [Caenorhabditis elegans]		UNCLASSIFIED	55811150, 264691, 60431528, 55810764
323	94653725 (645, 646)			UNCLASSIFIED	264488, 265009, 264593, 264628, 264635
324	79174383 (647, 648)			UNCLASSIFIED	264687
325	79862891 (649, 650)			UNCLASSIFIED	264693
326	28774974 (651, 652)			UNCLASSIFIED	264288, 18108385
327	79776267 (653, 654)	Novel Protein sim. GBank gij451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]			264488, 264805, 264509, 264910
328	80253202 (655, 656)			UNCLASSIFIED	264592
329	10173821 (657, 658)			UNCLASSIFIED	264510
330	86597767 (659, 660)	Novel Protein sim. GBank gij4191358 (AF087825) - claudin-7 [Mus musculus]		UNCLASSIFIED	264259, 264908
331	79754888 (661, 662)	Novel Protein sim. GBank gij80741]pirjS20912 - regulatory protein whiB - Streptomyces coelicolor		transcriptfactor	264910, 264687, 264689, 264636, 264567
332	80071440 (663, 664)	Novel Protein sim. GBank gij114049]spjP19480]AHPF_SALTY - ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F (ALKYL HYDROPEROXIDE REDUCTASE F52A PROTEIN)		reductase	35696423, 264636, 264638, 264565
333	13009555 (665, 666)				264687

334	80230771 (667, 668)	Novel Protein sim. GBank gij3222228jiprj[S32227 - glutamate dehydrogenase (NADP+)] (EC 1.4.1.4) - Corynebacterium glutamicum	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264805, 264600, 264604, 264486
335	80057026 (668, 670)	Novel Protein sim. GBank gij2193638jemb[CAB09802] - (Z96800) glpQ2 [Mycobacterium tuberculosis]		esterase	264907, 264803, 264683, [18108374, 264636, 18108387]
336	80414319 (671, 672)			UNCLASSIFIED	265009, 264766, 264686
337	11080829 (673, 674)				264502
338	95413134 (675, 676)	Novel Protein sim. GBank gij5454074ref[NP_006303.1pSMRT - silencing mediator for retinoid and thyroid hormone receptors	Contains protein domain (PF00249) - Myb-like DNA-binding domain	nud_rept	264569, 18108397, 22278998, 29331822, 20281099, 29331824, 56182181, 68714117, 29331825, 35696052, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 265008, 264910, 265009, 264758, 55812038, 65274444, 265011, 87168559, 265017, 265018, 265019, 264780, 55811150, 264681, 264762, 18108351, 264682, 264764, 264766, 264685, 264686, 264768, 52644229, 264689, 55811957, 35695917, 264692, 264693, 264628, 18108370, 18108374, 55811578, 35696423, 35695855, 264635, 264555, 264636, 264556, 264637, 264557, 18108380, 264638, 264558, 264639, 18108381, 83373044, 18108385, 87168518, 60432113
339	11398513 (677, 678)	Novel Protein sim. GBank gij4001713jdbj[BAA35087.1] - (AB015879) DnaK [Porphyrromonas gingivalis]		eph	264593
340	80504149 (679, 680)	Novel Protein sim. GBank gij2842699isp[Q92353]UBPC_SCHPO - PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C8G9.08 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)		ubiquitin	264905, 265019, 264769, 18108374
341	11075188 (681, 682)	Novel Protein sim. GBank gij2688580 (AE001166) - conserved hypothetical protein [Borrelia burgdorferi]	Contains protein domain (PF00290) - Tryptophan synthase alpha chain	isomerase	264605
342	80054186 (683, 684)	Novel Protein sim. GBank gij1684738jemb[CAA70601] - (Y09452) Yed J hypothetical protein [Pseudomonas syringae]			264603, 264604
343	20466782 (685, 686)				264605
344	80428870 (687, 688)	Novel Protein sim. GBank gij2117275jemb[CAB09104] - (Z95818) hypothetical protein Rv0807 [Mycobacterium tuberculosis]		UNCLASSIFIED	264600, 264605, 264768, 18108370, 18108374, 35695855
345	80258853 (689, 690)	Novel Protein sim. GBank gij3023317isp[Q48935]APHA_MYCRA - ACETYL POLYAMINE AMINOHYDROLASE		histone	264593
346	79831058 (691, 692)	Novel Protein sim. GBank gij4239787jemb[CAA75437] - (Y15166) NADP-glutamate dehydrogenase [Pseudomonas aeruginosa]	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264905



347	79158195 (693, 694)	Novel Protein sim. GBank gll731675 sp P38795 YHN4_YEAST - HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION		UNCLASSIFIED	265006, 265008, 265010, 265018, 263987, 263981
348	80020208 (695, 696)	Novel Protein sim. GBank gll1073610 pir S47672 - ugpB protein - Escherichia coli		transport	264602, 18108351, 18108387
349	17282112 (697, 698)	Novel Protein sim. GBank gll3261599 emb CAB009171 - (Z77137) hypothetical protein Rv1277 (Mycobacterium tuberculosis)		nuclease	265007 265008, 264769, 264689, 18108370
350	80502370 (699, 700)	Novel Protein sim. GBank gll2959367 emb CAA179211 - (AL022117) hypothetical protein [Schizosaccharomyces pombe]		glycoprotein	264769, 264805, 264808
351	80501805 (701, 702)	Novel Protein sim. GBank gll4416302 gb AAD203071 - (AF105716) copia-type pol polyprotein [Zea mays]		protease	264595
352	11811585 (703, 704)	Novel Protein sim. GBank gll1174887 sp P42873 URE1_STAXY - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) - Urease	UNCLASSIFIED	264604
353	80061653 (705, 706)	Novel Protein sim. GBank gll115157 sp P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA	Contains protein domain (PF00072) - Response regulator receiver domain	UNCLASSIFIED	264628
354	56926130 (707, 708)	Novel Protein sim. GBank gll497637 (J03939) - cytochrome oxidase d subunit I [Escherichia coli]		oxidase	264605
355	80046344 (709, 710)	Novel Protein sim. GBank gll2290990 (AF006000) - Brg1 [Bordetella pertussis]		UNCLASSIFIED	264768
356	80043835 (711, 712)	Novel Protein sim. GBank gll3510639 (AF049344) - UDP- GalNAc:polypeptide N-acetylglucosaminyltransferase T5 [Rattus norvegicus]		UNCLASSIFIED	264604, 264769
357	80070568 (713, 714)	Novel Protein sim. GBank gll113764 sp P25718 AMY1_ECOLI - ALPHA-AMYLASE PRECURSOR (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		UNCLASSIFIED	264594
358	37032756 (715, 716)	Novel Protein sim. GBank gll113764 sp P25718 AMY1_ECOLI - ALPHA-AMYLASE PRECURSOR (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		transferase	22278998, 264259, 29331822, 29331824, 264605, 55811957, 265022
359	80501488 (717, 718)	Novel Protein sim. GBank		amylase	264688
360	80026748 (719, 720)	Novel Protein sim. GBank			
361	80584075 (721, 722)	Novel Protein sim. GBank			
362	13089485 (723, 724)	Novel Protein sim. GBank			
363	78750145 (725, 726)	Novel Protein sim. GBank			
364	82443593 (727, 728)	Novel Protein sim. GBank gll2829816 sp P95171 NUOK_MYCTU - NADH DEHYDROGENASE I CHAIN K (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11)	Contains protein domain (PF00420) - NADH-ubiquinone/plastoquinone oxidoreductase chain 4L	dehydrogenase	264568 264789, 264602, 264604, 264508, 264762, 264638, 264486

365	88040288 (729, 730)	Novel Protein sim. GBank gij4929268 gb AAD33924.1  - (AF144237) LOMP protein [Homo sapiens]	Contains protein domain (PF00412) - LIM domain containing proteins	264488, 21906766, 21906767, 55811576, 21906769, 26148629, 22278985, 22278986, 265020, 265022, 264634, 264891, 264593, 33857023, 33857402, 264693, 264639, 264594, 29331824, 264758, 18108385, 29331827, 87168559, 265018, 22279000, 265019, 264482, 264761, 264681, 18108351, 265017, 264757
366	81821838 (731, 732)	Novel Protein sim. GBank gij4503843 re NP_003908.1 pG2AD - UNKNOWN	Contains protein domain (PF01802) - glycoprotein	26424179, 65274572, 56182575, 22278994, 56984075, 22278998, 264259, 29331822, 29331824, 56182181, 60424289, 68714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264905, 264828, 56182435, 285008, 264512, 265008, 264591, 55812038, 55813868, 265010, 87168559, 265017, 265018, 264604, 265019, 55811550, 264448, 264369, 264288, 264688, 264768, 56181582, 21906768, 21906769, 55811957, 35885917, 265022, 60170615, 33857023, 65274620, 18108365, 263967, 33857109, 33857349, 35895763, 264828, 18108376, 55811576, 65274791, 35895855, 56182323, 83373044, 60432113, 264563, 264564, 264567
367	95357471 (733, 734)			
368	79607265 (735, 736)	Novel Protein sim. GBank gij3913029 sp P94967 ALR_MYCSM - ALANINE RACEMASE	UNCLASSIFIED	264509
369	95292917 (737, 738)	Novel Protein sim. GBank gij3249559 (AF018261) - EH domain binding protein Epsin [Rattus norvegicus]	UNCLASSIFIED	264508, 264604, 264605, 264636
370	88090966 (739, 740)	Novel Protein sim. GBank gij2995299 emb CAA18328  - (AL022268) putative tRNA delta(2)-isopentenylpyrophosphate transferase [Streptomyces coelicolor]	UNCLASSIFIED	264805, 264592, 264603, 264766, 264691
371	95292599 (741, 742)	Novel Protein sim. GBank gij5456934 gb AAD43716.1  - (AF182322) protocadherin gamma A2 [Homo sapiens]	transferase	264805, 264806, 264510, 264600, 264601, 264602, 264603, 265018, 264604, 264605, 265021, 264692, 264636, 264564
372	80021107 (743, 744)	Novel Protein sim. GBank gij2506393 sp P31576 FIXX_ECOLI - FERREDOXIN LIKE PROTEIN		264564
373	79863766 (745, 746)	Novel Protein sim. GBank gij3341640 emb CAA13164  - (AJ231122) z61f [Vibrio cholerae]	UNCLASSIFIED	264809
374	78847568 (747, 748)	Novel Protein sim. GBank gij5456934 gb AAD43716.1  - (AF182322) protocadherin gamma A2 [Homo sapiens]	UNCLASSIFIED	264905, 264906
375	91230181 (749, 750)	Novel Protein sim. GBank gij1805408 dbj BAA08970  - (D50453) homologues to nitrile hydratase region 3'-hypothetical protein P47K of P. chlororaphis [Bacillus subtilis]	cadherin	65274572, 264259, 29331826, 56182435, 60433356, 60433438, 264757, 55812038, 264758, 55811957, 264690, 33857023
376	80505214 (751, 752)		UNCLASSIFIED	264769
377	10339083 (753, 754)			264906

378	80056153 (755, 756)	Novel Protein sim. GBank gij1076013 pir A49930 - carB protein homolog - <i>Mycobacterium bovis</i> (strain BCG) (fragment)	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	UNCLASSIFIED	265008, 264555
378	80503437 (757, 758)	Novel Protein sim. GBank gij1076013 pir A49930 - carB protein homolog - <i>Mycobacterium bovis</i> (strain BCG) (fragment)	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	synthase	264769
380	80060837 (759, 760)	Novel Protein sim. GBank gij216556 dbj BAA02174 - (D12651) glucose dehydrogenase [Escherichia coli]	Contains protein domain (PF01011) - PQQ enzyme repeat	dehydrogenase	264604
381	11768027 (761, 762)			UNCLASSIFIED	264684
382	80054377 (763, 764)				264592
383	83259025 (765, 766)	Novel Protein sim. GBank gij3327136 dbj BAA31636 - (AB014561) KIAA0661 protein [Homo sapiens]			264595, 265017, 265021, 264638, 87168518, 22279002
384	95314255 (767, 768)			UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264288, 264786, 263987, 65274791, 35695855, 263981, 83373044, 264567
385	10237679 (769, 770)				264692
386	79633434 (771, 772)	Novel Protein sim. GBank gij1073456 pir S47810 - probable alcohol dehydrogenase (EC 1.1.1.1) - <i>Escherichia coli</i>	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases	dehydrogenase	264908
387	17960637 (773, 774)	Novel Protein sim. GBank gij1460074 emb CA801049 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]	Contains protein domain (PF01841) - Transglutaminase-like superfamily	UNCLASSIFIED	264760
388	87741376 (775, 776)	Novel Protein sim. GBank gij4240169 dbj BAA74863.1 - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	homeobox	35686286, 264905, 66712502, 60432229, 264593, 60433356, 264688, 264688, 21906765, 264691, 22279000, 264482
389	78316971 (777, 778)			UNCLASSIFIED	18108394, 22278996, 264630, 264556, 22279002
390	80079949 (779, 780)			UNCLASSIFIED	264600
391	7857302 (781, 782)	Novel Protein sim. GBank gij854065 emb CAA56337 - (X83413) U88 [Human herpesvirus 6]			264482
392	79786058 (783, 784)			UNCLASSIFIED	264908
393	33206031 (785, 786)	Novel Protein sim. GBank gij3378523 emb CAA08867 - (AJ009832) cyclomaltohexanase glucanotransferase [Thermotoga neapolitana]		synthase	264602, 21906764
394	10104463 (787, 788)				
395	80228010 (789, 790)			UNCLASSIFIED	264563
396	20436224 (781, 792)	Novel Protein sim. GBank gij2677780 (U70327) - unknown [Paretiplus polyactis]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	264556
397	80417014 (793, 794)	Novel Protein sim. GBank gij4507809 ref NP_000388.1 pWAS - Wiskott-Aldrich syndrome (eczema-thrombocytopenia)			265007, 265009, 264508, 264556, 264629, 264766
398	91230517 (795, 796)	Novel Protein sim. GBank gij1518458 (U45998) - mitochondrial solute carrier [Onchocerca volvulus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	18108398, 22278995, 22278996, 56994075, 22278999, 264259, 29331824, 29331826, 264905, 264908, 265007, 265008, 265009, 21906754, 33657084, 265017, 264448, 264288, 264766, 21906765, 21906766, 21908767, 265020, 265021, 33657023, 33657109, 264628, 35696423, 35695855, 264952, 18108380, 264567, 18108391

399	80055278 (797, 798)	Novel Protein sim. GBank gij3356081 dbj BAA31995  - (AB015974) glycerol kinase [Pseudomonas tolaasii]	Contains protein domain (PF00370) - kinase FGGY family of carbohydrate kinases	264592, 264595
400	84117480 (799, 800)	Novel Protein sim. GBank gij728635 sp P39192 ALU5_HUMAN - !!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!	Contains protein domain (PF00560) - cadherin Leucine Rich Repeat	18108394, 56182575, 22278895, 22278897, 22278899, 264259, 26331824, 265006, 265007, 265009, 60432228, 33657402, 21806754, 265010, 265017, 265018, 265019, 18108351, 18108357, 21906765, 265021, 265022, 264691, 264692, 33657023, 18108370, 65274791, 264634, 264636, 60170394, 56182323
401	11397491 (801, 802)	Novel Protein sim. GBank gij4928292 gb AAD33527.1 AF13211 - (AF132117) FhuA [Staphylococcus aureus]	transport	264594
402	85420264 (803, 804)	Novel Protein sim. GBank gij5689487 dbj BAA83027.1  - (AB028998) KIAA1075 protein [Homo sapiens]	Contains protein domain (PF00017) - phosphatase Src homology domain 2	65274572, 56182575, 35686286, 22278898, 22278899, 264093, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264906, 264907, 264908, 265006, 264511, 285007, 265008, 264910, 264591, 33657402, 60433356, 60433438, 264596, 21806754, 52644286, 265010, 265011, 87168559, 265017, 265018, 265019, 284681, 18108351, 264692, 284448, 264288, 264684, 264766, 264767, 264686, 21806765, 21906766, 21808767, 21808768, 21806769, 55811957, 265020, 265021, 265022, 264690, 264693, 65274620, 35695763, 264628, 18108370, 264629, 18108379, 35698423, 55811576, 264635, 264636, 264557, 264639, 18108385, 22279002, 264563, 264564, 264565, 264566
403	80439913 (805, 806)		UNCLASSIFIED	264768, 264632, 264639, 264563
404	11809865 (807, 808)			264682
405	79471280 (809, 810)	Novel Protein sim. GBank gij2661649 emb CAA15755  - (AL009198) dnaE2 [Mycobacterium tuberculosis]	polymerase	265009, 264682
406	78634172 (811, 812)		Contains protein domain (PF00159) - Pancreatic hormone peptides	18108357, 264693
407	80478229 (813, 814)		UNCLASSIFIED	264769
408	80079956 (815, 816)		UNCLASSIFIED	264600
409	5640527 (817, 818)	Novel Protein sim. GBank gij3047117 (AF058919) - similar to ATP-dependent RNA helicases [Arabidopsis thaliana]	helicase	264259

410	95357488 (819, 820)	Novel Protein sim. GBank gij475016[dbj BAA06184] - (D28801) Unknown [Mus musculus]		UNCLASSIFIED	264489, 52646365, 52646842, 56181686, 35696286, 52645080, 29331822, 29331824, 56182181, 29331825, 60424289, 35696052, 33656970, 264508, 264509, 264905, 264906, 264907, 264908, 52644045, 264909, 264510, 265007, 264512, 285008, 264910, 33657402, 264758, 52646317, 55811386, 265010, 285011, 285017, 264604, 285018, 55811150, 284762, 284764, 264768, 264687, 264768, 264769, 52644228, 21806768, 285020, 265021, 264534, 52644150, 264692, 33657023, 65274620, 33657109, 33657182, 27486281, 35695783, 264628, 264629, 60431528, 18108376, 263978, 35696423, 35695855, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 56182323, 264559, 60432113, 22279002, 264563, 264565, 264486
411	80501870 (821, 822)			UNCLASSIFIED	264769
412	80241662 (823, 824)				284907, 264910, 263973, 22278002
413	11076446 (825, 826)	Novel Protein sim. GBank gij3261784[emb CAB08897] - (Z95558) htpX [Mycobacterium tuberculosis]		eph	284605
414	82050554 (827, 828)	Novel Protein sim. GBank gij129038[sp P20707 ODO1_AZOVI - 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE)]		dehydrogenase	18108374, 264760, 264769, 264602, 264638, 264603, 264909, 264805
415	84453144 (829, 830)	Novel Protein sim. GBank gij4686350[gb AAD31273.1 AF13202 - (AF132025) rhophilin [Drosophila melanogaster]		UNCLASSIFIED	264908, 87168518
416	80402775 (831, 832)	Novel Protein sim. GBank gij2555172 (AF023543) - ArcC; carbamate kinase [Rhizobium etli]		kinase	264488, 264600, 264602, 264764, 264636
417	20153797 (833, 834)	Novel Protein sim. GBank gij170817[sp P52311 MTX2_XANOR - MODIFICATION METHYLASE XORII (CYTOSINE-SPECIFIC METHYLTRANSFERASE XORII) (M.XORII)]	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase		264605
418	94125841 (835, 836)			UNCLASSIFIED	264689, 264693
419	95314273 (837, 838)			collagen	264908, 264910, 264764, 264639
420	37036349 (839, 840)	Novel Protein sim. GBank gij3261659[emb CAB03751] - (Z81388) hypothetical protein Rv2419c [Mycobacterium tuberculosis]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	phosphatase	264769
421	95292842 (841, 842)	Novel Protein sim. GBank gij2916942[emb CAA17580] - (AL021999) hypothetical protein Rv0991 [Mycobacterium tuberculosis]	Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	264908, 264600, 264601, 264603, 264604, 264760, 264769
422	78471293 (843, 844)	Novel Protein sim. GBank gij231752[sp Q00767 CH61_STRAL - 80 KD CHAPERONIN 1 (PROTEIN CPN60 1) (GROEL PROTEIN 1) (HSP58)]	Contains protein domain (PF00118) TCP-1/cpn60 chaperonin family	eph	22278996, 264682, 18108376, 18108387
423	78604948 (845, 846)			UNCLASSIFIED	264509

424	78966557 (847, 848)	Novel Protein sim. GBank gi 4826814 ref NP_004977.1 p KTIN1 - kinesin 1 (kinesin receptor)		struct	265019
425	80431450 (849, 850)	Novel Protein sim. GBank gi 170370 bb s 178462 - KRP5=kinesin-related protein (rats, testes, Peptide Partial, 167 aa)	Contains protein domain (PF00225) - Kinesin motor domain	struct	264908, 265007, 55811386, 264768, 55810764
426	80064522 (851, 852)				264605, 264559
427	80057232 (853, 854)	Novel Protein sim. GBank gi 231829 sp P29929 COBN_PSEDE - COBN PROTEIN		UNCLASSIFIED	264603, 264636
428	78487788 (855, 856)	Novel Protein sim. GBank gi 81286 p S22697 - extensin - Volvox carterii (fragment)		UNCLASSIFIED	264683
429	80091252 (857, 858)	Novel Protein sim. GBank gi 1808154 emb CAB08451 - (Z84395) hypothetical protein Rv0588 [Mycobacterium tuberculosis]		UNCLASSIFIED	35698423, 35695763, 35695855, 265017, 264584, 264782
430	80504192 (859, 860)	Novel Protein sim. GBank gi 1808154 emb CAB08451 - (Z84395) hypothetical protein Rv0588 [Mycobacterium tuberculosis]		reductase	264508, 264805, 264509, 264808, 264809, 265008, 264800, 264887, 264789, 264689, 264636, 264638, 18108385, 264486
431	20824249 (861, 862)				264566
432	16523372 (863, 864)				265020
433	81484303 (865, 866)	Novel Protein sim. GBank gi 3123552 emb CAA18608 - (AL022578) DJ393P12.2 (hypothetical Proline-rich protein - KIAA0269 LIKE) [Homo sapiens]		UNCLASSIFIED	264907, 264908, 264909, 264910, 264592, 264595, 264758, 264804, 264760, 264762, 264763, 264636, 264837, 22279002
434	94326323 (867, 868)	Novel Protein sim. GBank gi 2495272 sp Q99826 CDX2_HUMAN - HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3)	Contains protein domain (PF00189) - PH domain	UNCLASSIFIED	55812038, 56182181, 58181562, 29331828, 35698052, 55810764, 55811576, 65274791, 35695855, 80432113, 55811150, 264636, 264768
435	80502738 (869, 870)	Novel Protein sim. GBank gi 114105 sp P08532 ARAH_ECOLI - L-ARABINOSE TRANSPORT SYSTEM PERMEASE PROTEIN ARAH		transport	264595, 264789
436	41085953 (871, 872)			UNCLASSIFIED	265020, 22279002
437	11399291 (873, 874)			UNCLASSIFIED	264593
438	11773835 (875, 876)			UNCLASSIFIED	264688
439	80019495 (877, 878)	Novel Protein sim. GBank gi 3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana]			264905, 264600, 264602, 264604
440	79841062 (879, 880)	Novel Protein sim. GBank gi 2281232 gb AAB65351.1 - (AF016427) Contains similarity to Pfam domain: PF00004 (AAA), Score=268.1, E-value=3.7e-77, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00004) - ATPases associated with various cellular activities (AAA)	ATPase-associated	35698052, 264905, 264808, 264909, 265011, 35698423
441	20398935 (881, 882)	Novel Protein sim. GBank gi 5639846 gb AAD45904.1 AF16132 - (AF16132) histidine kinase CstS [Corynebacterium diphtheriae]			264605
442	85281058 (883, 884)	Novel Protein sim. GBank gi 1184790 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264909
443	82456427 (885, 886)	Novel Protein sim. GBank gi 5689893 emb CAB52056.1 - (AL109732) putative ATP-binding RNA helicase [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	35698052, 264508, 264808, 264512, 264604, 264782, 264769, 264689, 264636
444	11395897 (887, 888)	Novel Protein sim. GBank gi 1783249 db BAA11726 - (D63026) homologous to citrate-sodium symport (citrate transporters), hypothetical [Bacillus subtilis]		UNCLASSIFIED	264591

445	79552709 (889, 890)	Novel Protein sim. GBank gij5531272[embjCAB50897.1]- (A243800) WSC4 homolog [Kluyveromyces fragilis]		UNCLASSIFIED	264693
446	78810937 (891, 892)	Novel Protein sim. GBank gij538413 (L36315) - zinc finger protein [Mus musculus]	Contains protein domain (PF00098) - zinc finger, C2H2 type		264509
447	80438888 (893, 894)	Novel Protein sim. GBank gij1542814[embjCAB02185] - (Z80108) fms [Mycobacterium tuberculosis]	Contains protein domain (PF00551) - formyl transferase	transcript factor	264768, 55811576
448	80238110 (895, 896)	Novel Protein sim. GBank gij118794[spjP10443]DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		dehydrogenase	264508, 264600, 264803, 264605, 264682, 264769, 18108362, 264634, 18108387
449	20460634 (897, 898)	Novel Protein sim. GBank gij118794[spjP10443]DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	264605, 264559
450	94631210 (898, 900)	Novel Protein sim. GBank gij458950[embjBAA76775.1] - (AB023148) KIAA0931 protein [Homo sapiens]	Contains protein domain (PF00481) - protein phosphatase 2C	phosphatase	65274572, 22278988, 29331824, 29331826, 264906, 264910, 264592, 52646317, 265017, 21906767, 55811957, 56528486, 22279002
451	21433609 (901, 902)	Novel Protein sim. GBank gij2850614 (AE001104) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	264486
452	10267278 (903, 904)	Novel Protein sim. GBank gij2493000[spjQ08450]SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3'-OXOACID COA-TRANSFERASE)		UNCLASSIFIED	264692
453	52560098 (905, 906)	Novel Protein sim. GBank gij2493000[spjQ08450]SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3'-OXOACID COA-TRANSFERASE)		UNCLASSIFIED	264907, 264600
454	39523922 (907, 908)	Novel Protein sim. GBank gij2493000[spjQ08450]SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3'-OXOACID COA-TRANSFERASE)		transferase	264603
455	13089692 (909, 910)	Novel Protein sim. GBank gij448689[embjCAB38153.1] - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]		UNCLASSIFIED	264687
456	78563081 (911, 912)	Novel Protein sim. GBank gij3411053 (AF034863) - synaptic scaffolding molecule [Rattus norvegicus]	Contains protein domain (PF00595) - POZ domain (Also known as DHR or GLGF)	UNCLASSIFIED	264691
457	79631273 (913, 914)	Novel Protein sim. GBank gij3411053 (AF034863) - synaptic scaffolding molecule [Rattus norvegicus]		UNCLASSIFIED	264905
458	78581227 (915, 916)	Novel Protein sim. GBank gij448689[embjCAB38153.1] - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]	Contains protein domain (PF00595) - POZ domain (Also known as DHR or GLGF)	kinase	55812038, 265010, 265018, 264681
459	80567359 (917, 918)	Novel Protein sim. GBank gij4506075[spjNP_002733.1]pPRKC - protein kinase C, mu	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	22278997, 264259, 29331826, 265018, 264448, 264369, 21906765, 35696423
460	78245890 (919, 920)	Novel Protein sim. GBank gij113158[spjP25516]ACO1_ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDRO-LYASE 1) (ACONITASE 1)		UNCLASSIFIED	264906
461	95287618 (921, 922)	Novel Protein sim. GBank gij1168574[spjP42464]ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	264602, 264605, 264768, 264769, 265021, 33857023, 264559

462	79606589 (923, 924)	Novel Protein sim. GBank gi11348891 slpIP45597 PTF1_XANCP - MULTIPHOSPHORYL TRANSFER PROTEIN (MTP) (CONTAINS: PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I); PHOSPHOCARRIER PROTEIN HPR (PROTEIN H); PTS SYSTEM, FRUCTOSE-SPECIFIC IIA COMPONENT ...	Contains protein domain (PF00391) - PEP-utilizing enzymes	284907
463	79796417 (925, 926)	Novel Protein sim. GBank gi1854065 emb CAA583371 - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	284905, 284908, 284909, 284910, 284591, 284595, 285011, 284632, 284635, 284636, 284637, 284638, 284639
464	82340151 (927, 928)	Novel Protein sim. GBank gi15689776 emb CAB52137.1 - (AJ242832) calpain [Homo sapiens]	UNCLASSIFIED	284834
465	83005730 (929, 930)	Novel Protein sim. GBank gi11806175 emb CAB06470 - (Z84395) rpsC [Mycobacterium tuberculosis]	Contains protein domain (PF00848) - Calpain family cysteine protease	265017, 21906764, 265020
466	20460645 (931, 932)	Novel Protein sim. GBank gi11806175 emb CAB06470 - (Z84395) rpsC [Mycobacterium tuberculosis]	Contains protein domain (PF00417) - Ribosomal protein S3, N-terminal domain.	284605, 284559
467	80408035 (933, 934)	Novel Protein sim. GBank gi1548705 slpIP36949 RRSB_BACSU - D-RIBOSE-BINDING PROTEIN PRECURSOR	UNCLASSIFIED	264764
468	52582208 (935, 936)	Novel Protein sim. GBank gi12114024 emb CAB08957 - (Z95558) grcC1 [Mycobacterium tuberculosis]	UNCLASSIFIED	284692
469	19520527 (937, 938)	Novel Protein sim. GBank gi12809459 emb CAA17347 - (AL021829) cobQ [Mycobacterium tuberculosis]	UNCLASSIFIED	284488
470	80502756 (939, 940)	Novel Protein sim. GBank gi114921 slpIP17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN	synthase	264602, 264769
471	17937351 (941, 942)	Novel Protein sim. GBank gi114921 slpIP17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN	transport	265019
472	80047458 (943, 944)	Novel Protein sim. GBank gi1862343 (L10908) - Gcap1 gene product [Mus musculus]	UNCLASSIFIED	284596, 284685, 284557
473	20558793 (945, 946)	Novel Protein sim. GBank gi1862343 (L10908) - Gcap1 gene product [Mus musculus]	UNCLASSIFIED	264369
474	80593385 (947, 948)	Novel Protein sim. GBank gi1543856 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	UNCLASSIFIED	22278897, 264682, 264288
475	82454665 (949, 950)	Novel Protein sim. GBank gi1543856 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	UNCLASSIFIED	264907, 284908, 284511, 265009, 284762, 264448, 284636, 264638
476	94143857 (951, 952)	Novel Protein sim. GBank gi1543856 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	glycoprotein	85274572, 60432049, 284259, 264508, 52644045, 55812038, 284758, 265011, 264288, 284686, 52844229, 65274791, 264638, 284586
477	79175933 (953, 954)	Novel Protein sim. GBank gi1543856 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	UNCLASSIFIED	284638
478	79633483 (955, 956)	Novel Protein sim. GBank gi1543856 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	UNCLASSIFIED	284690, 284693
479	80189746 (957, 958)	Novel Protein sim. GBank gi1543856 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	collagen	264686, 35695855, 265008, 264631, 264910, 264632, 264638, 265018, 264389, 284909
480	78390729 (959, 960)	Novel Protein sim. GBank gi1127551 (U18939) - orf2 [Batrachocottus baikalensis]	mapolymerase	264369
481	78624578 (961, 962)	Novel Protein sim. GBank gi14063042 (AF068065) - GP900; mucin-like glycoprotein [Cryptosporidium parvum]	UNCLASSIFIED	264693
482	83050611 (963, 964)	Novel Protein sim. GBank gi14063042 (AF068065) - GP900; mucin-like glycoprotein [Cryptosporidium parvum]	UNCLASSIFIED	284809, 284686, 264768, 284693, 55811576, 56182323, 18108385



483	20283306 (965, 966)	Novel Protein sim. GBank gij2104303[emb]CAB08632] - (Z95387) hypothetical protein Rv2610c [Mycobacterium tuberculosis]	Contains protein domain (PF00534) - Glycosyl transferases group 1		284600
484	11618048 (967, 968)	Novel Protein sim. GBank gij3450883 (AF083334) - fibrin [Antheraea pernyi]		UNCLASSIFIED	284594
485	80191234 (969, 970)	Novel Protein sim. GBank gij5042272[emb]CAB44526.1] - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]		UNCLASSIFIED	284369, 21908765, 22279000, 22279002
486	80059042 (971, 972)			dehydrogenase	284604
487	11813339 (973, 974)				284638
488	91222383 (975, 976)	Novel Protein sim. GBank gij5724778[gib]AAC53522.2] - (AF012273) rho-type GTPase-activating protein rhoGAPX-1 [Mus musculus]	Contains protein domain (PF00620) - RhoGAP domain		284686, 66714117, 284768, 18108385, 55811578, 265008, 265008, 265009, 265019, 22279002, 284259, 18108370, 264907, 264764, 56182323, 264288, 264693
489	10867710 (977, 978)	Novel Protein sim. GBank gij3882223[dbj]BAA34471.1] - (AB018294) KIAA0751 protein [Homo sapiens]		kinase	284639
490	95361124 (979, 980)	Novel Protein sim. GBank gij8209[ipir]A25494 - hydroxyproline-rich glycoprotein - tomato (fragment)		collagen	22278996, 29331822, 29331828, 264107, 264909, 264110, 265009, 264592, 264593, 60433358, 264288, 264693, 263974, 263976, 20281071, 60432113
491	80498412 (981, 982)	Novel Protein sim. GBank gij2894206[emb]CAA17072] - (AL021840) hypothetical protein Rv3258c [Mycobacterium tuberculosis]		UNCLASSIFIED	284769
492	87421264 (983, 984)				284600
493	11692942 (985, 986)			UNCLASSIFIED	284638
494	87726604 (987, 988)	Novel Protein sim. GBank gij5262605[emb]CAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]		UNCLASSIFIED	35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 33657402, 264762, 264764, 264768, 264769, 264688, 21908765, 21908769, 35695917, 265020, 264693, 33657109, 264629, 35696423, 35695855, 264634, 264638
495	80028599 (989, 990)	Novel Protein sim. GBank gij2791517[emb]CAA16054] - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]	Contains protein domain (PF00005) - ABC transporter	transport	284602, 264682, 264638
496	78985624 (991, 992)	Novel Protein sim. GBank gij230281[dbj]R169] - 434 Repressor (Amino-Terminal Domain) (R1-69)	Contains protein domain (PF01381) - Helix-turn-helix		284601, 265021
497	78949661 (993, 994)	Novel Protein sim. GBank gij128736[ip]P28225[PDXH_ECOLI - PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP)MP OXIDASE]		oxidase	265006

498	88095488 (995, 998)	Novel Protein sim. GBank gij1145789 (U41662) - neuroligin 2 [Rattus norvegicus]	Contains protein domain (PF00135) - Carboxylesterases	esterase	264259, 29331826, 35698052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265008, 264910, 264591, 33657402, 264758, 265010, 265011, 264600, 264601, 264605, 264683, 264764, 264766, 264767, 264768, 264687, 264769, 21908767, 33657023, 264693, 264628, 264629, 35696423, 264630, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 18108385, 264563, 264564, 264565, 264566, 264567
499	20438222 (897, 998)	Novel Protein sim. GBank gij97480[pri]S18739 - integral membrane protein - Rhodobacter capsulatus		UNCLASSIFIED	264605
500	11076810 (899, 1000)				264605
501	13418034 (1001, 1002)	Novel Protein sim. GBank gij5708250[emb]CAB52363.1] - (AL108747) putative integral membrane protein [Sireptomycetes coelicolor A3(2)]		UNCLASSIFIED	264688
502	80021176 (1003, 1004)	Novel Protein sim. GBank gij4486678[emb]CAB38132.1] - (AL035591) glucose-6-phosphate isomerase [Sireptomycetes coelicolor]	Contains protein domain (PF00342) - Phosphoglucose isomerase	isomerase	22278986, 265011, 264602, 264603, 264635
503	20284483 (1005, 1006)			UNCLASSIFIED	264564
504	10887321 (1007, 1008)			UNCLASSIFIED	264687
505	95003068 (1009, 1010)			UNCLASSIFIED	264369
506	16454282 (1011, 1012)	Novel Protein sim. GBank gij4033509[sp]P02598[CALM_TETPY - CALMODULIN	Contains protein domain (PF00036) - EF hand	struct	265010
507	20451588 (1013, 1014)	Novel Protein sim. GBank gij2501069[sp]Q46127[SYW_CLOLO - TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN-TRNA LIGASE) (TRPRS)		UNCLASSIFIED	264604
508	78841424 (1015, 1016)	Novel Protein sim. GBank gij466069[sp]P34618[YO82_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN ZK1236.2 IN CHROMOSOME III		UNCLASSIFIED	264908
509	11776385 (1017, 1018)				264638
510	83373465 (1019, 1020)			UNCLASSIFIED	264687, 264639
511	16525578 (1021, 1022)				265007
512	20389484 (1023, 1024)	Novel Protein sim. GBank gij2497419[sp]P55635[Y4RB_RHISM - PUTATIVE INTEGRASE/RECOMBINASE Y4RB		UNCLASSIFIED	264565
513	78457404 (1025, 1026)	Novel Protein sim. GBank gij12768897 (U41809) - cyclin J [Drosophila melanogaster]	Contains protein domain (PF00134) - Cyclin	cyclin	264683, 264688, 35696423, 264639
514	79813805 (1027, 1028)	Novel Protein sim. GBank gij1184790 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264909
515	78462581 (1029, 1030)				22278999, 264690
516	9862020 (1031, 1032)	Novel Protein sim. GBank gij2127400[pri]S65770 - maltotriose trehalase - Arthrobacter sp. (strain Q36)		amylase	264910

517	95292894 (1033, 1034)	Novel Protein sim. GBank gi 2983605 (AE000725) - ribose 5 phosphate isomerase B [Aquilifex aelificus]		isomerase	265018, 264605, 264764, 264766, 264687, 264691, 264565
518	8491831 (1035, 1036)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 8]		UNCLASSIFIED	264487
519	91677886 (1037, 1038)	Novel Protein sim. GBank gi 5689365 dbj BAA83073.1  - (AB024075) B120 [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	dna_rna_bind	52644507, 22278997, 22278998, 60432049, 264259, 52645080, 28331824, 88714117, 60424269, 28331826, 35696052, 264905, 29331830, 68712502, 264511, 265007, 264591, 60432228, 33657402, 60433438, 21908754, 33109854, 52644286, 87168474, 87168559, 265017, 265018, 264604, 265019, 264681, 264448, 264369, 264288, 264685, 21908765, 21908766, 21908767, 21908769, 265021, 60170615, 33657023, 264692, 52845129, 33657109, 27486262, 27486264, 35895763, 18108370, 264629, 52644332, 56182323, 264639, 83373044, 18108385, 56526486, 80432113
520	79859188 (1038, 1040)	Novel Protein sim. GBank gi 1169126 sp P46839 CTPA MYCLE - CATION-TRANSPORTING P-TYPE ATPASE A		transport	264789
521	11076821 (1041, 1042)	Novel Protein sim. GBank gi 1172669 sp P44331 RBSK_HAEN - RIBOKINASE	Contains protein domain (PF00284) - pfrB family carbohydrate kinase	kinase	264605
522	80435060 (1043, 1044)	Novel Protein sim. GBank gi 1172669 sp P44331 RBSK_HAEN - RIBOKINASE			264905, 264768
523	18356013 (1045, 1046)	Novel Protein sim. GBank gi 2132243 pir J591028 - hypothetical protein YPL236c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	264629
524	80261805 (1047, 1048)	Novel Protein sim. GBank gi 4033608 dbj BAA35136  - (AB012308) B2HC [Anthracis crassispina]		ATPase_associated	264092, 264596, 265011
525	76610046 (1048, 1050)	Novel Protein sim. GBank gi 4108610 emb CAA21365  - (AL031866) ORF42, len=386 aa, similarity to an aminotransferase, in P95957 Sulfolobus solfataricus, (401 aa), 33.1% identity in 393 aa overlap. FastA scores: opt:468, E(): 8.5e-24, in Q64602 R. norvegicus, (425 aa), 28.6% ident...		UNCLASSIFIED	264907
526	36827630 (1051, 1052)	Novel Protein sim. GBank gi 731088 sp P24215 UXUA_ECOLI - MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE)		UNCLASSIFIED	264758
527	80504728 (1053, 1054)	Novel Protein sim. GBank gi 731088 sp P24215 UXUA_ECOLI - MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE)		UNCLASSIFIED	264769
528	85484134 (1055, 1056)	Novel Protein sim. GBank gi 42144 emb CAA25200  - (X00513) NusA protein (nusA) [Escherichia coli]		UNCLASSIFIED	56182375, 265017, 265018
529	17836810 (1057, 1058)	Novel Protein sim. GBank gi 42144 emb CAA25200  - (X00513) NusA protein (nusA) [Escherichia coli]		hydrolase	265019
530	10887338 (1059, 1060)	Novel Protein sim. GBank gi 5262640 emb CAB45758.1  - (AL080170) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264687
531	80226576 (1061, 1062)	Novel Protein sim. GBank gi 5262640 emb CAB45758.1  - (AL080170) hypothetical protein [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	264555, 264556, 264557, 264558, 18108385
532	90933444 (1063, 1064)	Novel Protein sim. GBank gi 5262640 emb CAB45758.1  - (AL080170) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264488, 264489, 264259, 264592, 264760, 265021, 264690, 263976, 264558

533	87761531 (1065, 1066)	Novel Protein sim. GBank gi 4883636 gb AAD31593.1 AF11229 - (AF11229) Integral inner nuclear membrane protein MAN1 [Homo sapiens] (AJ001206) pep1 [Streptomyces coelicolor]			264907, 264909, 264768, 35685917, 264630, 264555
534	82368284 (1067, 1068)	Novel Protein sim. GBank gi 2899352 emb CAA04608.1  - (AJ001206) pep1 [Streptomyces coelicolor]	UNCLASSIFIED		264905, 265011, 264601, 264602, 264605, 264762, 264768, 265020, 264693, 264636 264906
535	79641850 (1069, 1070)	Novel Protein sim. GBank gi 3878636 emb CAA88953  - (Z49128) similar to cAMP-dependant protein kinase; cDNA EST EMBL: T00719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk49214.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		
536	79907207 (1071, 1072)	Novel Protein sim. GBank gi 2486828 sp P55757 YOH1_SERMA - HYPOTHETICAL 10.1 KD PROTEIN IN BIOA 5 REGION	reductase		18108376, 264805, 264908, 264807, 264909
537	84147448 (1073, 1074)	Novel Protein sim. GBank			265008, 264605, 65274791
538	87821863 (1075, 1076)	gi 134920 sp P21897 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	collagen		29331822, 29331824, 29331825, 29331826, 29331827, 264908, 52844045, 33657402, 265017, 264762, 264883, 264288, 264685, 21806765, 35685763, 264558, 60170394, 264559, 22279002 264602, 265019
539	28396269 (1077, 1078)	Novel Protein sim. GBank gi 24868433 sp Q12341 HAT1_YEAST - HISTONE ACETYLTRANSFERASE	histone		
540	76637077 (1078, 1080)	Novel Protein sim. GBank gi 3882241 dbj BAA34480.1  - (AB018303) KIAA0760 protein [Homo sapiens]	transcript factor		264893
541	87762268 (1081, 1082)		Contains protein domain (PF00096) - Zinc finger, C2H2 type		18108394, 22278897, 22278898, 264259, 264112, 265009, 33657402, 55812038, 52846317, 265017, 21908765, 264693, 55811578, 264635, 56528486, 264566 264910, 265018, 264688, 264638, 264486
542	95285838 (1083, 1084)	Novel Protein sim. GBank gi 5042272 emb CAB44526.1  - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]	dehydrogenase		
543	78788280 (1085, 1086)	Novel Protein sim. GBank gi 2791398 emb CAA15994  - (AL021184) hypothetical protein Rv1464 [Mycobacterium tuberculosis]	UNCLASSIFIED		264602, 264908
544	20437191 (1087, 1088)		UNCLASSIFIED		264605
545	80434504 (1089, 1090)	Novel Protein sim. GBank			
546	80248018 (1091, 1092)	gi 4887211 gb AAD3237.1 AF14744 - (AF14744) penicillin binding protein 1B [Pseudomonas aeruginosa]			264768, 264634, 264907, 264592, 264809 264600, 264602, 21908785
547	11077563 (1093, 1094)	Novel Protein sim. GBank gi 1350855 sp P19176 RPOC_PSEPU - DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT)	mapolymerase		264604
548	8214936 (1095, 1096)	Novel Protein sim. GBank gi 2330021 (AF019250) - kinesin- related protein; KRP; Costal2 [Drosophila melanogaster]	UNCLASSIFIED		264488, 264905, 264910, 264760, 264693, 264639, 264563, 264564

549	95421804 (1097, 1098)	Novel Protein sim. GBank gll4337460[gb]AAD181331 - (AF058195) neuroblastoma-amplified protein [Homo sapiens]		UNCLASSIFIED	264488, 65274572, 18108398, 22278995, 22278998, 22278997, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 29331826, 35686052, 265007, 265008, 264910, 264592, 33657402, 33109954, 265017, 265018, 265019, 18108351, 264448, 264764, 264368, 264288, 264768, 264686, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264691, 33657023, 264692, 264693, 65274620, 52645128, 33657108, 27486261, 27486262, 27486264, 33657349, 55811576, 18108397, 60432113, 22279002
550	10866816 (1099, 1100)	Novel Protein sim. GBank		UNCLASSIFIED	264688
551	80439980 (1101, 1102)	Novel Protein sim. GBank gll312893[sp]P94985[SYFB MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)]		UNCLASSIFIED	264908, 264909, 264768
552	94672870 (1103, 1104)	Novel Protein sim. GBank		UNCLASSIFIED	264689, 264639, 264563
553	80106002 (1105, 1106)	Novel Protein sim. GBank gll5019771[gb]AAD37857.1[AF13326 - (AF133263) histidine protein kinase-response regulator hybrid protein CvgSY (Pseudomonas syringae pv. syringae)]	Contains protein domain (PF000008) - EGF-like domain	glycoprotein	55811957, 264628
554	79618378 (1107, 1108)	Novel Protein sim. GBank gll131515[sp]P02908[PTGA_SALTY - PTS SYSTEM, GLUCOSE-SPECIFIC IIA COMPONENT (EIIA-GLC) (GLUCOSE-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIIA-GLC)]		kinase	264906
555	78966347 (1109, 1110)	Novel Protein sim. GBank gll3914014[sp]P96380[MFD MYCTU - TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)]	Contains protein domain (PF00358) - phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1	transport	264762
556	20457127 (1111, 1112)	Novel Protein sim. GBank gll5042273[emb]CAB44527.1[ - (AL078618) nuoE, NADH dehydrogenase subunit (Streptomyces coelicolor)]		transcriptfactor	284508, 264605, 264559
557	19523405 (1113, 1114)	Novel Protein sim. GBank gll170933[sp]P45331[METE_HAEIN - 5-METHYLTRAHYDROXYLTRYGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE)]		dehydrogenase	264488
558	20724428 (1115, 1116)	Novel Protein sim. GBank gll4980587[gb]AAD35173.1[AE001694] iron(III) ABC transporter, permease protein [Thermotoga maritima]		UNCLASSIFIED	264602
559	80084353 (1117, 1118)	Novel Protein sim. GBank		UNCLASSIFIED	264634

560	80066533 (1118, 1120)	Novel Protein sim. GBank gij2492595[sp]Q53193Y4TR_RHISN - PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TR	Contains protein domain (PF000005) - ABC transporter	transport	18108396, 264806, 264602, 264604, 18108374
561	20293187 (1121, 1122)			UNCLASSIFIED	264600
562	11698161 (1123, 1124)			UNCLASSIFIED	264689
563	79761420 (1125, 1126)	Novel Protein sim. GBank gij4104925 (AF042276) - poly(hydroxycalcinate) granule associated protein GA2 [Pseudomonas putida]		UNCLASSIFIED	264910, 264691
564	56716390 (1127, 1128)	Novel Protein sim. GBank gij2792310 (AF040570) - unknown [Amycolatopsis mediterranea]	dehydrogenase		264592
565	56465618 (1129, 1130)	Novel Protein sim. GBank gij3448294[dbj]BAA32462] - (AB011532) MEGF6 [Rattus norvegicus]	synthase		265010
566	94323888 (1131, 1132)	Novel Protein sim. GBank gij4539588[emb]CAB38487.1] - (AL035636) putative helicase [Streptomyces coelicolor]	helicase		264808, 264510, 265008, 264910, 264758, 264600, 264602, 264604, 264805, 264788, 264687, 264689, 35695917, 264693, 65274620, 264486
567	79560955 (1133, 1134)	Novel Protein sim. GBank gij100506[pir]S17455 - Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flaveria trinervia (fragment)	UNCLASSIFIED		264681, 264691, 264593
568	94681793 (1135, 1136)	Novel Protein sim. GBank gij3915843[sp]O31212[RS2_STRCO - 30S RIBOSOMAL PROTEIN S2	Malic enzyme		264689
569	39506897 (1137, 1138)	Novel Protein sim. GBank gij115122[sp]P21627[BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD	ribosomalprot		264565
570	78375927 (1139, 1140)	Novel Protein sim. GBank	Contains protein domain (PF00318) - Ribosomal protein S2		
571	79793981 (1141, 1142)	Novel Protein sim. GBank gij115122[sp]P21627[BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD	UNCLASSIFIED	transport	18108376, 18108387, 264565 264907, 264909
572	36986838 (1143, 1144)	Novel Protein sim. GBank gij453923[emb]CAB39881.1] - (AL049497) putative integral membrane protein [Streptomyces coelicolor]	UNCLASSIFIED		264762
573	20715521 (1145, 1146)	Novel Protein sim. GBank gij115122[sp]P21627[BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD	UNCLASSIFIED		265007, 264601
574	13521592 (1147, 1148)	Novel Protein sim. GBank			264636
575	13076416 (1149, 1150)	Novel Protein sim. GBank gij118794[sp]P10443[DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN	polymerase		264687
576	20482246 (1151, 1152)	Novel Protein sim. GBank gij5457625[emb]CAB49116.1] - (AJ248283) PAB2227 [Pyrococcus abyssi]			264605
577	66727102 (1153, 1154)	Novel Protein sim. GBank gij5042274[emb]CAB44528.1] - (AL078618) nuoD, NADH dehydrogenase subunit [Streptomyces coelicolor]	Contains protein domain (PF00346) - Respiratory-chain NADH dehydrogenase, 49 Kd subunit	dehydrogenase	35696052, 264636
578	11804477 (1155, 1156)	Novel Protein sim. GBank			264638
579	11794723 (1157, 1158)	Novel Protein sim. GBank gij1723081[sp]Q11046[Y089_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.09	transport		264682, 264556

580	80059417 (1159, 1160)				22278999, 35696052, 264555, 264556, 264558
581	79230833 (1161, 1162)			UNCLASSIFIED	265008, 264564
582	80049617 (1163, 1164)	Novel Protein sim. GBank gi 3243131 (AF045777) - ilin [Drosophila melanogaster]	Contains protein domain (PF00047) - situat immunoglobulin domain	struct	265021, 264555, 264557
583	78321392 (1165, 1166)	Novel Protein sim. GBank gi 2501162 sp P77726 YAJR_ECOLI - HYPOTHETICAL 49.0 KD PROTEIN IN ABPA-CYOE INTERGENIC REGION		transport	264594
584	79845024 (1167, 1168)	Novel Protein sim. GBank gi 3882221 dbj BAA34470.1  - (AB018293) KIAA0750 protein [Homo sapiens]		UNCLASSIFIED	264488, 264806, 264766, 264987, 35696423
585	79581454 (1169, 1170)			UNCLASSIFIED	265018, 264684, 21006769
586	38277486 (1171, 1172)	Novel Protein sim. GBank gi 4467250 emb CAB37575  - (AL035589) probable Glu-IRNA Gln amidotransferase subunit [Streptomyces coelicolor]		UNCLASSIFIED	264908, 265007
587	80497359 (1173, 1174)	Novel Protein sim. GBank gi 5689519 dbj BAA83043.1  - (AB028014) KIAA1091 protein [Homo sapiens]		hydrolase	264600, 264602, 264605, 264769, 264680, 264557
588	79557239 (1175, 1176)			UNCLASSIFIED	265020, 264692
589	79805828 (1177, 1178)			UNCLASSIFIED	
590	78815628 (1178, 1180)			UNCLASSIFIED	22278996, 264907, 264909, 264510, 265008, 265010, 264687, 264769, 35695917, 18108376, 264634, 264636, 264638
591	10313540 (1181, 1182)	Novel Protein sim. GBank gi 2143293 emb CAB09390  - (Z95972) rpoB [Mycobacterium tuberculosis]		UNCLASSIFIED	264906, 264909
592	13889767 (1183, 1184)	Novel Protein sim. GBank gi 4311983 gb AAD21543.1  - (AF088886) electrotransfer ubiquinone oxidoreductase [Zymomonas mobilis]		mapolymerase	264691
593	82346599 (1185, 1186)			MHC	263972
594	20212392 (1187, 1188)	Novel Protein sim. GBank gi 1272368 (U51896) - LfGE [Vibrio parahaemolyticus]		dehydrogenase	264511, 264762, 264769, 264486
595	10064064 (1189, 1190)	Novel Protein sim. GBank gi 131490 sp P20966 PTFB_ECOLI - PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU) (PHOSPHOTRANSFERASE IIBC COMPONENT) (COMPONENT) (EIIF-FRU)		UNCLASSIFIED	264605
596	13085170 (1191, 1192)				264769
597	80259003 (1193, 1194)			UNCLASSIFIED	264636
598	94140216 (1195, 1196)			UNCLASSIFIED	264592
599	20385137 (1197, 1198)	Novel Protein sim. GBank gi 125329 sp P04951 KDSB_ECOLI - 3-DEOXY-MANNO- OCTULONATE CYTIDYLTRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULONIC ACID SYNTHETASE) (CKS)		UNCLASSIFIED	264758, 55810764, 264555, 264556, 264637, 83373044
600	10357663 (1199, 1200)			UNCLASSIFIED	264603
601	78610404 (1201, 1202)	Novel Protein sim. GBank gi 2127414 pir J560064 - hypothetical protein 2 - Corynebacterium glutamicum		UNCLASSIFIED	264806, 264510

602	79250602 (1203, 1204)	Novel Protein sim. GBank gij3522961[gblAAC34243.1] - (AC004411) putative pto kinase [Arabidopsis thaliana]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	265007
603	11466067 (1205, 1206)			UNCLASSIFIED	264595
604	81675420 (1207, 1208)				264758
605	20436657 (1209, 1210)	Novel Protein sim. GBank gij1175322[spIP44917]Y883_HAEIN - HYPOTHETICAL PROTEIN H0883		UNCLASSIFIED	264605
606	80334562 (1211, 1212)	Novel Protein sim. GBank gij5020264[gblAAD38043.1]AF15136 - (AF151363) Cdc42 GTPase-activating protein [Mus musculus]		UNCLASSIFIED	264784
607	95361506 (1213, 1214)	Novel Protein sim. GBank gij180864 (M74027) - mucin [Homo sapiens]		UNCLASSIFIED	264508, 264908, 856558542, 264682, 264687, 264689, 264534, 18108376, 35696423, 264636, 264555, 264638
608	11810888 (1215, 1216)			UNCLASSIFIED	264682
609	80064775 (1217, 1218)	Novel Protein sim. GBank gij2496701[spIP55552]Y4LL_RHISN - HYPOTHETICAL 91.8 KD PROTEIN Y4LL	Contains protein domain (PF00989) - PAS domain	UNCLASSIFIED	264605
610	79629413 (1219, 1220)				264682
611	87586205 (1221, 1222)				264508, 264905, 264907, 264908, 264909, 264511, 264910, 264758, 264604, 264684, 264766, 264688, 264692, 264628, 264635, 264636, 264637, 264558
612	95287851 (1223, 1224)	Novel Protein sim. GBank gij1877366[emb]CAB07118] - (Z92772) recD [Mycobacterium tuberculosis]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	nuclease	264600, 264601, 264604, 264769, 264558, 264565
613	7523475 (1225, 1226)			UNCLASSIFIED	264369
614	79989348 (1227, 1228)	Novel Protein sim. GBank gij5114231[gblAAD40238.1]AF13670 - (AF136709) histidine kinase YycG [Staphylococcus aureus]		kinase	18108372, 264563
615	39586688 (1229, 1230)	Novel Protein sim. GBank gij1339950[dbj]BAA12741] - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]		synthase	264600, 264602, 264629
616	20465331 (1231, 1232)	Novel Protein sim. GBank gij544367[spIP35673]GALE_ERWAM - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		isomerase	264605
617	91227222 (1233, 1234)	Novel Protein sim. GBank gij2498087[spIQ60769]TNP3_MOUSE - TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20)	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	Inf	52645156, 21906765, 35696423, 21906768, 21906769, 22278994, 35696286, 22278996, 265020, 265021, 265007, 265008, 264638, 52644150, 33657023, 264692, 264693, 29331822, 29331824, 55812038, 83373044, 58182181, 60424268, 66714117, 29331825, 33657109, 29331826, 33657182, 29331827, 35696052, 29331828, 27486262, 33657349, 56526486, 265018, 265019, 22279002, 264482, 264448, 29331830, 66712502, 264909



618	20632843 (1235, 1236)	Novel Protein sim. GBank gij5459388[embjCAB50746.1] - (AL098839) putative aminotransferase [Streptomyces coelicolor]		isomerase	284603	
619	91227224 (1237, 1238)				56994075, 28331826, 33656970, 265008, 33657402, 33109954, 87108559, 264448, 18108374, 83373044	
620	81183143 (1239, 1240)	Novel Protein sim. GBank gij464335[spjQ05922]DUS2_MOUSE - DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 (DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1)		phosphatase	28148498, 264756, 264369, 29148627	
621	80239251 (1241, 1242)			UNCLASSIFIED	264558, 264558, 264639	
622	20456427 (1243, 1244)	Novel Protein sim. GBank gij2633557[embjCAB13060] - (Z89110) yjdf [Bacillus subtilis]		UNCLASSIFIED	264605	
623	10131798 (1245, 1246)	Novel Protein sim. GBank gij1857710[gbjAAB48482] - (U87224) contacin associated protein [Rattus norvegicus]	Contains protein domain (PF00054) - Laminin G domain	laminin	264906	
624	18534127 (1247, 1248)	Novel Protein sim. GBank gij1705703[spjP52225]CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK		cytochrome	264596	
625	13084619 (1249, 1250)	Novel Protein sim. GBank gij2894252[embjCAA17114.1] - (AL021841) hypothetical protein Rv3342 [Mycobacterium tuberculosis]		UNCLASSIFIED	264688	
626	88062603 (1251, 1252)	Novel Protein sim. GBank gij416592[spjP32323]AGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR		UNCLASSIFIED	29331822, 264905, 264908, 33657023, 33657109, 264558	
627	80255457 (1253, 1254)	Novel Protein sim. GBank gij3098418 (AF040944) - P140 [Mus musculus]		UNCLASSIFIED	18108394, 264112, 264593, 265022, 264635	
628	80077096 (1255, 1256)	Novel Protein sim. GBank gij1711543[spjP50526]SSP1_SCHPO - SERINE/THREONINE-PROTEIN KINASE SSP1	Contains protein domain (PF00069) - Kinase Eukaryotic protein kinase domain	kinase	264600	
629	78851602 (1257, 1258)	Novel Protein sim. GBank gij1143204 (U34305) - ORF2; Method: conceptual translation supplied by author. [Shigella sonnei]		isomerase	264906, 264907	
630	38565158 (1259, 1260)	Novel Protein sim. GBank gij3236368 (AF064748) - S3-12 [Mus musculus]		UNCLASSIFIED	264490	
631	20598718 (1261, 1262)	Novel Protein sim. GBank gij140887[spjP11666]YGBB_ECQLI - HYPOTHETICAL 30.9 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 4) (F286)			263978	
632	27843880 (1263, 1264)			UNCLASSIFIED	264908, 264600, 264605, 264769, 264689, 264488	
633	80477772 (1265, 1266)			UNCLASSIFIED	264769	
634	17938608 (1267, 1268)				265019	
635	78574508 (1269, 1270)			UNCLASSIFIED	264689	
636	79910981 (1271, 1272)			UNCLASSIFIED	264596, 264762, 264693	

637	82455796 (1273, 1274)	Novel Protein sim. GBank gi 2326739 emb CAB10953  - (Z98288) recN [Mycobacterium tuberculosis]		nuclease	264906, 264907, 264510, 264511, 264601, 264602, 264603, 264604, 264605, 18108351, 264762, 264766, 264687, 264769, 264689, 35695917, 264693, 264634, 264638, 264639, 264559, 18108385
638	14997457 (1275, 1276)	Novel Protein sim. GBank gi 467662 emb CAB1074.1  - (AL049845) putative large ATP-binding protein [Streptomyces coelicolor]			264636
639	80204210 (1277, 1278)	Novel Protein sim. GBank gi 4589628 dbj BAA76836.1  - (AB023209) KIAA0992 protein [Homo sapiens]		struct	264112, 263974
640	17929579 (1279, 1280)	Novel Protein sim. GBank gi 1432083 (U60981) - homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana]	Contains protein domain (PF01466) - (mapolymerase Skp1 family		265009, 265010
641	79636398 (1281, 1282)			UNCLASSIFIED	264693
642	19898737 (1283, 1284)			UNCLASSIFIED	264565
643	81516220 (1285, 1286)			UNCLASSIFIED	264906, 264908, 264758, 264288, 264632, 264635, 264639, 264584
644	11751367 (1287, 1288)			UNCLASSIFIED	264684
645	95010907 (1289, 1290)			UNCLASSIFIED	264906, 264762, 264693, 264639, 264559
646	80089083 (1291, 1292)				264595, 264566
647	80257085 (1293, 1294)	Novel Protein sim. GBank gi 4507813 ref NP_003738.1 pTINKS - TANKYRASE	Contains protein domain (PF00023) - (Ank repeat		264909, 264591
648	80077428 (1295, 1296)	Novel Protein sim. GBank gi 1044963 pbls 169646 - protamine [Monodonta turbinata, gonads, Peptide, 106 aa]		UNCLASSIFIED	264600
649	80247447 (1297, 1298)			UNCLASSIFIED	263978
650	11798316 (1299, 1300)			UNCLASSIFIED	264686
651	11776932 (1301, 1302)	Novel Protein sim. GBank gi 1346816 sp P12283 PURA, ECOLI - ADENYLOSUCCINATE SYNTHETASE (IMP--ASPARTATE LIGASE)		UNCLASSIFIED	264602, 264638
652	85516704 (1303, 1304)			UNCLASSIFIED	264905, 264907, 264909, 263978, 264637
653	82124947 (1305, 1306)	Novel Protein sim. GBank gi 1722977 sp Q10639 Y03C_MYCTU - HYPOTHETICAL 82.8 KD PROTEIN CY130.12C		UNCLASSIFIED	22278998, 264510, 264511, 264512, 264593, 21908754, 264603, 264760, 18108376, 264556
654	95010589 (1307, 1308)			UNCLASSIFIED	264906, 264595, 264632
655	79320692 (1309, 1310)	Novel Protein sim. GBank gi 130327 sp P28647 PLSC_ECOLI - 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE) (LPAAT)	Contains protein domain (PF01553) - (Acy/transferase		264592
656	80416739 (1311, 1312)			UNCLASSIFIED	264602, 264605, 264766, 264681
657	20611010 (1313, 1314)			UNCLASSIFIED	264557, 264558

658	87761915 (1315, 1316)	Novel Protein sim. GBank gij5689493dbj BAA83030.1  - (AB029001) KIAA1078 protein (Homo sapiens)		UNCLASSIFIED	22278996, 60432049, 29331822, 29331824, 29331828, 265007, 265009, 33657402, 33657084, 265017, 264448, 21906765, 21906768, 263967, 20281149, 18108370, 18108374, 264482
659	87718663 (1317, 1318)	Novel Protein sim. GBank gij2137872pir 48724 - zinc finger protein PZF - mouse	Contains protein domain (PF000096) - Zinc finger, C2H2 type	transcript/factor	22278998, 60432049, 66714117, 29331827, 265007, 264766, 66181562, 18108359, 18108365, 18108370, 18108381
660	81897922 (1319, 1320)			UNCLASSIFIED	264757
661	80028023 (1321, 1322)	Novel Protein sim. GBank gij134180 spIP15401 SACY, BACSU - LEVANSUCRASE AND SUCRASE SYNTHESIS OPERON ANTI-TERMINATOR	Contains protein domain (PF00874) - Transcriptional antiterminator bglG family	UNCLASSIFIED	264510, 265009, 264600, 264602, 264603, 264604, 264605, 32833986, 18108376, 264636, 18108387, 22279000
662	20463731 (1323, 1324)	Novel Protein sim. GBank gij4545228 gb AAD22450.1 AF11618 - (AF116183) SecA homolog [Actinobacillus actinomycetemcomitans]		UNCLASSIFIED	264605
663	20628080 (1325, 1326)	Novel Protein sim. GBank gij5689250dbj BAA82881.1  - (AB024335) similar to orf5 [Comamonas testosteronii]		dehydrogenase	264605
664	80508512 (1327, 1328)	Novel Protein sim. GBank gij1852848 dbj BAA17766  - (D90909) DNA photolyase [Synecococcus sp.]		UNCLASSIFIED	264768
665	80079053 (1329, 1330)	Novel Protein sim. GBank gij116641 spIP21640 COBJ_PSEDE - PRECORRIN-3B C17 METHYLTRANSFERASE (PRECORRIN-3 METHYLTRANSFERASE) (PRECORRIN-3 METHYLTRANSFERASE)		isomerase	264600
666	79603142 (1331, 1332)	Novel Protein sim. GBank gij3261829 emb CAB10927  - (Z98260) hypothetical protein Rv1230c [Mycobacterium tuberculosis]		glycoprotein	264907, 265007
667	94631802 (1333, 1334)	Novel Protein sim. GBank gij5688851 dbj BAA82702.1  - (AB017438) Orf5 [Streptomyces coelicolor]		UNCLASSIFIED	264689, 264602, 264593
668	82051891 (1335, 1336)	Novel Protein sim. GBank gij3581853 emb CAA20809  - (AL031541) 50S ribosomal protein L20 [Streptomyces coelicolor]	Contains protein domain (PF00453) - Ribosomal protein L20	ribosomal prot	264905, 264908, 264908, 264600, 264601, 264603, 264605, 264760, 264689, 264636, 264638, 264639
669	12967154 (1337, 1338)			UNCLASSIFIED	264637
670	80238549 (1339, 1340)	Novel Protein sim. GBank gij2582531 (AF026444) - 2- isopropylmalate synthase [Streptomyces coelicolor]		synthase	264905, 264906, 264908, 264601, 264762, 264766, 264689, 264638, 18108385, 264486
671	79601368 (1341, 1342)		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264690, 264692, 264693, 264636, 18108387
672	79634371 (1343, 1344)	Novel Protein sim. GBank gij2114430 (U92703) - Oil-1/EBF-like-3 transcription factor [Mus musculus]		transcript/factor	264910, 265017
673	82285798 (1345, 1346)	Novel Protein sim. GBank gij4589285 gb AAD26430.1 AF13515 - (AF135154) ferric alkaline siderophore receptor [Bordetella pertussis]			264759
674	78189259 (1347, 1348)			UNCLASSIFIED	264629

675	8789870 (1349, 1350)	Novel Protein sim. GBank gi4980755 gb AAD35347.1 AE00170. (AE001708) D- alanine-D-alanine ligase [Thermotoga maritima]	Contains protein domain (PF01820) - D-ala D-ala ligase	UNCLASSIFIED	264488, 22278999, 66714117, 264508, 264511, 285008, 6043338, 264600, 264601, 264602, 264603, 264604, 264605, 264782, 264687, 264789, 60431802, 18108374, 264636, 264638 265010
676	78898607 (1351, 1352)	Novel Protein sim. GBank gi1723566 sp Q10479 YDF7 SCHPO - PUTATIVE GLUCOSYLTRANSFERASE C17C9.07		ATPase-associated	264591, 264632
677	21644312 (1353, 1354)	Novel Protein sim. GBank gi187208 (U03976) - dynein heavy chain isotype 5C [Tritreustes gratilla]			
678	84225200 (1355, 1356)	Novel Protein sim. GBank gi1586274 pt 2203365A - laminin alpha5 [Mus musculus]	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	264758, 264682, 264557
679	78868855 (1357, 1358)	Novel Protein sim. GBank gi13928723 emb CAA22218  - (AL034355) putative ABC transporter [Streptomyces coelicolor]		UNCLASSIFIED	22278986, 264693
680	20726424 (1359, 1360)	Novel Protein sim. GBank			264600, 264602
681	84322017 (1361, 1362)	gi15174493 ref NP_006050.1 pLAMC - laminin, gamma 3	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	264102, 264907, 264808, 265006, 264693, 263972, 83373044, 264568
682	11392478 (1363, 1364)	Novel Protein sim. GBank		UNCLASSIFIED	264595
683	80083680 (1365, 1366)	gi4758208 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	264634
684	20465387 (1367, 1368)	Novel Protein sim. GBank gi15420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]			264605
685	80246735 (1369, 1370)				264809, 263867, 263881
686	79208608 (1371, 1372)				264631
687	80085629 (1373, 1374)				264693, 264635
688	79853412 (1375, 1376)	Novel Protein sim. GBank gi12688962 (AF027768) - LspA [Serratia marcescens]		peptidase	264907, 264638
689	88064256 (1377, 1378)	Novel Protein sim. GBank gi13046931 (AF049330) - PPAR gamma coactivator [Mus musculus]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264806, 264907, 265007, 265008, 60433338, 21806754, 264760, 18108358, 21808786, 21906769, 265021, 18108381, 263974, 18108379, 264557, 18108385, 22278002
690	80388750 (1379, 1380)	Novel Protein sim. GBank gi2498941 sp Q15428 SP62 HUMAN - SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)		UNCLASSIFIED	264510, 264511, 264784, 264769
691	81854392 (1381, 1382)				264757
692	83608936 (1383, 1384)	Novel Protein sim. GBank gi15420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	55812038, 55811957, 265018, 55811150, 18108351, 264908, 60431528, 264594
693	78586116 (1385, 1386)	Novel Protein sim. GBank gi1854085 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264635
694	8245983 (1387, 1388)	Novel Protein sim. GBank gi1267327 sp Q1033 VG48_HSVSA - HYPOTHETICAL GENE 48 PROTEIN			22278996, 264510, 264602, 264603, 264762, 264687, 264769, 264693

695	94147849 (1389, 1390)	Novel Protein sim. GBank gjl4466339[emb]CAB38059.1] - (AJ010901) MUC4 [Homo sapiens]	Contains protein domain (PF000094) - von Willebrand factor type D domain	UNCLASSIFIED	55182575, 264509, 264905, 264907, 29331830, 264908, 264909, 264511, 265007, 264910, 264758, 264764, 264288, 65274791, 264905, 264595
696	79830882 (1381, 1392)	Novel Protein sim. GBank gjl2649950 (AE001058) - glutamine ABC transporter, ATP-binding protein (glnQ) [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	
697	11767889 (1393, 1394)	Novel Protein sim. GBank gjl1731343[sp]Q10694[Y25_MYCTU - HYPOTHETICAL 24.4 KD PROTEIN CY48.25]	Contains protein domain (PF01836) - Transposase	UNCLASSIFIED	264682
698	6685862 (1395, 1396)			UNCLASSIFIED	264688, 35895917
699	79582553 (1397, 1398)			UNCLASSIFIED	264682
700	79639098 (1399, 1400)			UNCLASSIFIED	264693
701	80230242 (1401, 1402)	Novel Protein sim. GBank gjl1001236[db]BAA10471] - (D84003) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	264488, 264510, 264511, 264602, 264605, 264689
702	78814789 (1403, 1404)			UNCLASSIFIED	264909
703	20446820 (1405, 1406)	Novel Protein sim. GBank gjl2498935[sp]Q46338[SOXG_CORSP - SARCOSINE OXIDASE GAMMA SUBUNIT	oxidase	264604	
704	94312224 (1407, 1408)	Novel Protein sim. GBank gjl3150513 (AF067219) - contains similarity to the kelch/MIPP family [Caenorhabditis elegans]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	264288, 56181562, 33657109, 264629, 55811576
705	17932141 (1409, 1410)	Novel Protein sim. GBank gjl421091[pir]S30730 - hypothetical protein o206 - Escherichia coli		UNCLASSIFIED	265006
706	20288062 (1411, 1412)	Novel Protein sim. GBank gjl3024872[sp]Q55790[Y074_SYNNY3 - HYPOTHETICAL 52.8 KD PROTEIN SLR0074]			264600
707	20638065 (1413, 1414)	Novel Protein sim. GBank gjl3420608[gb]AAC31907.1] - (AF075709) ABC transporter ATP-binding subunit [Pseudomonas putida]	transport		264603
708	20708292 (1415, 1416)				264601, 264692
709	88001439 (1417, 1418)	Novel Protein sim. GBank gjl3649741[emb]CAA03985] - (AJ000281) mucin [Homo sapiens]	struct		18108398, 264637, 264908, 264909
710	11356683 (1419, 1420)	Novel Protein sim. GBank gjl3080425[emb]CAA18744.1] - (AL022604) putative protein [Arabidopsis thaliana]			264369
711	17931418 (1421, 1422)				265019
712	80258164 (1423, 1424)	Novel Protein sim. GBank gjl4758686[ref]NP_002323.1[pl]LRP1 - low density lipoprotein related protein 1 (alpha-2-macroglobulin receptor)	Contains protein domain (PF00058) - Low-density lipoprotein receptor repeat class B	apolipoprotein	264591
713	79263126 (1425, 1426)	Novel Protein sim. GBank gjl1703266[sp]Q11056[AM12_MYCTU - PUTATIVE AMIDASE CY50.19C]	hydrolase		264906, 264907
714	27847651 (1427, 1428)	Novel Protein sim. GBank gjl4502351[ref]NP_001692.1[p]BAAT - bile acid Coenzyme A: amino acid N-acyltransferase; glycine N-choyltransferase			264508, 264555

715	78639423 (1429, 1430)	Novel Protein sim. GBank gll1789035 (AE000352) - ori, hypothetical protein [Escherichia coli]		UNCLASSIFIED	264907	
716	78558072 (1431, 1432)				264692	
717	78491842 (1433, 1434)	Novel Protein sim. GBank gll2494074[sp]P55653[IGABD_RHISN - PROBABLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+)] (SSDH)		dehydrogenase	264636	
718	94318658 (1435, 1436)	Novel Protein sim. GBank gll3873679[emb]CAA94886] - (Z71178) similar to pro-collagen domains; cDNA EST EMBL:D27878 comes from this gene; cDNA EST EMBL:D27977 comes from this gene; cDNA EST EMBL:D34189 comes from this gene; cDNA EST EMBL:D64392 comes from this gene; cDNA EST EMBL:....	Contains protein domain (PF00093) - von Willebrand factor type C domain	kinase	18108392, 22278994, 22278998, 265008, 265018, 264681, 18108354, 264684, 264685, 264686, 264687, 264689, 21906789, 18108361, 264691, 264692, 55810764, 264635, 18108381, 18108382, 83373044, 18108388	
719	176789564 (1437, 1438)	Novel Protein sim. GBank gll2104302[emb]CAB08631] - (Z95387) hypothetical protein Rv2811c [Mycobacterium tuberculosis]		UNCLASSIFIED	265011	
720	79841684 (1439, 1440)				264808	
721	15020180 (1441, 1442)	Novel Protein sim. GBank gll123530[sp]P04929[HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	264629	
722	9862603 (1443, 1444)	Novel Protein sim. GBank gll498253 (U02372) - integrase [Vibrio cholerae]			264910	
723	19755599 (1445, 1446)	Novel Protein sim. GBank gll2253054[emb]CAB10705] - (Z97559) hypothetical protein Rv2114 [Mycobacterium tuberculosis]		UNCLASSIFIED	264691	
724	10126484 (1447, 1448)	Novel Protein sim. GBank gll4083015 (AF083061) - protease PrtA [Pseudomonas fluorescens]	Contains protein domain (PF00353) - Hemolysin-type calcium-binding proteins	protease	264909	
725	78878678 (1449, 1450)			UNCLASSIFIED	264905, 264907	
726	13086282 (1451, 1452)			UNCLASSIFIED	264636	
727	13522872 (1453, 1454)				264634	
728	20268471 (1455, 1456)	Novel Protein sim. GBank gll2633910[emb]CAB13411] - (Z99112) similar to hypothetical proteins [Bacillus subtilis]			264567	
729	11293753 (1457, 1458)			UNCLASSIFIED	264490	
730	19900373 (1459, 1460)	Novel Protein sim. GBank gll2494660[sp]Q45291[GALE_BRELA - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		isomerase	264564	
731	80058750 (1461, 1462)	Novel Protein sim. GBank gll1146192 (L47838) - putative [Bacillus subtilis]		UNCLASSIFIED	264605	
732	80258175 (1463, 1464)	Novel Protein sim. GBank gll1168398[sp]P46681[AIIP2_YEAST - ACTIN INTERACTING PROTEIN 2		struct	264591, 264594, 264595	
733	20446839 (1465, 1466)				264804	
734	20435987 (1467, 1468)	Novel Protein sim. GBank gll3184080[emb]CAA19336] - (AL023781) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	264804	

735	11607959 (1469, 1470)	Novel Protein sim. GBank gi401582 sp p27432 YICE_ECOLI - HYPOTHETICAL 48.9 KD PROTEIN IN GLTS-SELIC INTERGENIC REGION			264594
736	10879734 (1471, 1472)	Novel Protein sim. GBank gi400831 sp p31135 POTH_ECOLI - PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTH	Contains protein domain (PF00528) - transport Binding-protein-dependent transport systems inner membrane component	transport	264636
737	78945340 (1473, 1474)		Contains protein domain (PF00815) - Regulator of G protein signaling domain	UNCLASSIFIED	265020
738	17895353 (1475, 1476)	Novel Protein sim. GBank		oxidase	265008
739	79833670 (1477, 1478)	Novel Protein sim. GBank gi2506867 sp p33225 TORA_ECOLI - TRIMETHYLAMINE- N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) (TRIMETHYLAMINE OXIDASE)			264910
740	19881557 (1479, 1480)	Novel Protein sim. GBank gi3261828 emb CAB10925  - (Z88260) mmp [Mycobacterium tuberculosis]			264907, 264764, 264634, 264637
741	79827273 (1481, 1482)	Novel Protein sim. GBank gi3877484 emb CAA88472.1  - (Z48583) ATP binding protein with similarity to the CDC48/PAS1/SEC18 family; cDNA EST EMBL:D65037 comes from this gene; cDNA EST EMBL:D68340 comes from this gene; cDNA EST EMBL:D65048 comes from this gene; cDNA EST EMBL:D6845...	Contains protein domain (PF01883) - Domain of unknown function	UNCLASSIFIED	264688, 35696286, 264510, 264808, 18108362
742	82393795 (1483, 1484)	Novel Protein sim. GBank gi3877484 emb CAA88472.1  - (Z48583) ATP binding protein with similarity to the CDC48/PAS1/SEC18 family; cDNA EST EMBL:D65037 comes from this gene; cDNA EST EMBL:D68340 comes from this gene; cDNA EST EMBL:D65048 comes from this gene; cDNA EST EMBL:D6845...		UNCLASSIFIED	26331822, 264910, 264762
743	82300051 (1485, 1486)	Novel Protein sim. GBank gi127420 sp p19888 MTBA_BACAR - MODIFICATION METHYLASE BANI (CYTOSINE-SPECIFIC METHYLTRANSFERASE BANI) (M.BANI)	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase	UNCLASSIFIED	264488, 264259, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264596, 264759, 265010, 265011, 18108351, 264763, 264288, 264766, 264768, 264693, 18108370, 264629, 18108372, 264630, 264631, 264634, 264558, 18108385, 264482, 264584, 264567
744	80230421 (1487, 1488)				18108397, 264511, 264690, 264628, 264638, 264692, 264639, 264766
745	9841963 (1489, 1490)	Novel Protein sim. GBank gi78921 pir S04846 - UDP-N- acetyluramoylalanine-D-glutamate-2, 6-diaminopimelate--D- alanine-D-alanine ligase (EC 6.3.2.15) precursor - Escherichia coli		glycoprotein	264906
746	11073229 (1491, 1492)	Novel Protein sim. GBank gi3386354 (AF074705) - pyochelin synthetase [Pseudomonas aeruginosa]		synthase	264600
747	94322044 (1493, 1494)	Novel Protein sim. GBank gi2887411 dbj BAA24848  - (AB007876) KIAA0418 [Homo sapiens]	Contains protein domain (PF00018) - oxidase SH3 domain	oxidase	56714117, 264905, 264509, 264906, 264907, 264908, 264809, 264511, 264910, 265011, 264681, 264288, 264766, 264687, 264768, 264769, 21906768, 35695917, 264691, 264693, 264628, 264634, 264635, 264639, 56182323, 83373044
748	11617923 (1495, 1496)				264690

749	20469118 (1497, 1498)	Novel Protein sim. GBank		UNCLASSIFIED	264604
750	20296427 (1489, 1500)	g11189727sp1P44948IFPG_HAEIN - FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY-DNA GLYCOSYLASE)			264600
751	21636169 (1501, 1502)	Novel Protein sim. GBank	Contains protein domain (PF000069) - kinase Eukaryotic protein kinase domain	kinase	264605, 264559
752	82450366 (1503, 1504)	g11360088gb1AAD42851.1(AF159689) serine/threonine kinase PKN3 [Mycoccus xanthus]	Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate	UNCLASSIFIED	264508, 264907, 264510, 265011, 264762, 264689, 35695855, 264638, 18108387
753	80508718 (1505, 1508)	Novel Protein sim. GBank		UNCLASSIFIED	264908, 264600, 264602, 264604, 264760, 264769, 264634
754	95083741 (1507, 1508)	g12851530sp1P32389YHGE_BACSU - HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLT INTERGENIC REGION (ORF8)		UNCLASSIFIED	264508, 264906, 264907, 264808, 264909, 264759, 264802, 264764, 264769, 264628, 264629, 264630, 264632, 264634, 264635, 264637, 264638, 83373044, 18108385
755	80185449 (1509, 1510)	Novel Protein sim. GBank		UNCLASSIFIED	264448, 264690
756	94631688 (1511, 1512)	g13449276lamb(CAA20420) - (AL031317) putative dehydrogenase [Streptomyces coelicolor]		UNCLASSIFIED	264769, 264689, 264638, 264639
757	79488533 (1513, 1514)	Novel Protein sim. GBank		UNCLASSIFIED	264682, 264685
758	78963176 (1515, 1516)	g14580331lamb(CAB40107.1) - (A001206) putative glycogen debranching enzyme [Streptomyces coelicolor]		amylase	265007, 18108387, 265007, 18108387
759	79475667 (1517, 1518)	Novel Protein sim. GBank		UNCLASSIFIED	264684, 264686
760	87628888 (1519, 1520)	g12911858 (AF047659) - No definition line found [Caenorhabditis elegans]	Contains protein domain (PF00122) - transport E1-E2 ATPase	transport	29331822, 264908, 52644045, 56182435, 60170831, 21908754, 265017, 265019, 264681, 264687, 264688, 21906766, 21906768, 265020, 265021, 265022, 264635, 22279000
761	79877968 (1521, 1522)	Novel Protein sim. GBank		UNCLASSIFIED	264768
762	80023563 (1523, 1524)	g13327158lamb(BAA31647) - (AB014572) KIAA0872 protein [Homo sapiens]		UNCLASSIFIED	264907, 264593, 265020
763	20294813 (1525, 1526)	Novel Protein sim. GBank			264600
764	39515024 (1527, 1528)	g14981268gb1AAD35822.1(AE00174) - (AE001744) lipopolysaccharide core biosynthesis protein KdtB [Thermotoga maritima]			264603



765	80025347 (1529, 1530)	Novel Protein sim. GBank gl 3845093 (AE001371) - erythrocyte membrane protein PIEMP3 [Plasmodium falciparum]		struct	264805, 264806, 264594, 264666, 33657023
766	82417404 (1531, 1532)	Novel Protein sim. GBank gl 541121 pir S40827 - hypothetical protein o300 - Escherichia coli		UNCLASSIFIED	264605, 264762, 18108374
767	10296742 (1533, 1534)	Novel Protein sim. GBank gl 2982501 emb CAA061641 - (AJ004832) neuropathy target esterase [Homo sapiens]		UNCLASSIFIED	264592, 264595
768	78416080 (1535, 1536)	Novel Protein sim. GBank gl 283437 pir S27850 - hypothetical protein - Trypanosoma cruzi (fragment)		esterase	35810764, 264559
769	80086554 (1537, 1538)	Novel Protein sim. GBank gl 4769004 gb AAD29715.1 AF14059 - (AF140598) ring-box protein 1 [Homo sapiens]		UNCLASSIFIED	264805, 264807, 264828, 264809, 265010, 264766, 264628, 264629, 264634, 264636, 264555
770	80417847 (1539, 1540)	Novel Protein sim. GBank gl 5531324 emb CAB51045.1 - (AJ009579) putative alkane 1-monooxygenase [Pseudomonas fluorescens]	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	56182575, 35686286, 264259, 66714117, 264107, 66712502, 56182435, 264112, 55812038, 87168559, 264288, 21906766, 33657023, 65274620, 65274791, 18108381
771	95329509 (1541, 1542)	Novel Protein sim. GBank gl 4769004 gb AAD29715.1 AF14059 - (AF140598) ring-box protein 1 [Homo sapiens]		UNCLASSIFIED	264910
772	78971362 (1543, 1544)	Novel Protein sim. GBank gl 5531324 emb CAB51045.1 - (AJ009579) putative alkane 1-monooxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	265020
773	78945363 (1545, 1546)	Novel Protein sim. GBank gl 5531324 emb CAB51045.1 - (AJ009579) putative alkane 1-monooxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	264909
774	78856129 (1547, 1548)	Novel Protein sim. GBank gl 5531324 emb CAB51045.1 - (AJ009579) putative alkane 1-monooxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	
775	20820141 (1549, 1550)	Novel Protein sim. GBank gl 5531324 emb CAB51045.1 - (AJ009579) putative alkane 1-monooxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	264555
776	78942693 (1551, 1552)	Novel Protein sim. GBank gl 5531324 emb CAB51045.1 - (AJ009579) putative alkane 1-monooxygenase [Pseudomonas fluorescens]	Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	UNCLASSIFIED	265019
777	79960378 (1553, 1554)	Novel Protein sim. GBank gl 4505461 rat NP_003624.1 pNRPB - nuclear restricted protein, BTB domain-like (brain)	Contains protein domain (PF01344) - Kelch motif	protease	21906754, 265020, 60170615, 264691
778	20681310 (1555, 1556)	Novel Protein sim. GBank gl 1144520 (U34856) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]		UNCLASSIFIED	264511
779	80054024 (1557, 1558)	Novel Protein sim. GBank gl 1144520 (U34856) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]		synthase	264603
780	95288987 (1559, 1560)	Novel Protein sim. GBank gl 1144520 (U34856) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]			264907, 264600, 264601, 264602, 264603, 264604, 264605, 264486
781	80250049 (1561, 1562)	Novel Protein sim. GBank gl 4505461 rat NP_003624.1 pNRPB - nuclear restricted protein, BTB domain-like (brain)		UNCLASSIFIED	264905, 264907, 265010, 264600, 264601, 18108362, 18108374, 264556
782	8758529 (1563, 1564)	Novel Protein sim. GBank gl 4505461 rat NP_003624.1 pNRPB - nuclear restricted protein, BTB domain-like (brain)		UNCLASSIFIED	264605
783	16410791 (1565, 1566)	Novel Protein sim. GBank gl 4505461 rat NP_003624.1 pNRPB - nuclear restricted protein, BTB domain-like (brain)		UNCLASSIFIED	285020
784	80051197 (1567, 1568)	Novel Protein sim. GBank gl 4505461 rat NP_003624.1 pNRPB - nuclear restricted protein, BTB domain-like (brain)		UNCLASSIFIED	264635, 33657023, 29331828, 265017, 264585, 264568
785	56073541 (1569, 1570)	Novel Protein sim. GBank gl 3451335 (AC005526) - F22162.1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	35686052, 264604
786	20438842 (1571, 1572)	Novel Protein sim. GBank gl 38748 sp P10905 UGPA_ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA		transport	264603
787	80258364 (1573, 1574)	Novel Protein sim. GBank gl 38748 sp P10905 UGPA_ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA		UNCLASSIFIED	264593

788	80507844 (1575, 1578)	Novel Protein sim. GBank gi 2748079 (AF015310) - BTH1 [Brassica napus]				264908, 264602, 264603, 264769, 264638
789	17294715 (1577, 1578)	Novel Protein sim. GBank gi 2351849 (U93357) - 40 kDa heat shock chaperone protein [Halobacterium salinarum]			UNCLASSIFIED	265007
790	86284408 (1578, 1580)	Novel Protein sim. GBank gi 5706378 (dbj BAA03099.1) - (AB026118) MALT1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain		glycoprotein	22278998, 26331824, 264828, 87188559, 265018, 21908765, 21908787, 21908798, 21908769, 265020, 264692, 22279000, 264583
791	94651827 (1581, 1582)	Novel Protein sim. GBank gi 5689948 (emb CAB51885.1) - (AL109863) putative isoleucyl-IRNA synthetase [Streptomyces coelicolor A3(2)]				264601, 264605, 264638
792	80056786 (1583, 1584)	Novel Protein sim. GBank gi 393184 (L02375) - S-antigen [Plasmodium falciparum]			struct	265021, 264631, 264635, 264556
793	79838730 (1585, 1586)	Novel Protein sim. GBank gi 1345408 (dbj BAA05046) - (D26046) AT motif-binding factor [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain		homeobox	264693
794	81839284 (1587, 1588)	Novel Protein sim. GBank gi 105884 (pir S24023) - dopamine receptor D4 - human (fragment)			UNCLASSIFIED	264603, 264604, 264910, 264762, 264806, 264639, 264909, 264757
795	80074988 (1588, 1590)	Novel Protein sim. GBank gi 1877334 (emb CAB07082) - (Z92771) birA [Mycobacterium tuberculosis]			carboxylase	264488, 35696052, 264905, 264907, 265010, 35698423, 264636
796	86669451 (1591, 1592)					60432229, 55811150, 264630, 264637, 264565
797	87771781 (1593, 1594)	Novel Protein sim. GBank gi 2954447 (emb CAA71519) - (Y10495) CDV-1R protein [Mus musculus]			struct	22278998, 264093, 264094, 66714117, 21908767, 21908769, 265020, 265022
798	79865209 (1595, 1596)				transcript factor	264687, 264768, 264693
799	79557816 (1597, 1598)	Novel Protein sim. GBank gi 4467250 (emb CAB37575) - (AL035569) probable Glu-IRNA Gin amidotransferase subunit [Streptomyces coelicolor]			hydrolase	264908, 264910, 264638, 264638
800	79970199 (1599, 1600)				UNCLASSIFIED	264488
801	80499399 (1601, 1602)	Novel Protein sim. GBank gi 2791517 (emb CAA16054) - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]			transport	264508, 264511, 265006, 265009, 264789, 264567, 264486
802	79834598 (1603, 1604)	Novel Protein sim. GBank gi 4887211 (gb AAD32237.1) [AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]				264905, 264693
803	20467520 (1605, 1606)				struct	264605
804	10174239 (1607, 1608)	Novel Protein sim. GBank gi 176152 (sp P44507) [YHAD_HAEIN - HYPOTHETICAL PROTEIN H10091]			kinase	264510
805	79599993 (1609, 1610)					
806	80484113 (1611, 1612)	Novel Protein sim. GBank gi 2764612 (emb CAA04683) - (AJ001330) ornithine transcarbamoylase [Lactobacillus sakei]	Contains protein domain (PF00185) - Aspartate/ornithine carbamoyltransferase		transferase	264508, 264769
807	80381812 (1613, 1614)	Novel Protein sim. GBank gi 2833311 (sp Q21828) [YNF_D_CAEEL - HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III]				264764

808	35108817 (1615, 1616)	Novel Protein sim. GBank gi3913092[sp]Q46170[ARCO_CLOPE - ARGININE/ORNITHINE ANTIporter]		transport	264909, 264602, 21908764, 18108374
809	81454254 (1617, 1618)	Novel Protein sim. GBank gi3913016[sp]P74309[ALF1_SUNY3 - FRUCTOSE- BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE)]	Contains protein domain (PF00274) - Fructose-bisphosphate aldolase class-I	UNCLASSIFIED	264508, 264906, 264909, 265007, 264910, 264758, 264600, 264602, 264603, 264605, 264687, 264769, 264689, 264636, 264486
810	80192761 (1619, 1620)	Novel Protein sim. GBank gi401472[sp]P30863[YAFB_ECOLI - HYPOTHETICAL OXIDOREDUCTASE IN ASPU-MLTD INTERGENIC REGION]	Contains protein domain (PF00248) - Aldo/keto reductase family	reductase	264389
811	80079280 (1621, 1622)			UNCLASSIFIED	264558
812	10297854 (1623, 1624)			UNCLASSIFIED	264692
813	79612280 (1625, 1626)			UNCLASSIFIED	264906
814	80473427 (1627, 1628)	Novel Protein sim. GBank gi1146168 (J01617) - glutaminyl- [RNA synthetase [Escherichia coli]]		synthase	264905, 264602, 264605, 264682, 264687, 264789, 264636
815	95419513 (1629, 1630)	Novel Protein sim. GBank gi4589652[dbj]BAA76848.1] - (AB023221) KIAA1004 protein [Homo sapiens]		UNCLASSIFIED	264488, 22278998, 22278999, 29331822, 29331824, 29331825, 29331827, 29331828, 29146499, 264905, 264908, 265007, 33657402, 60433356, 60433438, 264758, 265011, 265017, 265018, 265019, 264389, 264286, 264685, 21906765, 21906787, 265020, 265021, 264682, 65274820, 33857109, 264628, 18108376, 264635, 264638, 80170394, 56182323, 264564 264600
816	18881910 (1631, 1632)	Novel Protein sim. GBank gi11781144[emb]CAB06254] - (Z83866) hypothetical protein Rv3069 [Mycobacterium tuberculosis]		UNCLASSIFIED	264595
817	95293316 (1633, 1634)	Novel Protein sim. GBank gi1477468 (U35244) - vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]			65274572, 22278998, 60424269, 35696052, 55812038, 21906768, 55811957, 35695917, 33857023, 18108370, 18108374, 55810764, 35696423, 55811578, 264636
818	90938180 (1635, 1636)			transport	264565
819	80254977 (1637, 1638)	Novel Protein sim. GBank gi1001352[dbj]BAA10839] - (D64006) ABC transporter [Synecocystis sp.]		UNCLASSIFIED	264600, 264602, 264604
820	80059688 (1639, 1640)	Novel Protein sim. GBank gi586814[sp]P37484[YVBT_BACSU - HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION]			
821	79762590 (1641, 1642)			UNCLASSIFIED	264910
822	80215310 (1643, 1644)	Novel Protein sim. GBank gi3878400[emb]CAA95828] - (Z71264) predicted using GeneFINDER: Weak similarity to Mouse T-complex-associated-testes-expressed-1 protein (PIR Acc. No. A45841); cDNA EST EMBL:D32742 comes from this gene; cDNA EST EMBL:D33617 comes from this gene; cDNA EST...		UNCLASSIFIED	264510, 264594, 264637
823	94992299 (1645, 1646)			struct	264508, 264687, 264691
824	80411171 (1647, 1648)	Novel Protein sim. GBank gi137007[emb]CAA66887] - (X98235) type I [Drosophila melanogaster]	Contains protein domain (PF01429) - Methyl-CpG binding domain		264910, 264783, 264769, 264693

825	20638600 (1649, 1650)	Novel Protein sim. GBank gi 3025132 sp p77391 YEAG_ECOLI - HYPOTHETICAL 74.5 KD PROTEIN IN GAPA-RND INTERGENIC REGION		UNCLASSIFIED	264592	
826	11075047 (1651, 1652)	Novel Protein sim. GBank gi 3242281 emb CAA16669  - (AL021646) hypothetical protein Rv3202c [Mycobacterium tuberculosis]			264605	
827	80054207 (1653, 1654)	Novel Protein sim. GBank gi 3417424 emb CAA20312  - (AL031261) putative transport protein [Schizosaccharomyces pombe]			264603	
828	95106322 (1655, 1656)	Novel Protein sim. GBank gi 4336692 gb AAD17897  - (AF101361) Abnormal X segregation [Drosophila melanogaster]		UNCLASSIFIED	52645080, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264512, 264910, 264591, 264758, 264600, 264768, 264768, 21908768, 35695917, 264691, 264628, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 264639, 83373044, 18108385, 264563, 264566, 264488	
829	81742215 (1657, 1658)	Novel Protein sim. GBank gi 3820539 (AF080002) - UDP-N- acetyl(muramyl tripeptide synthetase MurC [Helicobacter mobilis]		UNCLASSIFIED	264758, 264634	
830	20396091 (1659, 1660)			UNCLASSIFIED	264603	
831	87112435 (1661, 1662)	Novel Protein sim. GBank gi 1870004 emb CAB06855  - (Z92539) hypothetical protein Rv1024 [Mycobacterium tuberculosis]		UNCLASSIFIED	56714117, 264910, 264639	
832	19536322 (1663, 1664)			UNCLASSIFIED	264906	
833	20726654 (1665, 1666)	Novel Protein sim. GBank gi 2500056 sp Q46267 PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	264602	
834	21428762 (1667, 1668)	Novel Protein sim. GBank gi 2497531 sp Q46078 KPYK_CORGL - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase		264600, 264602, 264769, 264689, 264636	
835	94140482 (1669, 1670)				264768, 263994, 21908767, 264910, 264632, 264635, 264259, 264639, 264693, 83373044, 264758, 35696052, 22279002, 264508, 264905, 264906, 264448, 263972, 264908, 264909	
836	66126552 (1671, 1672)	Novel Protein sim. GBank gi 699315 (U15184) - phosphate transport protein PSTC [Mycobacterium leprae]		transport	35695917, 264557	
837	70450450 (1673, 1674)	Novel Protein sim. GBank gi 728867 sp P40802 APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		UNCLASSIFIED	264595	
838	79184203 (1675, 1676)	Novel Protein sim. GBank gi 2496533 sp Q50598 YOD8_MYCTU - HYPOTHETICAL 69.9 KD PROTEIN CY1A11.08		UNCLASSIFIED	264687	
839	79641125 (1677, 1678)			UNCLASSIFIED	264906	
840	80059851 (1679, 1680)	Novel Protein sim. GBank gi 4557753 ref NP_000372.1 pMID1 - midline 1 protein (finger)	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	264762, 264556	

841	80376318 (1681, 1682)	Novel Protein sim. GBank gll139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN gll139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00096) Zinc finger, C2H2 type	- transcript factor	284784
842	80078724 (1683, 1684)	Novel Protein sim. GBank gll139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00569) Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	284905, 284908, 265008, 265009, 18108374, 56182323, 264558
843	87002847 (1685, 1686)	Novel Protein sim. GBank gll139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00170) bZIP transcription factor	- struct	264081, 29331825, 284806, 264768, 264563
844	17941439 (1687, 1688)	Novel Protein sim. GBank gll139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00096) Zinc finger, C2H2 type	- transcript factor	265011
845	18346844 (1689, 1690)	Novel Protein sim. GBank gll139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN (D88733) membrane glycoprotein [Equine herpesvirus 1]			284829
846	78863441 (1691, 1692)	Novel Protein sim. GBank gll139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN (D88733) membrane glycoprotein [Equine herpesvirus 1]		kinase	284907
847	78695348 (1693, 1694)	Novel Protein sim. GBank gll139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN (D88733) membrane glycoprotein [Equine herpesvirus 1]			264809
848	78489365 (1695, 1696)	Novel Protein sim. GBank gll139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN (D88733) membrane glycoprotein [Equine herpesvirus 1]			285020
849	78756367 (1697, 1698)	Novel Protein sim. GBank gll139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN (D88733) membrane glycoprotein [Equine herpesvirus 1]		UNCLASSIFIED	264566
850	78817649 (1699, 1700)	Novel Protein sim. GBank gll139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00120) Glutamine synthetase	UNCLASSIFIED	264909
851	95320333 (1701, 1702)	Novel Protein sim. GBank gll139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF01608) VLWEQ domain		284488, 52644507, 264488, 18108398, 65274572, 56182575, 22278994, 22278995, 22278996, 35686286, 22278997, 22278998, 22278999, 20281171, 264490, 264259, 52845080, 29331822, 29331824, 86714117, 29331825, 60432289, 29331826, 29331827, 35686052, 29331828, 29146498, 29146499, 264107, 264905, 264906, 264907, 264908, 52844045, 56182435, 265006, 265007, 265008, 265009, 264910, 60432229, 60431735, 60433356, 33657402, 60433438, 264595, 264758, 264759, 21908754, 33109954, 52644298, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 264762, 264681, 18108351, 264763, 284448, 284682, 284784, 284683, 18108354, 284288, 284369, 264685, 264766, 264687, 264768, 264769, 21908765, 21908766, 21906767, 21906768, 29148627, 21906769, 29148628, 55811957, 35685917, 265020, 265021, 265022, 60170815, 52844150, 264691, 264692, 33657023, 264693, 263986, 33657109, 27486281, 27486282, 27486284, 27486285, 35685763, 60431602, 18108370, 20281069, 264629, 18108374, 18108376, 55811576, 35686423, 35685855, 264634, 264635, 264636, 264555, 60431850, 264556, 264691
852	10147366 (1703, 1704)				

[illegible]

874	80077692 (1747, 1748)	Novel Protein sim. GBank gil134318 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)		UNCLASSIFIED	264600
875	86608446 (1748, 1750)	Novel Protein sim. GBank gil481000 p JIS37594 - mucin - human (fragment)			264259, 264448, 264288, 264557, 87168518
876	86455157 (1751, 1752)	Novel Protein sim. GBank gil3128283 (AF010496) - Iron(iii) dicitrate transport ATP-binding protein [Rhodobacter capsulatus]	Contains protein domain (PF00005) - ABC transporter	transport	264907, 264601, 264602, 264605, 265020, 60431602
877	87802548 (1753, 1754)	Novel Protein sim. GBank gil731074 sp P40349 URB1_USTMA - SIDEROPHORE BIOSYNTHESIS REGULATORY PROTEIN URBS1	Contains protein domain (PF00320) - GATA zinc finger	transcriptionfactor	22278998, 264909, 264369
878	80187289 (1755, 1756)	Novel Protein sim. GBank gil1351614 sp Q09853 YAED_SCHPO - HYPOTHETICAL 181.5 KD PROTEIN C23D3.13C IN CHROMOSOME 1		ATPase-associated	264369, 264555
879	94328962 (1757, 1758)	Novel Protein sim. GBank gil3875304 emb CAA98434  - (Z74030) predicted using Genefinder; cDNA EST EMBL: C07609 comes from this gene; cDNA EST EMBL: C09023 comes from this gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com....			56182575, 29331824, 264508, 264906, 265018, 18108351, 264448, 264683, 21908768, 21908768, 80170815, 33657023, 65274820, 33657109, 18108374, 35898855, 264563
880	8491135 (1759, 1760)	Novel Protein sim. GBank gil137120 sp P11214 UROT_MOUSE - TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (TPA) (T- PLASMINOGEN ACTIVATOR)	Contains protein domain (PF00051) - Kringle domain	cathepsin	264508
881	11290122 (1761, 1762)	Novel Protein sim. GBank gil2632098 emb CAA75667  - (Y15513) Prodos protein [Drosophila melanogaster]		UNCLASSIFIED	264508
882	11077011 (1763, 1764)	Novel Protein sim. GBank gil1155068 emb CAA64425  - (X94976) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED	264558
883	78582989 (1765, 1766)	Novel Protein sim. GBank gil1155068 emb CAA64425  - (X94976) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED	264688
884	13517921 (1767, 1768)	Novel Protein sim. GBank gil1155068 emb CAA64425  - (X94976) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED	264636
885	80052457 (1769, 1770)	Novel Protein sim. GBank gil2078027 emb CAB08467  - (Z95208) hypothetical protein Rv2372c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 18108362
886	11685138 (1771, 1772)	Novel Protein sim. GBank gil2695834 emb CAA15904  - (AL021008) sucA [Mycobacterium tuberculosis]			264690
887	94315307 (1773, 1774)	Novel Protein sim. GBank gil5689395 dbj BAA82981.1  - (AB028952) KIAA1029 protein [Homo sapiens]		dehydrogenase	35688052, 264906, 264600, 264603, 35695917, 35695855, 264636
888	10083399 (1775, 1776)	Novel Protein sim. GBank gil1881338 dbj BAA19365  - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE [Bacillus subtilis]		UNCLASSIFIED	264908
889	20385917 (1777, 1778)	Novel Protein sim. GBank gil1881338 dbj BAA19365  - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE [Bacillus subtilis]			264603
890	19904337 (1779, 1780)	Novel Protein sim. GBank gil854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]			264629

891	13516879 (1781, 1782)	Novel Protein sim. GBank gi 4959396 gb AAD34331.1 AF11248 - (AF112481) RAD54B protein [Homo sapiens]		UNCLASSIFIED	264636
892	87634157 (1783, 1784)	Novel Protein sim. GBank gi 545526 bbs 143833 - LBP- 1b=transcription factor binding to initiation site of HIV-1 (alternatively spliced) [human, Namakwa cells, Peptide, 541 aa]		transcriptfactor	22278986, 22278999, 29331828, 35696052, 264808, 264809, 265009, 265011, 264602, 265019, 264766, 21908765, 21908768, 21908769, 265020, 265021, 56528486
893	79168037 (1785, 1786)	Novel Protein sim. GBank gi 2829888 sp P80609 CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIOL)-LYASE) (CSASE)		synthase	264689, 263967
894	11102240 (1787, 1788)				263978
895	80239888 (1789, 1790)			UNCLASSIFIED	264508, 264600, 264555, 264559
896	79747803 (1791, 1792)				264632
897	84981923 (1793, 1794)		Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	264886, 29331828, 264511
898	87895109 (1795, 1796)				56182575, 604322289, 56182435, 60432228, 55811957, 22279000, 264486
899	11100463 (1797, 1798)				264601
900	80499768 (1799, 1800)	Novel Protein sim. GBank gi 1750127 (U66480) - YncC [Bacillus subtilis]	transport		264769, 264691, 264563
901	80502410 (1801, 1802)	Novel Protein sim. GBank gi 3122879 sp O07438 SVA_MYCTU - ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)	Contains protein domain (PF01411) - IRNA synthetases class II (A)	synthase	264907, 264602, 264605, 264769, 35695917, 18108376, 264563
902	80503301 (1803, 1804)	Novel Protein sim. GBank gi 3355701 emb CAA20001 - (AL031124) 3-isopropylmalate dehydratase large subunit [Streptomyces coelicolor]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	isomerase	264909, 265008, 264602, 264604, 264769, 264689, 264693
903	82060208 (1805, 1806)	Novel Protein sim. GBank gi 2960120 emb CAA18018.1  - (AL022121) gipK [Mycobacterium tuberculosis]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	kinase	35696052, 264905, 264510, 264511, 264512, 264605, 264760, 18108351, 264762, 264687, 264768, 264769, 264688, 21908764, 35695917, 27486262, 35695855, 264634, 264638, 264486
904	20451078 (1807, 1808)	Novel Protein sim. GBank gi 728887 sp P40906 ARGI_COCIM - ARGINASE	Contains protein domain (PF00491) - Arginase family	hydrolase	264604
905	9398483 (1809, 1810)	Novel Protein sim. GBank gi 4567200 gb AAD23616.1 AC00716 - (AC007168) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264809
906	80052628 (1811, 1812)	Novel Protein sim. GBank gi 3738200 emb CAA21292  - (AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]			264595, 264605
907	87913201 (1813, 1814)				
908	11754482 (1815, 1816)	Novel Protein sim. GBank gi 3868940 db BAA34296  - (AB015054) Alg2 [Rhizomucor pusillus]		UNCLASSIFIED	60432288, 264601, 264690
909	20727907 (1817, 1818)	Novel Protein sim. GBank gi 4599726 db BAA76883.1  - (AB003137) DnaJ homolog protein [Salix glauca]		UNCLASSIFIED	264638
910	16776206 (1819, 1820)		Contains protein domain (PF00684) - DnaJ central domain (4 repeats)	eph	264602



911	87454340 (1821, 1822)	Novel Protein sim. GBank gi 548774 sp P35685 RL7A_ORYSA - 60S RIBOSOMAL PROTEIN L7A		ribosomalprot	265010, 264604, 60432113
912	20448663 (1823, 1824)	Novel Protein sim. GBank gi 2314008 gb AA07921.1  - (AE000597) CDP-diglyceride hydrolase (cdh) [Helicobacter pylori 26695]		hydrolase	264559
913	20469357 (1825, 1826)				
914	79183351 (1827, 1828)	Novel Protein sim. GBank gi 417657 sp Q03604 RI1_CAEEL - PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (RIBONUCLEOTIDE REDUCTASE)	Contains protein domain (PF00317) - Ribonucleotide reductase	UNCLASSIFIED - reductase	264604 264636
915	87606703 (1829, 1830)	Novel Protein sim. GBank gi 568957 dbj BAA83069.1  - (AB028040) KIAA1117 protein [Homo sapiens]			18108398, 22276996, 86714117, 264908, 264591, 21908768, 265020, 55811576, 264638
916	79444091 (1831, 1832)	Novel Protein sim. GBank gi 4186110 emb CAA71790  - (Y10831) putative integrase [Ralstonia eutropha]		UNCLASSIFIED	264595
917	20195985 (1833, 1834)				
918	91226795 (1835, 1836)	Novel Protein sim. GBank gi 1655699 emb CAA69032  - (Y07752) pterophorin-S [Volvox carter]		UNCLASSIFIED synthase	264605 264259, 29331826, 264908, 265019, 264448, 265020, 264835, 83373044
919	80436785 (1837, 1838)	Novel Protein sim. GBank gi 5689968 emb CAB52005.1  - (AL109663) putative membrane protein (Streptomyces coelicolor A3(2))			265006, 264512, 264600, 264602, 264604, 264768, 18108370, 264563
920	79608095 (1839, 1840)	Novel Protein sim. GBank gi 1168448 sp Q05813 AMP1_STRJ - XAA-PRO AMINOPEPTIDASE I (X-PRO AMINOPEPTIDASE I) (AMINOPEPTIDASE P I) (APP) (PEPP I) (AMINOACYLPROLINE AMINOPEPTIDASE I)		peptidase	264508
921	19858634 (1841, 1842)	Novel Protein sim. GBank gi 3850084 emb CAA21911.1  - (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]		UNCLASSIFIED	264600
922	78982605 (1843, 1844)				
923	86695830 (1845, 1846)	Novel Protein sim. GBank gi 267079 sp P29514 TB86_ARATH - TUBULIN BETA-6 CHAIN		tubulin	265019, 22279002 264907, 265008, 265009, 265010, 18108351, 264689, 265021, 18108370, 18108374, 18108385
924	21431341 (1847, 1848)				264510
925	20630332 (1849, 1850)	Novel Protein sim. GBank gi 2497688 sp Q60963 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...		esterase	264603
926	79397657 (1851, 1852)	Novel Protein sim. GBank gi 3882325 dbj BAA34522.1  - (AB018345) KIAA0802 protein [Homo sapiens]			55811957, 263972, 264639
927	37036201 (1853, 1854)			UNCLASSIFIED	264769

928	80070610 (1855, 1856)	Novel Protein sim. GBank gij156146 (M30316) - xanthine dehydrogenase (AA at 2538) [Caliphora vicina]		dehydrogenase	264605
929	20630336 (1857, 1858)	Novel Protein sim. GBank gij115936 [gb]AAD03446.1] - (AF118223) No definition line found [Arabidopsis thaliana]		UNCLASSIFIED	264603
930	5496348 (1859, 1860)	Novel Protein sim. GBank gij4490609 [emb]CAB38642.1] - (AJ1133495) ribonucleotide reductase major subunit [Staphylococcus aureus]			264259
931	10245731 (1861, 1862)	Novel Protein sim. GBank gij5459336 [emb]CAB50754.1] - (AL096839) putative integral membrane transport protein [Streptomyces coelicolor]	Contains protein domain (PF00317) - Ribonucleotide reductase	reductase	264486
932	80420813 (1863, 1864)	Novel Protein sim. GBank gij5689523 [dbj]BAA83045.1] - (AB028016) KIAA1093 protein [Homo sapiens]		transport	264508, 264905, 264906, 264909, 264600, 264602, 264603, 264605, 264766, 264558, 18108387, 264486
933	94326010 (1865, 1866)	Novel Protein sim. GBank gij119111 [sp]P12978 [EBN2_EBV - EBNA-2 NUCLEAR PROTEIN]	Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	264508, 264686, 264693, 27486281, 18108370, 65274791, 264636, 264559, 22279002
934	80039105 (1867, 1868)	Novel Protein sim. GBank gij119111 [sp]P12978 [EBN2_EBV - EBNA-2 NUCLEAR PROTEIN]			264369, 22279002
935	80063162 (1869, 1870)				
936	80026632 (1871, 1872)	Novel Protein sim. GBank gij845686 (M32103) - ORF-27 [Staphylococcus aureus]		UNCLASSIFIED	264604, 264605, 264693, 18108370, 18108374
937	80250273 (1873, 1874)	Novel Protein sim. GBank gij1360669 [pir]CGHU1V - collagen alpha 1(V) chain precursor - human		UNCLASSIFIED	22278995, 22278996, 264602, 264687, 32833986, 18108387
938	80026633 (1875, 1876)	Novel Protein sim. GBank gij226243 [emb]CAA74531.1] - (Y14083) hypothetical protein [Bacillus subtilis]		synthase	263978
939	11071694 (1877, 1878)	Novel Protein sim. GBank gij3560166 [emb]CAA20678] - (AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]		UNCLASSIFIED	264602
940	94144252 (1879, 1880)		Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2		264600
941	11398414 (1881, 1882)				264905, 264906, 264907, 264908, 264909, 264511, 264910, 264592, 33857402, 264596, 264758, 264760, 264683, 264766, 264769, 264769, 33657023, 33657109, 264628, 264629, 264630, 264635, 264636, 264555, 264637, 264556, 264638, 264639, 83373044, 18108385, 264585, 18108391
942	19484122 (1883, 1884)				264593
943	80080258 (1885, 1886)	Novel Protein sim. GBank gij4033729 (AF038595) - apolipoprotein N-acyltransferase [Pseudomonas aeruginosa]		UNCLASSIFIED	264760
944	80216096 (1887, 1888)	Novel Protein sim. GBank gij2494764 [sp]Q50729 [GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)]		UNCLASSIFIED	264600, 264687, 264689, 264563
945	80052477 (1889, 1890)	Novel Protein sim. GBank gij732353 [sp]P39606 [YWCH_BACSU - HYPOTHETICAL 38.8 KD PROTEIN IN QOXD-VPR INTERGENIC REGION]	Contains protein domain (PF00818) - Ice nucleation protein repeat	synthase	264511, 264603
946	78246402 (1891, 1892)			UNCLASSIFIED	264906, 264604, 264605, 265020, 18108387
					265017

947	81802699 (1893, 1894)	Novel Protein sim. GBank gl 2886770 emb CAA172471 - (AL021899) hypothetical protein Rv2033c [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	18108394, 22278996, 264907, 264909, 265008, 265009, 264910, 264758, 264600, 264602, 265018, 264605, 264769, 264699, 264693
948	88165538 (1895, 1898)	Novel Protein sim. GBank gl 2827284 (AF041037) - novel antagonist of FGF signaling [Homo sapiens]		tgf	18108398, 58182575, 22278997, 22278999, 60432049, 29331822, 29331826, 264907, 56182435, 55811386, 265011, 264600, 265017, 265018, 265019, 18108351, 265020, 265021, 265022, 27486265, 263972, 55811576, 264638, 60170394, 264566
949	88081786 (1897, 1898)	Novel Protein sim. GBank gl 4507985 ref NP_003427.1 pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF000098) - Zinc finger, C2H2 type	transcriptfactor	29331825, 21906764, 27486261, 21906766, 52844296, 33657349, 87188518, 56994075, 265020, 265021, 87168559, 52644150, 264637
950	79465872 (1899, 1900)	Novel Protein sim. GBank gl 1079461 pir IS43865 - cytokeratin 8, type II - potoroo (fragment)	Contains protein domain (PF000038) - Intermediate filament proteins	struct	264683, 18108361
951	20451411 (1901, 1902)	Novel Protein sim. GBank gl 5420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264604
952	79566954 (1903, 1904)	Novel Protein sim. GBank gl 5305702 gb AAD41779.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		calhepsin	264910, 264691
953	10196003 (1905, 1906)	Novel Protein sim. GBank gl 2495842 sp Q4714 VFHS ECOLI - HYPOTHETICAL 41.8 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION		transport	264510
954	9893328 (1907, 1908)	Novel Protein sim. GBank gl 2360995 (AF016253) - D-amino acid dehydrogenase [Klebsiella aerogenes]		dehydrogenase	264508
955	95313410 (1908, 1910)	Novel Protein sim. GBank gl 5454064 ref NP_008319.1 pSIP1 - SYT interacting protein	Contains protein domain (PF000076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	56994075, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264910, 264758, 264759, 265010, 264601, 264760, 18108351, 264762, 264763, 264764, 264766, 264686, 264767, 264687, 264768, 264769, 264689, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 56182333, 264639, 18108388, 264563, 264564
956	80064224 (1911, 1912)	Novel Protein sim. GBank gl 2052129 emb CAB08155  - (Z94752) rimJ [Mycobacterium tuberculosis]			264605
957	80056208 (1913, 1914)	Novel Protein sim. GBank gl 1709787 sp Q00451 PRF1_LYCES - 36.4 KD PROLINE-RICH PROTEIN		UNCLASSIFIED	264603, 18108362
958	80036446 (1915, 1916)	Novel Protein sim. GBank gl 2129478 pir IS51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264908, 264910, 284762, 263978, 264637
959	80026647 (1917, 1918)	Novel Protein sim. GBank gl 2131050 emb CAB09260  - (Z95844) opcA [Mycobacterium tuberculosis]		UNCLASSIFIED	264602, 264692
960	37815408 (1918, 1920)	Novel Protein sim. GBank gl 2129478 pir IS51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264259
961	20567383 (1921, 1922)				263978
962	11399318 (1923, 1924)				264593

963	80590374 (1925, 1926)				UNCLASSIFIED	264510, 264288, 264555, 264558, 264559, 264486
964	79832019 (1927, 1928)	Novel Protein sim. GBank gl 4598622 dbj BAA76833.1  - (AB023206) KIAA0989 protein [Homo sapiens]			UNCLASSIFIED	264112, 264910, 264689
965	81228485 (1928, 1930)	Novel Protein sim. GBank gl 5420387 emb CAB46678.1  - (AJ243459) proteophosphoglycan [Leishmania major]			UNCLASSIFIED	264488, 265017, 264448, 264634, 264558, 83373044
966	95292815 (1931, 1932)				UNCLASSIFIED	264908, 264592, 264598, 264604, 264788, 21908764, 264692, 264693, 264638
967	79255708 (1933, 1934)	Novel Protein sim. GBank gl 1731207 sp Q11156 RGX3_MYCTU - SENSORY TRANSDUCTION PROTEIN REGX3	Contains protein domain (PF00072) - Response regulator receiver domain		phosphatase	264760
968	79560289 (1935, 1936)	Novel Protein sim. GBank gl 2661836 emb CAA75187  - (Y14964) putative transport protein [Methylophilus methylotrophus]			transport	264693
969	79918470 (1937, 1938)	Novel Protein sim. GBank gl 5419878 emb CAB46422.1  - (AL098747) hypothetical protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, C2H2 type		dna_ma_bind	35698288, 264685, 264686, 35695917, 264692, 18108374, 264635
970	95085947 (1939, 1940)				UNCLASSIFIED	18108382, 18108394, 18108398, 22278995, 22278998, 22278998, 22278998, 28147820, 264828, 265006, 265007, 265008, 265009, 18108348, 33109954, 265010, 265011, 18108351, 264288, 21908767, 21906768, 18108370, 18108374, 18108377, 264630, 264635, 18108380, 83373044, 18108387, 18108388
971	78919770 (1941, 1942)				UNCLASSIFIED	265007, 265020, 22279002
972	20710704 (1943, 1944)					264557
973	20370183 (1945, 1946)	Novel Protein sim. GBank gl 1723119 sp P53990 Y174_HUMAN - HYPOTHETICAL PROTEIN KIAA0174				264604
974	80057103 (1947, 1948)				UNCLASSIFIED	264565
975	10196018 (1949, 1950)				UNCLASSIFIED	264510
976	80205742 (1951, 1952)	Novel Protein sim. GBank gl 3881459 emb CAA92988.1  - (Z68753) predicted using GeneFinder; Similarity to Yeast hypothetical protein YIK9 (SW:YIK9_YEAST); cDNA EST EMBL:D27680 comes from this gene; cDNA EST EMBL:D27679 comes from this gene; cDNA EST EMBL:D64477 comes from this ge...			UNCLASSIFIED	264508, 264906, 264758, 264632, 264639, 264563
977	10355349 (1953, 1954)	Novel Protein sim. GBank gl 549456 sp Q05335 XYS3_PSEPU - XYLDLEOF OPERON TRANSCRIPTIONAL ACTIVATOR 3			UNCLASSIFIED	264906
978	80025927 (1955, 1956)				UNCLASSIFIED	264600, 264602, 264603, 264604
979	80447820 (1957, 1958)	Novel Protein sim. GBank gl 3171904 emb CAA75869  - (Y15908) DIA-12C protein [Homo sapiens]			UNCLASSIFIED	264767, 264788, 265008, 265007, 264906
980	80025928 (1959, 1960)				UNCLASSIFIED	264600, 264602, 264605
981	80098550 (1961, 1962)	Novel Protein sim. GBank gl 3599940 (AF017368) - facicgenital dysplasia protein 2 [Mus musculus]			UNCLASSIFIED	264692, 264555, 264556, 264557, 264559

982	80195670 (1963, 1964)	Novel Protein sim. GBank gij2950220jemb[CAA71575] - (Y10545) fused-ccdB [Escherichia coli]		UNCLASSIFIED	264404
983	90995041 (1965, 1966)	Novel Protein sim. GBank gij476389[prj]B43402 - myosin heavy chain-B, neuronal - chicken		struct	65274572, 56182575, 264808, 264809, 265007, 265008, 264758, 265010, 55811150, 33657023, 264634, 264557, 264558
984	20466878 (1967, 1968)			UNCLASSIFIED	264605
985	85461368 (1969, 1970)	Novel Protein sim. GBank gij3451504jemb[CAA07660.1] - (AJ007747) hypothetical protein BbLPS1.21 [Bordetella bronchiseptica]	Contains protein domain (PF00534) - Glycosyl transferases group 1	transferase	58182435, 264600
986	87102888 (1971, 1972)			UNCLASSIFIED	264106, 264110, 265020, 60170615
987	79867231 (1973, 1974)				264809
988	19858661 (1975, 1976)			UNCLASSIFIED	264600
989	88095329 (1977, 1978)			UNCLASSIFIED	264508, 265017, 264534, 264584
990	88057748 (1979, 1980)	Novel Protein sim. GBank gij5725506jgb[AA4080.1]AF08015 - (AF080152) METH1 protein [Homo sapiens]	Contains protein domain (PF01421) - Reprolysin (M128) family zinc metalloprotease	oxidase	264259, 264908, 265009, 264910, 264596, 264369, 264288, 264768, 264628, 264635, 264568
991	10106140 (1981, 1982)			UNCLASSIFIED	264809
992	78845694 (1983, 1984)	Novel Protein sim. GBank gij2105049jemb[CAB08835] - (Z85438) hypothetical protein Rv3845 [Mycobacterium tuberculosis]	Contains protein domain (PF00211) - Adenylate and Guanylate cyclase catalytic domain	UNCLASSIFIED	264508, 264593
993	10814053 (1985, 1986)				264907
994	11090590 (1987, 1988)	Novel Protein sim. GBank gij3329297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]		reductase	264602
995	94321811 (1989, 1990)	Novel Protein sim. GBank gij5106572jgb[AAD39760.1]AF14394 - (AF143946) transcriptional activator SRCAP [Homo sapiens]	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	18108398, 65274572, 22278998, 264490, 60432049, 29331827, 28146498, 264508, 264905, 264907, 264908, 56182435, 265008, 264591, 264592, 60432228, 60431735, 33657402, 264595, 264758, 21906754, 265010, 265017, 265018, 264605, 264760, 264448, 264763, 264768, 21906765, 21906768, 21906769, 55811957, 264692, 264693, 264629, 35696423, 55811576, 35695855, 264638, 264555, 264556, 264558, 83373044, 22279002, 264563
996	91013745 (1991, 1992)	Novel Protein sim. GBank gij2911719 (AC004227) - KIA001LB [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	phosphatase	83373044, 29331824, 283978, 55811957, 56528486, 87188518, 284910, 284906, 264585, 264566, 264693, 264766
997	80503347 (1993, 1994)	Novel Protein sim. GBank gij2649101 (AE001001) - ABC transporter, ATP-binding protein [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	35696286, 22278997, 22278998, 264508, 264905, 264908, 265010, 264600, 264602, 264605, 264688, 264769, 265021, 264565, 18108391
998	11397390 (1995, 1996)	Novel Protein sim. GBank gij123530jgpf04929jhrpx_plalo - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR			18108391, 264595

999	11768047 (1997, 1998)	Novel Protein sim. GBank gij2506697[sp]P46490[YFCA_HAEIN - HYPOTHETICAL PROTEIN H0198]		UNCLASSIFIED	284882	
1000	20727844 (1999, 2000)			UNCLASSIFIED	284602	
1001	86673131 (2001, 2002)	Novel Protein sim. GBank gij2224899[gb]BAA20833] - (AB002377) KIAA0379 [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	60432049, 284907, 284908, 284511, 284803, 284683, 284684, 284687, 284689, 29148827, 21908769, 284692, 18108385, 22278000	
1002	80189603 (2003, 2004)	Novel Protein sim. GBank gij1586121[sp]P37709[TRHY_RABIT - TRICHOHYALIN]		struct	285009, 284369, 285020	
1003	17833491 (2005, 2006)				285019	
1004	18314987 (2007, 2008)	Novel Protein sim. GBank gij854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]			284635	
1005	79617144 (2008, 2010)	Novel Protein sim. GBank gij114073[sp]P07672[APT_ECOLI - ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)]		UNCLASSIFIED	284508	
1006	37815429 (2011, 2012)					
1007	79620871 (2013, 2014)	Novel Protein sim. GBank gij4062979[gb]BAA36210.1] - (AB017138) epsilon subunit of malonate decarboxylase [Pseudomonas putida]		UNCLASSIFIED	284259 284905	
1008	86094444 (2015, 2016)	Novel Protein sim. GBank gij2808807[emb]CAA04607.1] - (AJ001206) putative trehalose synthase [Streptomyces coelicolor]		synthase	285007, 284602, 284605, 284760, 284636	
1009	57451289 (2017, 2018)	Novel Protein sim. GBank gij3639077 (AF090113) - AMPA receptor binding protein [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	284102, 284288	
1010	94672537 (2019, 2020)	Novel Protein sim. GBank gij3746332 (AF016307) - possible NADH-dependent oxidase, may function as a demethylase [Sinorhizobium meliloti]		dehydrogenase	284592	
1011	85546916 (2021, 2022)	Novel Protein sim. GBank gij2342847[gb]AAB86591.1] - (U90653) DHC-domain-containing cysteine-rich protein [Homo sapiens]		UNCLASSIFIED	35896052, 284905, 284784, 284788, 35695917, 284629	
1012	95284456 (2023, 2024)	Novel Protein sim. GBank gij3413411[emb]CAA20272] - (AL031231) guanosine pentaphosphate synthetase/ polyribonucleotide nucleotidyltransferase [Streptomyces coelicolor]	Contains protein domain (PF00013) - KH domain	phosphorylase	35896052, 284905, 284600, 284601, 284602, 284605, 284762, 284768, 284768, 284689	
1013	86095772 (2025, 2026)			UNCLASSIFIED	284591, 21908768	
1014	86608628 (2027, 2028)			UNCLASSIFIED	29331824, 285019, 285020	

1015	95418878 (2029, 2030)	Novel Protein sim. GBank gij4159995 (AF063095) - SELIL (Mus musculus)	Contains protein domain (PF00040) - Fibronectin type II domain	struct	22278994, 22278995, 56994075, 22278996, 22278999, 284258, 29331825, 29331828, 264807, 56182435, 284510, 264591, 264593, 60433358, 284594, 55812038, 284758, 21906754, 33657084, 265010, 264600, 265017, 265018, 265019, 18108351, 21906765, 21806766, 21906767, 21906768, 55811957, 265022, 33657023, 65274620, 33657182, 32833986, 18108370, 18108377, 55811576, 35698423, 264630, 22279000, 264565
1016	78559694 (2031, 2032)	Novel Protein sim. GBank gij25089694p41407ACPD, ECOLI - ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)		esterase	264686, 264693
1017	11069213 (2033, 2034)	Novel Protein sim. GBank gij5103943jdbjBAA79259.1 - (AP000059) 802aa long hypothetical oligopeptide-binding protein oppA (Aeropyrum pernix)	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	transport	264600
1018	80072430 (2035, 2036)	Novel Protein sim. GBank gij4493973lenb CAB39032.1 - (AL034559) predicted using hexExon; MAL3P7.14 (PFC0925w). Hypothetical protein, len. 489 aa [Plasmodium falciparum]			22278986, 29148627, 264563
1019	11703607 (2037, 2038)			UNCLASSIFIED	264686
1020	80234432 (2038, 2040)				264508, 264509, 264512, 264600, 264762, 264769, 264688, 18108370, 264636, 264638, 264486
1021	37036243 (2041, 2042)	Novel Protein sim. GBank gij4633807jgb AAD26859.1 AF12779 - (AF127795) trehalose biosynthetic enzyme TreY [Rhizobium leguminosarum bv. viciae]		synthase	264789
1022	80502627 (2043, 2044)	Novel Protein sim. GBank gij1781230lenb CAB062771 - (Z83687) hypothetical protein Rv3137 [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	35696052, 264508, 265008, 265009, 264769, 18108387, 264563
1023	11399341 (2045, 2046)	Novel Protein sim. GBank gij3777495 (U92083) - calcium transporting ATPase [Pichia angustia]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase-associated	264593
1024	80057129 (2047, 2048)			UNCLASSIFIED	52646842, 33657402, 33657023, 18108379, 55811576, 264631, 264556, 264557, 264559, 18108388, 264586
1025	78644200 (2048, 2050)	Novel Protein sim. GBank gij3483045lenb CAA20556 - (AL031371) putative transport system permease protein [Streptomyces coelicolor]		transport	264693
1026	80025946 (2051, 2052)	Novel Protein sim. GBank gij1174922jpc Q02322 UVRD, HAEIN - DNA HELICASE II		helicase	264602
1027	17659234 (2053, 2054)	Novel Protein sim. GBank gij4757728ref NP_004886.1 pAGTA - angiotensin/vasopressin receptor AII/AVP-like		UNCLASSIFIED	265017

1028	20287928 (2055, 2056)	Novel Protein sim. GBank gij2791409[emb CAA16003] - (AL021184) acn [Mycobacterium tuberculosis]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	UNCLASSIFIED	264600	
1029	94565090 (2057, 2058)			UNCLASSIFIED	264595	
1030	88095343 (2059, 2060)			UNCLASSIFIED	264907, 264908, 264510, 264512, 265009, 265010, 265011, 264600, 264602, 264603, 264605, 264769, 18108372, 18108374	
1031	95289117 (2061, 2062)			UNCLASSIFIED	264905, 264906, 264909, 264595, 264692, 264630, 264634, 264638	
1032	94673275 (2063, 2064)	Novel Protein sim. GBank gij4503895[ref NP_000145.1 pGALK - galactokinase 1		UNCLASSIFIED	264689	
1033	86464818 (2065, 2066)	Novel Protein sim. GBank gij2982990 (AE000682) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	35896052, 264908, 264510, 18108354, 264687, 264769, 264689, 60431602, 18108385, 264486	
1034	79245837 (2067, 2068)	Novel Protein sim. GBank gij405895 (U00007) - methionyl-tRNA synthetase [Escherichia coli]		UNCLASSIFIED	264906	
1035	79956355 (2069, 2070)			UNCLASSIFIED	264692	
1036	85804998 (2071, 2072)			UNCLASSIFIED	264905, 66712502, 264908, 264768	
1037	87896058 (2073, 2074)			UNCLASSIFIED	29331824, 264909, 60433438, 265019	
1038	20481015 (2075, 2076)	Novel Protein sim. GBank gij790819 (L39881) - polycystic kidney disease-associated protein [Homo sapiens]	Contains protein domain (PF01477) - PLAT/LH2 domain		264604, 264634	
1039	87260021 (2077, 2078)	Novel Protein sim. GBank gij2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	264092, 264093, 264094, 264683, 264689, 263987	
1040	80026840 (2079, 2080)	Novel Protein sim. GBank gij2352095 (U97022) - DNA topoisomerase I [Fervidobacterium islandicum]	Contains protein domain (PF01131) - Prokaryotic DNA topoisomerase	isomerase	264595	
1041	10156862 (2081, 2082)	Novel Protein sim. GBank gij3256535[db BAA29218.1  - (AP000001) 301aa long hypothetical 2-phosphoglycerate kinase [Pyrococcus horikoshii]		kinase	264907	
1042	11084375 (2083, 2084)	Novel Protein sim. GBank gij2058299[emb CAA66953] - (X88309) ARI protein [Drosophila melanogaster]			264605	
1043	80057136 (2085, 2086)	Novel Protein sim. GBank gij1670167[emb CAA70125] - (Y08921) msK [Streptomyces reticuli]	Contains protein domain (PF00005) - ABC transporter	transport	264565, 264567	
1044	80025952 (2087, 2088)			UNCLASSIFIED	265006, 264602, 265017	
1045	52415482 (2089, 2090)	Novel Protein sim. GBank gij5688890[emb CA552053.1] - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]			29331825, 264637	
1046	11754862 (2091, 2092)	Novel Protein sim. GBank gij854065[emb CAA58337] - (X83413) U88 [Human herpesvirus 6]		helicase	264686	
1047	37036258 (2093, 2094)	Novel Protein sim. GBank gij4210471[db BAA74535.1] - (AB019033) orfSA [Pseudomonas sp.]		UNCLASSIFIED	264769	
1048	79186400 (2095, 2096)	Novel Protein sim. GBank gij3413419[emb CAA20279] - (AL031232) hypothetical protein SC10H5.07 [Streptomyces coelicolor]	Contains protein domain (PF00220) - Neurohypophysial hormones, N-terminal Domain	UNCLASSIFIED	264687	
1049	81755108 (2097, 2098)	Novel Protein sim. GBank gij5051636[gb AAD38326.1 AF07372] - (AF07372) EH domain-binding mitotic phosphoprotein [Homo sapiens]		UNCLASSIFIED	264905, 264634	
1050	79471521 (2099, 2100)			UNCLASSIFIED	264686	



1051	80475471 (2101, 2102)				UNCLASSIFIED	18108374, 264769, 265010, 265011, 264601, 265009, 264604, 264605, 264636, 18108351, 264692
1052	82442962 (2103, 2104)	Novel Protein sim. GBank gi 3123275 sp P35136 SERA_BACSU - D-3- PHOSPHOGLYCERATE DEHYDROGENASE (PGDH)	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases		dehydrogenase	264508, 264762, 264687, 264486
1053	94851640 (2105, 2106)	Novel Protein sim. GBank gi 5441319 emb CAB46717.1  - (AL034396) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]				264686, 18108374, 29331824, 83373044, 21906754, 52645156, 56182435, 264689, 29331827, 27486281, 35696052, 21908765, 35698423, 21908768, 56182575, 21908769, 55811957, 87168518, 35696286, 22278997, 265020, 265011, 265021, 265022, 265007, 265018, 22279000, 22279002, 264482, 264908, 52644150, 264909, 264288, 29331822, 52645080, 264766
1054	79580225 (2107, 2108)				UNCLASSIFIED	264686
1055	80594138 (2109, 2110)	Novel Protein sim. GBank gi 5052508 gb AA038584.1 AF14560 - (AF145609) BCDNA GH02833 [Drosophila melanogaster]	Contains protein domain (PF00270) - DEAD/DEAH box helicase		helicase	264907, 264602, 264681, 264288, 21906768, 33657109, 55810764, 35695855, 264631
1056	17882319 (2111, 2112)	Novel Protein sim. GBank gi 3021676 db BAA25358  - (D86033) RNA polymerase sigma-70 factor [Pseudomonas fluorescens]			mapolymerase	264906
1057	85667216 (2113, 2114)	Novel Protein sim. GBank gi 1226281 (U50308) - No definition line found [Caenorhabditis elegans]			UNCLASSIFIED	264682
1058	80376576 (2115, 2116)					264764
1059	94662754 (2117, 2118)	Novel Protein sim. GBank gi 170018 sp P46808 GREA_MYCLE - TRANSCRIPTION ELONGATION FACTOR GRE (TRANSCRIPT CLEAVAGE FACTOR GRE)			transcriptfactor	35696052, 35695855, 265009, 264636
1060	79481168 (2119, 2120)	Novel Protein sim. GBank gi 2499087 sp Q08332 UGGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)			glycoprotein	29146499, 264681, 264683, 264687
1061	11034025 (2121, 2122)	Novel Protein sim. GBank gi 90254 pir J28334 - protein- tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse			phosphatase	264634
1062	38557937 (2123, 2124)	Novel Protein sim. GBank gi 3334200 sp Q49954 GCSP_SOL_TU - GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)			dehydrogenase	264593
1063	8490481 (2125, 2126)	Novel Protein sim. GBank gi 2499968 sp Q41228 PSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A)				264508
1064	78891783 (2127, 2128)	Novel Protein sim. GBank gi 82654 pir J40086 - 10K zein precursor - maize				265007, 265008, 18108351, 18108385

1065	80021208 (2129, 2130)	Novel Protein sim. GBank gij212098[pri][S70682 - glycosyltransferase homolog - Bordetella pertussis]		transferase	264600, 264602, 264689
1066	17886879 (2131, 2132)	Novel Protein sim. GBank gij2506382[sp]P15042[DNLJ, ECOLI - DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (NAD+))]		synthase	265009
1067	10132178 (2133, 2134)	Novel Protein sim. GBank gij4007669[emb][CAA22355] - (AL034443) putative oxidoreductase [Streptomyces coelicolor]	Contains protein domain (PF00248) - Aldo/keto reductase family	reductase	264609 264688, 18108382, 264558, 264600, 264760
1068	82062057 (2135, 2136)	Novel Protein sim. GBank gij4589484[dbj][BAA76770.1] - (AB023143) KIAA0926 protein [Homo sapiens]		UNCLASSIFIED	264604
1069	83002954 (2137, 2138)	Novel Protein sim. GBank gij120304[sp]P15932[FLGK, SALT - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1)]		UNCLASSIFIED	264604, 264760
1070	82101992 (2139, 2140)	Novel Protein sim. GBank gij1750397 (U81261) - glutamate synthase large subunit [Pseudomonas aeruginosa]		synthase	264602
1071	20710589 (2141, 2142)	Novel Protein sim. GBank gij477532[pri][A49175 - Motch B protein - mouse (fragment)]	Contains protein domain (PF00008) - EGF-like domain	synthase	264606
1072	82358540 (2143, 2144)	Novel Protein sim. GBank gij3893109[emb][CAA76940] - (Y17820) CALO protein [Drosophila melanogaster]		UNCLASSIFIED	264687, 264688, 21908784, 35698052, 35695917, 35695855, 264600, 264601, 264602, 265008, 264605, 264508, 264805, 264690, 264906, 264762, 264828, 264768
1073	79814400 (2145, 2146)	Novel Protein sim. GBank gij1176203[sp]P46442[YHCM, ECOLI - HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (F375)]		ATPase-associated	264769
1074	80105992 (2147, 2148)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITD4, AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		kinase	264905
1075	81850293 (2149, 2150)	Novel Protein sim. GBank gij3413828[emb][CAA20296] - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	264600
1076	80477284 (2151, 2152)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITD4, AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		UNCLASSIFIED	18108394, 264769, 264634, 264636
1077	79831334 (2153, 2154)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITD4, AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		UNCLASSIFIED	264600
1078	20288874 (2155, 2156)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITD4, AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		UNCLASSIFIED	264600
1079	80494518 (2157, 2158)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITD4, AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		UNCLASSIFIED	264600
1080	11767188 (2159, 2160)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITD4, AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		UNCLASSIFIED	264684
1081	94747080 (2161, 2162)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITD4, AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		UNCLASSIFIED	83373044, 265019, 22278002, 264482, 18108351, 264682, 264688, 264608, 264693, 264487, 264758, 264768, 264769, 21908787, 284511, 264910, 264634, 264635, 264905, 264636, 264906, 264637, 264907, 264908, 264764, 264638, 20281099, 264766, 264595
1082	81490656 (2163, 2164)	Novel Protein sim. GBank gij4033487[sp]Q44472[ITD4, AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		UNCLASSIFIED	264684

1083	87446717 (2165, 2166)	Novel Protein sim. GBank gil1722945[sp]Q10523[Y01N_MYCTU - HYPOTHETICAL 44.6 KD PROTEIN CY427.23		UNCLASSIFIED	60424179, 264905, 264908, 264510, 60432229, 264759, 87168474, 264605, 264768, 264689, 18108364, 18108376, 35695855, 264636 264769
1084	37799308 (2167, 2168)	Novel Protein sim. GBank gil18384[sp]P32057[WCAI_ECOLI]; PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAI		UNCLASSIFIED	
1085	86475368 (2169, 2170)	Novel Protein sim. GBank gil1899190 (U90204) - heat shock protein 80 [Tukamurella tyrosinosolvens]	Contains protein domain (PF00116) - eph		60432229, 264687
1086	79608269 (2171, 2172)	Novel Protein sim. GBank gil1172956[sp]P46176[RL14_ACYKS - 50S RIBOSOMAL PROTEIN L14	Contains protein domain (PF00238) - ribosomalprot Ribosomal protein L14		264486
1087	79603979 (2173, 2174)	Novel Protein sim. GBank gil160198[emb]CAA15431 - (AL006583) dJ327J16.3 (novel CHROMObox family protein) [Homo sapiens]	Contains protein domain (PF00385) - "chromo" (CHRromatin Organization Modifier) domain		29331827, 264693
1088	79654963 (2175, 2176)	Novel Protein sim. GBank gil2983155 (AE000693) - phosphoglucosyltransferase/phosphomannomutase [Aquifex aerophilus]		UNCLASSIFIED	264905, 264601, 18108387
1089	80216800 (2177, 2178)	Novel Protein sim. GBank gil14981768[gb]AAD36290.1(AE001778) NADH dehydrogenase, 30 kDa subunit, putative [Thermotoga maritima]	Contains protein domain (PF00329) - Respiratory-chain NADH dehydrogenase, 30 kDa subunit	UNCLASSIFIED	264488, 264511, 265011, 264682, 264768, 264689, 21906764, 35695917, 265020, 32833986, 18108370, 35695855
1090	11083825 (2179, 2180)	Novel Protein sim. GBank gil4007680[emb]CAA22366 - (AL034443) putative oxidoreductase [Streptomyces coelicolor]			264604
1091	12917471 (2181, 2182)	Novel Protein sim. GBank gil2495562[sp]P77239[YLCD_ECOLI] - HYPOTHETICAL 44.3 KD PROTEIN IN NFRB-PHEP INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264637
1092	80252286 (2183, 2184)	Novel Protein sim. GBank gil2960098[emb]CAA17998.1 - (AL022121) ntl [Mycobacterium tuberculosis]	Contains protein domain (PF00730) - Endonuclease III		264566 264769, 35695917, 35695855, 264600, 264602, 264603, 264605, 18108351
1093	80496304 (2185, 2186)	Novel Protein sim. GBank gil1001642[db]BAA10373 - (DB4002) dGTP triphosphohydrolase [Synecococcus sp.]		UNCLASSIFIED	264686
1094	10860972 (2187, 2188)	Novel Protein sim. GBank gil4585587[emb]CAB40855.1 - (AL049628) putative adenine glycosylase [Streptomyces coelicolor]	Contains protein domain (PF00455) - Bacterial regulatory proteins, deoR family		264906, 265007, 264595, 264600, 264602, 264603, 264604, 264605, 264762, 264768, 264769, 264636, 264558, 18108387, 60432113, 264482, 264486
1095	87457250 (2189, 2190)	Novel Protein sim. GBank gil115001[sp]P19206[BIOB_BACSH] - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)			264600, 264602, 264603, 264604, 264605, 264631
1096	80025977 (2191, 2192)	Novel Protein sim. GBank gil114135[sp]P08205[ARGA_ECOLI] - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)			265019 264687
1097	79239560 (2193, 2194)	Novel Protein sim. GBank		UNCLASSIFIED	
1098	79186424 (2195, 2196)	Novel Protein sim. GBank gil114135[sp]P08205[ARGA_ECOLI] - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)		synthase	

1099	38523838 (2197, 2198)	Novel Protein sim. GBank gi 3915144 sp O33017 TRMD_MYCLE - TRNA (GUANINE- N1)-METHYLTRANSFERASE (M1G- METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)		UNCLASSIFIED	264603
1100	85738571 (2189, 2200)	Novel Protein sim. GBank gi 3023255 sp Q64420 ACOD_MESAU - ACYL-COA DESATURASE (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA9)-DESATURASE)		desaturase	284259, 284636
1101	80491857 (2201, 2202)	Novel Protein sim. GBank gi 1174735 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)	Contains protein domain (PF01396) - Topoisomerase DNA binding C4 zinc finger	isomerase	284769
1102	79777614 (2203, 2204)	Novel Protein sim. GBank gi 1908596 (U81788) - kinesin-73 [Drosophila melanogaster]		UNCLASSIFIED	284910, 284909
1103	81897259 (2205, 2206)	Novel Protein sim. GBank gi 2935448 (AF048976) - synaptic ras GTPase-activating protein p135 SynGAP [Rattus norvegicus]		struct	284757
1104	95003115 (2207, 2208)	Novel Protein sim. GBank gi 2935448 (AF048976) - synaptic ras GTPase-activating protein p135 SynGAP [Rattus norvegicus]		UNCLASSIFIED	284558, 22278002
1105	80255121 (2209, 2210)				284586
1106	79314110 (2211, 2212)			UNCLASSIFIED	284555, 284389
1107	80470019 (2213, 2214)				284908, 284769
1108	80440616 (2215, 2216)	Novel Protein sim. GBank gi 1173421 sp P43416 SECY_STRSC - PREPROTEIN TRANSLOCASE SECY SUBUNIT		transport	284907, 284510, 284511, 284600, 284602, 284605, 284768, 284769
1109	80084615 (2217, 2218)	Novel Protein sim. GBank gi 2995310 emb CAA18338  - (AL022268) putative ATP-dependent helicase [Streptomyces coelicolor]		helicase	284602, 284605, 284636
1110	80503554 (2219, 2220)				284908, 284593, 265010, 264601, 264603, 284604, 284605, 284682, 284768, 284689, 284636
1111	80071744 (2221, 2222)	Novel Protein sim. GBank gi 2622039 (AE000868) - type I restriction modification system, subunit S [Methanobacterium thermoautotrophicum]			18108370, 284557
1112	95010088 (2223, 2224)				284908
1113	82456352 (2225, 2226)	Novel Protein sim. GBank gi 3218376 emb CAA19628  - (AL023862) putative oxidoreductase [Streptomyces coelicolor]		UNCLASSIFIED	284600, 284602, 284604, 284605, 284762, 284768, 284565
1114	14898014 (2227, 2228)	Novel Protein sim. GBank gi 1083428 pir S54876 - NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor - mouse		dehydrogenase	284636
1115	11765583 (2229, 2230)				284686
1116	79841152 (2231, 2232)			UNCLASSIFIED	284908

1117	95305485 (2233, 2234)	Novel Protein sim. GBank gi 3255955 emb CAA94089  - (270200) U5 snRNP-specific 200kD protein [Homo sapiens]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108392, 264488, 263994, 264489, 18108398, 56182575, 22278995, 22278998, 35696286, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 68714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 26146488, 264508, 264905, 264509, 264908, 264907, 264908, 66712502, 264909, 52844045, 56182435, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 60170831, 264591, 264592, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264596, 264758, 264759, 21906754, 33109954, 33657084, 265011, 87168559, 264600, 264601, 264602, 264603, 265017, 264604, 265018, 264605, 265019, 264760, 55811150, 264681, 264762, 18108351, 264448, 264682, 264764, 264683, 264288, 264389, 264684, 264685, 264766, 264767, 264886, 264687, 264768, 264769, 264888, 18108359, 264889, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148784, 35695917, 265020, 265021, 265022, 60170815, 264690, 264691, 33657023, 264692, 264693, 65274620, 33657108, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695783, 264691
1118	79563326 (2235, 2236)			UNCLASSIFIED	264897
1119	79842463 (2237, 2238)			UNCLASSIFIED	264907
1120	79480463 (2239, 2240)	Novel Protein sim. GBank gi 5420387 emb CAB46678.1  - (AJ243459) proteophosphoglycan [Leishmania major]		collagen	29331827, 265018, 265019, 264681, 265021, 60170615, 18108387
1121	79471716 (2241, 2242)	Novel Protein sim. GBank gi 1644450 (U87884) - MEX-3 [Caenorhabditis elegans]	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	264683, 264632, 18108388
1122	79456246 (2243, 2244)			UNCLASSIFIED	264639, 264563
1123	79637119 (2245, 2246)	Novel Protein sim. GBank gi 98800 prj S17768 - 3-dehydroquininate synthase (EC 4.6.1.3) - Mycobacterium tuberculosis		synthase	264683, 27486265
1124	79811586 (2247, 2248)			UNCLASSIFIED	264909
1125	79757861 (2248, 2250)			UNCLASSIFIED	264910
1126	79758914 (2251, 2252)	Novel Protein sim. GBank gi 138154 sp P03643 VGG_BPPIX - MAJOR SPIKE PROTEIN (G PROTEIN) (GPG)		eph	264805, 264809, 264910
1127	11800930 (2253, 2254)			UNCLASSIFIED	264882
1128	8384885 (2255, 2256)	Novel Protein sim. GBank gi 5002704 emb CAB44358.1  - (AJ242630) DNA polymerase [Methylobacterium sp. DM4]	Contains protein domain (PF00476) - DNA polymerase family A	polymerase	264511

1129	80422480 (2257, 2258)	Novel Protein sim. GBank gij5689485[dj]BAA83026.1] - (AB028987) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	265011, 264766
1130	79420151 (2259, 2260)	Novel Protein sim. GBank		UNCLASSIFIED	264595
1131	80055391 (2261, 2262)	gi 4981328 gb AAD35881.1 AE00174 - (AE001747) bioY protein [Thermotoga maritima]		UNCLASSIFIED	35696286, 22278998, 28331828, 264603, 264605, 264559
1132	82062248 (2263, 2264)	Novel Protein sim. GBank gij1841552 (U89336) - unknown [Homo sapiens]		UNCLASSIFIED	22278998, 264906, 265009, 264600, 264602, 264604, 264605, 264780, 32833986, 18108374
1133	17290437 (2265, 2266)			UNCLASSIFIED	265018
1134	80233376 (2267, 2268)			UNCLASSIFIED	264512, 264534
1135	80029393 (2269, 2270)	Novel Protein sim. GBank gij4539171[emb]CAB39700.1] - (AL049485) conserved hypothetical protein [Streptomyces coelicolor]			264508, 264600, 264602, 264603, 18108376
1136	79842052 (2271, 2272)	Novel Protein sim. GBank gij4982454[gb]AAD36931.1 AE00182 - (AE001823) ATP-dependent protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	264906, 264808
1137	90931557 (2273, 2274)	Novel Protein sim. GBank gij4972746[gb]AAD34768.1] - (AF132180) unknown [Drosophila melanogaster]	Contains protein domain (PF00515) - collagen TPR Domain		22278998, 22278999, 35696052, 264907, 265009, 60433356, 264598, 265010, 264448, 264682, 264767, 264689, 265020, 264692, 55811576, 35695855, 264631, 264632, 22279002
1138	79841163 (2275, 2276)	Novel Protein sim. GBank gij731607[sp]P38739YHC8_YEAST - HYPOTHETICAL 63.8 KD PROTEIN IN CUT-1-RIM1 INTERGENIC REGION PRECURSOR	struct		264808
1139	76633561 (2277, 2278)	Novel Protein sim. GBank gij3650031 (AC005396) - putative proline-rich cell wall protein [Arabidopsis thaliana]	UNCLASSIFIED	264893	
1140	39480358 (2279, 2280)		UNCLASSIFIED	264593	
1141	79638019 (2281, 2282)		UNCLASSIFIED	265019, 264693	
1142	19635848 (2283, 2284)		UNCLASSIFIED	264631	
1143	87762158 (2285, 2286)	Novel Protein sim. GBank gij3928000[emb]CAA05880] - (A1003125) procollagen I N-proteinase [Homo sapiens]	Contains protein domain (PF00090) - oxidase Thrombospondin type 1 domain		56182575, 264808, 264600, 264632, 87168518
1144	80089988 (2287, 2288)		UNCLASSIFIED	264635, 264636, 264907, 264593, 264908, 264566, 264909	
1145	14610262 (2289, 2290)		UNCLASSIFIED	264112	
1146	82062082 (2291, 2292)		UNCLASSIFIED	264768, 264689, 35696286, 264780, 264805, 264488, 264559	
1147	80071761 (2293, 2294)	Novel Protein sim. GBank	kinase		264557
1148	80048433 (2295, 2296)	gi 2499003 sp P76422 THID_ECOLI - PHOSPHOMETHYL PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)			264591
1149	11607438 (2297, 2298)	Novel Protein sim. GBank gij2896734[emb]CAA17213.1] - (AL021897) hypothetical protein Rv1097c [Mycobacterium tuberculosis]			264591

1150	81325074 (2289, 2300)	Novel Protein sim. GBank gij2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]		ATPase-associated	264488, 35686286, 264807, 264908, 264909, 264910, 264593, 264596, 264758, 264764, 264766, 264768, 264693, 264628, 60431850, 264564, 264566, 264567, 264595
1151	80070874 (2301, 2302)	Novel Protein sim. GBank gij4324655jgb AAD16978  - (AF108181) DNA polymerase III alpha subunit [Streptomyces coelicolor]		polymerase	
1152	80235547 (2303, 2304)	Novel Protein sim. GBank gij387427jemb CAB07311.1  - (Z92825) predicted using GeneFinder; Similarity to Yeast low affinity glucose transporter HXT4 (PS:32467); cDNA EST EMBL.C12555 comes from this gene; cDNA EST YK404c10.3 comes from this gene; cDNA EST YK404c10.5 comes from this...		glycoprotein	264488, 22278988, 264905, 264629, 264486
1153	80027783 (2305, 2306)	Novel Protein sim. GBank gij4240315jdb BAA74938.1  - (AB020720) KIAA0913 protein [Homo sapiens]		UNCLASSIFIED	264910, 264555, 264557, 265008
1154	83002895 (2307, 2308)	Novel Protein sim. GBank gij4240315jdb BAA74938.1  - (AB020720) KIAA0913 protein [Homo sapiens]		UNCLASSIFIED	264690, 264636
1155	78411098 (2309, 2310)	Novel Protein sim. GBank gij4240315jdb BAA74938.1  - (AB020720) KIAA0913 protein [Homo sapiens]	Contains protein domain (PF00122) - transport E1-E2 ATPase	UNCLASSIFIED	264603
1156	57147843 (2311, 2312)	Novel Protein sim. GBank gij586655jdp P37617 ATZN_ECOLI - ZINC-TRANSPORTING ATPASE (ZINC(II)-TRANSLATING P-TYPE ATPASE)		UNCLASSIFIED	264908, 264807, 264758, 264768, 264769, 264689, 264638, 264566
1157	95287711 (2313, 2314)	Novel Protein sim. GBank gij418480jdp P32139 VHR_ECOLI - HYPOTHETICAL 34.0 KD PROTEIN IN GLNA-RBN INTERGENIC REGION		UNCLASSIFIED	264908, 264762, 264687, 264769, 264689, 18108374, 35695855
1158	82454917 (2315, 2316)	Novel Protein sim. GBank gij2486481jdp Q50724 Y09S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C			264687
1159	79186451 (2317, 2318)	Novel Protein sim. GBank gij1138408jdb BAA11490  - (D79995) similar to pig tubulin-tyrosine ligase. [Homo sapiens]			29331822, 29331824, 66714117, 29331826, 60433358, 265018, 265019, 83373044, 18108385, 22279000, 22279002, 264563
1160	91228893 (2318, 2320)	Novel Protein sim. GBank gij1138408jdb BAA11490  - (D79995) similar to pig tubulin-tyrosine ligase. [Homo sapiens]			264369
1161	7417143 (2321, 2322)	Novel Protein sim. GBank gij2443342jdb BAA22380  - (D88764) alpha 2 type I collagen [Rana catesbeiana]		UNCLASSIFIED	264693
1162	79635357 (2323, 2324)	Novel Protein sim. GBank gij4503375jref NP_001376.1 pDPYS - dihydropyrimidinase		UNCLASSIFIED	29331827, 264906
1163	79563186 (2325, 2326)	Novel Protein sim. GBank gij4503375jref NP_001376.1 pDPYS - dihydropyrimidinase		transport	18108398, 29331827, 29331828, 29146498, 29146499, 18108354, 21908768, 29148827, 21908769, 264693, 18108382, 18108385
1164	79650829 (2327, 2328)	Novel Protein sim. GBank gij5052554jgb AAD38607.1 AF14563 - (AF145632) BcDNA.GH06032 [Drosophila melanogaster]		UNCLASSIFIED	264602, 264605, 264769, 18108370, 18108374, 264565
1165	80491888 (2329, 2330)	Novel Protein sim. GBank gij4589476jdb BAA76766.1  - (AB023139) KIAA0922 protein [Homo sapiens]			264488, 35686286, 22278999, 264259, 66714117, 60432289, 35898052, 264905, 56182435, 265008, 60433438, 264759, 21906754, 33109954, 265017, 265019, 264448, 264288, 264766, 264685, 35696423, 35895855, 264558, 18108385, 60432113
1166	88098456 (2331, 2332)	Novel Protein sim. GBank gij4589476jdb BAA76766.1  - (AB023139) KIAA0922 protein [Homo sapiens]			

1167	79963862 (2333, 2334)	Novel Protein sim. GBank gij2580433[dbj][BAA23138] - (D76414) ppGpp hydrolase [Staphylococcus aureus]		kinase	264488
1168	80094678 (2335, 2336)			UNCLASSIFIED	264259, 29331827, 56182435, 60433438, 265019, 33657023, 35695855, 264586
1169	11805403 (2337, 2338)			UNCLASSIFIED	264681
1170	21632244 (2339, 2340)			UNCLASSIFIED	264602
1171	20434582 (2341, 2342)	Novel Protein sim. GBank gij2772914 (AF028249) - procollagen D [Mytilus edulis]		UNCLASSIFIED	264556
1172	78610113 (2343, 2344)	Novel Protein sim. GBank gij4757846[ref][NP_004317.1]pBCL9 - B-cell CLL/lymphoma 9		UNCLASSIFIED	55810764, 35696052, 264634, 264488
1173	80235713 (2345, 2346)	Novel Protein sim. GBank gij2564053[dbj][BAA22846] - (AB007832) Bm trachealless [Bombyx mori]			264508, 264906, 264907, 264809, 264591, 264632, 264638, 264639
1174	20283077 (2347, 2348)	Novel Protein sim. GBank gij2911027[emb][CAA17520] - (AL021958) mmsA [Mycobacterium tuberculosis]		dehydrogenase	264600
1175	20711847 (2349, 2350)	Novel Protein sim. GBank gij118333[sp][P23234][DCIP_ENTCL - INDOL-3-PYRUVATE DECARBOXYLASE (INDOLEPYRUVATE DECARBOXYLASE)]	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	carboxylase	264601
1176	80252845 (2351, 2352)	Novel Protein sim. GBank gij1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]	Contains protein domain (PF00586) - AIR synthase related protein	synthase	264509, 264905, 264583, 264602, 264605
1177	80064647 (2353, 2354)	Novel Protein sim. GBank gij119791[sp][P28643]FABG_CUPLA - 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)	Contains protein domain (PF00106) - short chain dehydrogenase	reductase	264605
1178	94128641 (2355, 2356)	Novel Protein sim. GBank gij5031697[ref][NP_005584.1]pFIC1 - familial intrahepatic cholestasis 1, (progressive, Byler disease and benign recurrent)	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase-associated	65274572, 18108398, 22278998, 22278999, 28331826, 284508, 264908, 264828, 33657402, 33109954, 264769, 21806765, 21806766, 21808768, 55811957, 33657023, 264629, 55811576, 35698423, 264636, 264556, 56182323, 60432113, 22279000, 22279002
1179	80055575 (2357, 2358)	Novel Protein sim. GBank gij2960090[emb][CAA17888.1] - (AL022121) dppA [Mycobacterium tuberculosis]	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	transport	264603
1180	11794446 (2359, 2360)	Novel Protein sim. GBank gij2558614[emb][CAA04787] - (AJ001493) dehydroquinase dehydratase [Streptomyces coelicolor]	Contains protein domain (PF01220) - Dehydroquinase class II	synthase	264638
1181	17846362 (2361, 2362)			UNCLASSIFIED	265017
1182	81494264 (2363, 2364)	Novel Protein sim. GBank gij5420387[emb][CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			265007, 265008, 264584, 264909, 264693
1183	78574044 (2365, 2366)	Novel Protein sim. GBank gij4091877 (AF061331) - alpha galactosidase precursor [Saccharopolyspora erythraea]			264689, 35696423, 264638, 18108385
1184	52559933 (2367, 2368)			UNCLASSIFIED	264602
1185	79491185 (2369, 2370)	Novel Protein sim. GBank gij2128478[pir][S51939] - chitinase (EC 3.2.1.14) precursor - beet		glycoprotein	263967



1188	20224012 (2371, 2372)				UNCLASSIFIED	264559	
1187	79248834 (2373, 2374)				UNCLASSIFIED	29331825, 265017, 18108351	
1188	79831387 (2375, 2376)	Novel Protein sim. GBank gij2996039 (AF054525) - hypothetical protein [Synecococcus PCC7002]			UNCLASSIFIED	264905, 264906	
1189	79609367 (2377, 2378)					284692	
1190	78930589 (2378, 2380)				UNCLASSIFIED	265018	
1191	80310105 (2381, 2382)				UNCLASSIFIED	284600, 264605, 264764, 36695855, 284638, 284486	
1192	13521641 (2383, 2384)			Contains protein domain (PF01581) - FMRfamide related peptide family		264636	
1193	11103584 (2385, 2386)				UNCLASSIFIED	263978	
1194	78893947 (2387, 2388)	Novel Protein sim. GBank gij854065 [emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	265007, 265008	
1195	20445442 (2389, 2390)	Novel Protein sim. GBank gij1780277 (AE000459) - putative oxidoreductase [Escherichia coli]			UNCLASSIFIED	264605	
1196	13000688 (2391, 2392)					264689	
1197	11382317 (2393, 2394)	Novel Protein sim. GBank gij2487360 [sp]Q50715 [IMDH_MYCTU - INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD)]		Contains protein domain (PF00571) - CBS domain		264594	
1198	95290101 (2395, 2396)					264603	
1199	81882011 (2397, 2398)	Novel Protein sim. GBank gij1708525 [sp]P54673 [P3K1_DICD1 - PHOSPHATIDYLINOSITOL 3-KINASE 1 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)]				284258, 264757, 33109954, 21906768	
1200	9848880 (2399, 2400)						
1201	80503751 (2401, 2402)	Novel Protein sim. GBank gij2499877 [sp]P70845 [BLMH_RAT - BLEOMYCIN HYDROLASE (BLM HYDROLASE) (BMH)]			UNCLASSIFIED	264910	
1202	80082633 (2403, 2404)	Novel Protein sim. GBank gij606342 (U18997) - ORF_0622; reading frame open far upstream of start; possible frameshift, linking to previous ORF [Escherichia coli]			cathepsin	264766, 264769	
1203	82125373 (2405, 2406)				ribosomalprol	264600, 264558	
1204	80503916 (2407, 2408)	Novel Protein sim. GBank gij2500728 [sp]Q59912 [SECY_STRGB - PREPROTEIN TRANSLOCASE SECY SUBUNIT]			UNCLASSIFIED	264768, 264769, 35695917, 264910, 264760, 264908, 264907, 264629, 264908, 264909, 264766	
1205	80053861 (2409, 2410)					264905, 264769, 264636	
1206	80241985 (2411, 2412)				UNCLASSIFIED	264566	
1207	78841192 (2413, 2414)				UNCLASSIFIED	264556, 264557, 264558	
1208	87755217 (2415, 2416)	Novel Protein sim. GBank gij2645560 (AF027854) - Bcl-2 related ovarian killer protein [Rattus norvegicus]		Contains protein domain (PF00452) - Apoptosis regulator proteins, Bcl-2 family		29331824, 264909, 265021, 18108370	
						29331824, 29331825, 29331827, 265007, 264764, 264683, 264769, 264688, 264689	

1209	79185742 (2417, 2418)	Novel Protein sim. GBank gij1175033 sp P44398 XYLA_HAEIN - XYLOSE ISOMERASE	Contains protein domain (PF00259) - Xylose isomerase	isomerase	264687, 264688
1210	56426884 (2419, 2420)				
1211	94665655 (2421, 2422)	Novel Protein sim. GBank gij1421095 pir S30688 - hypothetical protein o246 - Escherichia coli		UNCLASSIFIED transferase	264907, 264693 264591, 264592, 264595
1212	79167829 (2423, 2424)	Novel Protein sim. GBank gij380625 emb CAB07858  - (Z93785) predicted using GeneFinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf		264689, 263967
1213	79859633 (2425, 2426)	Novel Protein sim. GBank gij226292 pir J1505375A - vir gene [Bordetella pertussis]		kinase	264909
1214	10144306 (2427, 2428)	Novel Protein sim. GBank gij5726285 gb AAD48396.1 AF12616 - (AF126162) HERV-H LTR associating protein 2 [Homo sapiens]		UNCLASSIFIED	264908
1215	80050108 (2428, 2430)	Novel Protein sim. GBank gij2326739 emb CAB10953  - (Z98288) recN [Mycobacterium tuberculosis]		UNCLASSIFIED	265009, 264601, 264602, 264603, 33657109
1216	20438324 (2431, 2432)	Novel Protein sim. GBank gij417329 sp P33038 MURA_ENTCL - UDP-N- ACETYLGLUCOSAMINE 1- CARBOXYVINYLTRANSFERASE (ENOYLPIRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOLPYRUVYL TRANSFERASE) (EPT)		transferase	264604
1217	95011344 (2433, 2434)			UNCLASSIFIED	264905, 264907, 264908, 264591, 264766, 264691, 264693, 264629, 264630, 264636, 264564
1218	11093680 (2435, 2436)	Novel Protein sim. GBank gij1805460 dbj BAA08022  - (D50453) homologue of succinate semialdehyde dehydrogenase GabD of E. coli [Bacillus subtilis]		dehydrogenase	264601
1219	81216252 (2437, 2438)				56181686, 293331822, 60432289, 264601, 264692, 264629
1220	81241524 (2439, 2440)	Novel Protein sim. GBank gij4240315 dbj BAA74836.1  - (AB020720) KIAA0913 protein [Homo sapiens]		oncogene	52644507, 264905, 264909, 265008, 265019, 265020, 52644150, 33657023, 264693, 33657182, 35695763, 264634, 22279000, 22279002, 264482
1221	83045055 (2441, 2442)	Novel Protein sim. GBank gij2143886 pir J152523 - nucleoporin p82 homolog - rat (fragment)		UNCLASSIFIED	264768, 265020, 264906
1222	20711865 (2443, 2444)	Novel Protein sim. GBank gij730805 sp P39663 SPHR_SYN7P - ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY PROTEIN SPHR	Contains protein domain (PF00486) - Transcriptional regulatory protein, C terminal	- phosphatase	264601
1223	11615647 (2445, 2446)				264593
1224	80432645 (2447, 2448)	Novel Protein sim. GBank gij1172627 sp P46546 PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)	Contains protein domain (PF01472) - PUA domain	kinase	264593, 264600, 264601, 264603, 264605, 264768, 18108376, 264635, 18108387

1225	80434427 (2449, 2450)	Novel Protein sim. GBank gij2105050[emb]CAB08836] - (295436) hypothetical protein RV3844c [Mycobacterium tuberculosis]			264768
1226	80237518 (2451, 2452)	Novel Protein sim. GBank gij1706768[sp]P98133[FBN1_BOVIN - FIBRILLIN 1 PRECURSOR (MP340)]	polymerase		264905, 264512, 264689
1227	78422138 (2453, 2454)	Novel Protein sim. GBank gij1706768[sp]P98133[FBN1_BOVIN - FIBRILLIN 1 PRECURSOR (MP340)]	UNCLASSIFIED		264908, 264637, 264639
1228	78209027 (2455, 2456)	Novel Protein sim. GBank gij1653901[dbj]BAA18811] - (D90917) acriflavine resistance protein [Synectocystis sp.]			264605, 264634
1229	84329135 (2457, 2458)	Novel Protein sim. GBank gij1653901[dbj]BAA18811] - (D90917) acriflavine resistance protein [Synectocystis sp.]	UNCLASSIFIED		87168474, 265011, 87168559, 264681, 264689, 264693, 65274620, 18108374
1230	80049357 (2459, 2460)	Novel Protein sim. GBank gij116230[sp]P28598[CH60_BACSJ - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN)]	eph		264908, 264605, 18108388
1231	79843141 (2461, 2462)	Novel Protein sim. GBank gij1215733 [U48718] - OphC [Agrobacterium tumefaciens]	UNCLASSIFIED		264908
1232	79853104 (2463, 2464)	Novel Protein sim. GBank gij118298[sp]P20730[CHHC_BOMMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR (HC-B.13)]	transport		264909
1233	80255179 (2465, 2466)	Novel Protein sim. GBank gij118298[sp]P20730[CHHC_BOMMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR (HC-B.13)]	UNCLASSIFIED		265017, 264564
1234	78242158 (2467, 2468)	Novel Protein sim. GBank gij729671[sp]P40280[H2A_MAIZE - HISTONE H2A]	histone		265008, 265010, 18108381
1235	79914423 (2469, 2470)	Novel Protein sim. GBank gij3875133[emb]CAA94750] - (Z70750) similar to actin binding domain; cDNA EST EMBL:T00093 comes from this gene; cDNA EST EMBL:D34443 comes from this gene; cDNA EST EMBL:D37508 comes from this gene; cDNA EST EMBL:D84247 comes from this gene; cDNA EST EMBL:...	UNCLASSIFIED		264634, 264762
1236	81827147 (2471, 2472)	Novel Protein sim. GBank gij3875133[emb]CAA94750] - (Z70750) similar to actin binding domain; cDNA EST EMBL:T00093 comes from this gene; cDNA EST EMBL:D34443 comes from this gene; cDNA EST EMBL:D37508 comes from this gene; cDNA EST EMBL:D84247 comes from this gene; cDNA EST EMBL:...			265018, 55811150, 264565, 264757
1237	83371782 (2473, 2474)	Novel Protein sim. GBank gij3875133[emb]CAA94750] - (Z70750) similar to actin binding domain; cDNA EST EMBL:T00093 comes from this gene; cDNA EST EMBL:D34443 comes from this gene; cDNA EST EMBL:D37508 comes from this gene; cDNA EST EMBL:D84247 comes from this gene; cDNA EST EMBL:...			264758, 264601, 264766, 264687, 18108372, 264555, 264559
1238	87411577 (2475, 2476)	Novel Protein sim. GBank gij3885470 (AF061443) - G protein-coupled receptor LGR4 [Rattus norvegicus]	glycoprotein		264259, 28331822, 29331824, 35696052, 264508, 264908, 52844045, 52846317, 264288, 264769, 264893, 264632, 264634, 264558, 87168518, 264563
1239	82197449 (2477, 2478)	Novel Protein sim. GBank gij4007990[gb]AAC95339] - (AF084383) DOK protein [Mus musculus]	oncogene		264509, 264511, 264759, 264760, 264764, 264557
1240	80497259 (2479, 2480)	Novel Protein sim. GBank gij1176192[sp]P45420[YHCD_ECOLI - HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN IN GLTF-NANT INTERGENIC REGION PRECURSOR]			264769
1241	80020711 (2481, 2482)	Novel Protein sim. GBank gij121383[sp]P19904[GLNA_VIBAL - GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)]	UNCLASSIFIED		264601, 264604, 264638
1242	79775890 (2483, 2484)	Novel Protein sim. GBank gij121383[sp]P19904[GLNA_VIBAL - GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)]			264906, 264907, 264908, 264634

1243	78779458 (2485, 2486)	Novel Protein sim. GBank gij3355671[emb]CAA19971] - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor]		UNCLASSIFIED	18108374, 35695917, 35695855, 265009, 264508, 284909
1244	10284821 (2487, 2488)	Novel Protein sim. GBank gij2970846 (AF051945) - Xin [Mus musculus]		UNCLASSIFIED	264691
1245	80437103 (2489, 2490)	Novel Protein sim. GBank gij4586338[dbj]BAA76357.1] - (AB016787) cytochrome o ubiquinol oxidase B [Pseudomonas putida]	Contains protein domain (PF00115) - Cytochrome C and Quinol oxidase polypeptide I	oxidase	264768
1246	80059321 (2491, 2492)	Novel Protein sim. GBank gij3581849[emb]CAA20805] - (AL031541) putative phenylalanyl-tRNA synthetase beta chain [Streptomyces coelicolor]		UNCLASSIFIED	264604, 264636, 264557, 264564
1247	80084831 (2493, 2494)	Novel Protein sim. GBank gij2621684 (AE000842) - adhesion protein [Methanobacterium thermoautotrophicum]			264758, 264605, 264639
1248	88070353 (2495, 2496)	Novel Protein sim. GBank gij1352403[sp]P094671F16P HUMAN - FRUCTOSE-1,6-BISPHOSPHATASE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)	Contains protein domain (PF00316) - Fructose-1,6-bisphosphatase	UNCLASSIFIED	18108392, 264259, 28331826, 264106, 264508, 264907, 264828, 265009, 60433356, 264757, 264758, 21906754, 285010, 285011, 265018, 265019, 264760, 18108351, 18108354, 265021, 18108376, 18108377, 264630, 18108385
1249	80056657 (2497, 2498)	Novel Protein sim. GBank gij2791407[emb]CAA16001] - (AL021184) hypothetical protein Rv1473 [Mycobacterium tuberculosis]		transport	264908, 265010, 284600, 264603, 264691, 18108378
1250	12694385 (2499, 2500)	Novel Protein sim. GBank gij112785[sp]P051003MG1 ECOLI - DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)		UNCLASSIFIED	264689
1251	78850448 (2501, 2502)				264909
1252	78458087 (2503, 2504)			UNCLASSIFIED	264683, 263976
1253	80050121 (2505, 2506)	Novel Protein sim. GBank gij5670178[gb]AAD46616.1[AF16131] NRAMP manganese transport protein MntA [Salmonella typhimurium]		glycoprotein	264600, 264603, 18108376
1254	87716767 (2507, 2508)	Novel Protein sim. GBank gij103160[pir]j522126 - finger protein unkempt - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	35696286, 264910, 264764, 264688, 21906787, 55811957, 284692, 264556, 264639
1255	79169728 (2509, 2510)				264636
1256	87889508 (2511, 2512)	Novel Protein sim. GBank gij2995353[emb]CAA04608.1] - (AJ001206) pep2 [Streptomyces coelicolor]		UNCLASSIFIED	60432289, 264600, 264605, 264784, 264687, 264769, 264689, 27486265, 18108374, 18108376
1257	80201435 (2513, 2514)	Novel Protein sim. GBank gij3183308 (AF069300) - contains similarity to Arabidopsis membrane-associated salt inducible-like protein (GB:AL021637) [Arabidopsis thaliana]		UNCLASSIFIED	264094, 265019
1258	20708150 (2515, 2516)			UNCLASSIFIED	264602, 263978
1259	80186012 (2517, 2518)			UNCLASSIFIED	264906, 264448, 264808
1260	80084608 (2519, 2520)			UNCLASSIFIED	264634, 264639

1261	87412802 (2521, 2522)	Novel Protein sim. GBank gll5689511[dbj]BA03039.1] - (AB029010) KIAA1087 protein [Homo sapiens]	Contains protein domain (PF01699) - Sodium/calcium exchanger protein	cadherin	29331824, 264906, 264908, 264768, 264769, 264689, 264693, 264639, 18108384, 264563, 264634
1262	13504589 (2523, 2524)	Novel Protein sim. GBank gll95100[pir]S21334 - hypothetical protein 4 - Agrobacterium tumefaciens		UNCLASSIFIED	
1263	20710997 (2525, 2526)	Novel Protein sim. GBank gll3550958 (AF004840) - CDO [Rattus norvegicus]		struct	264602
1264	80063386 (2527, 2528)				264634
1265	80253578 (2529, 2530)				264563
1266	79914604 (2531, 2532)			UNCLASSIFIED	264768, 264636, 264638, 264567
1267	80558918 (2533, 2534)	Novel Protein sim. GBank gll1085002[pir]S55056 - mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264259, 21906754, 264369
1268	88178473 (2535, 2536)	Novel Protein sim. GBank gll4886445[emb]CAB43370.1] - (AL050269) hypothetical protein [Homo sapiens]	Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	18108398, 22278995, 56994075, 60424269, 29331827, 264108, 264512, 265007, 265008, 265009, 264595, 33109954, 33657084, 87168559, 264600, 265018, 265019, 264369, 264688, 21906767, 265020, 52644150, 264691, 33657023, 33657349, 18108374, 264556, 18108385, 60432113, 22279002, 264486
1269	78821948 (2537, 2538)	Novel Protein sim. GBank gll3334791[emb]CAA18939] - (AL031107) hypothetical protein SC5A7.10c [Streptomyces coelicolor]		UNCLASSIFIED	264508, 264905, 264906, 264687, 264693
1270	80031420 (2539, 2540)	Novel Protein sim. GBank gll2851634[sp]Q50591[V0D1_MYCTU - HYPOTHETICAL 50.0 KD PROTEIN CY1A11.01	Contains protein domain (PF01574) - IMP dehydrogenase / GMP reductase N terminus	dehydrogenase	265010, 264601
1271	79840499 (2541, 2542)			ATPase associated	35696052, 264908
1272	79462878 (2543, 2544)				264686, 264689
1273	80220315 (2545, 2546)	Novel Protein sim. GBank gll1655665[emb]CAB03731] - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]		UNCLASSIFIED	264509, 264639
1274	95010802 (2547, 2548)			UNCLASSIFIED	
1275	20730763 (2549, 2550)	Novel Protein sim. GBank gll123726[sp]P10413[HTPG_ECOLI - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C82.5)	Contains protein domain (PF00183) - Hsp90 protein	eph	264905, 264908, 264909, 264769, 264802
1276	21148644 (2551, 2552)	Novel Protein sim. GBank gll2129478[pir]S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264369
1277	20438185 (2553, 2554)				
1278	11088365 (2555, 2556)	Novel Protein sim. GBank gll1175473[sp]P44555[YAAJ_HAEIN - HYPOTHETICAL PROTEIN H10183		UNCLASSIFIED	264558
1279	21658756 (2557, 2558)	Novel Protein sim. GBank gll1929513 (U64318) - ATP synthase subunit beta [Moorella thermoacetica]		UNCLASSIFIED	264803
1280	78310959 (2559, 2560)	Novel Protein sim. GBank gll4938504[emb]CAB43862.1] - (AL078465) putative protein [Arabidopsis thaliana]		synthase	264605
				struct	263976

1281	94323988 (2561, 2562)	Novel Protein sim. GBank gji1138501 (U39546) - surface protein MCA-32 [Rattus norvegicus]	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	29331825, 29331828, 264766, 83373044
1282	87537685 (2563, 2564)	Novel Protein sim. GBank gji3328190 (AF074266) - proto-oncogene AF-4 [Mus musculus]		UNCLASSIFIED	265008
1283	20466305 (2565, 2566)	Novel Protein sim. GBank gji3261721 (emb CAB07057  - (Z92770) hypothetical protein Rv0153c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
1284	20536325 (2567, 2568)	Novel Protein sim. GBank gji3929022 (AF057696) - LspB [Haemophilus ducreyi]			264604
1285	80427330 (2569, 2570)	Novel Protein sim. GBank gji417154 (sp P33126 HS82_ORYSA - HEAT SHOCK PROTEIN 82 (Z95207) gorA [Mycobacterium tuberculosis]	Contains protein domain (PF00183) - eph Hsp90 protein		264766, 264689, 263987
1286	20465254 (2571, 2572)	Novel Protein sim. GBank gji2078004 (emb CAB08451  - (Z95207) gorA [Mycobacterium tuberculosis]	reductase		264605, 264639
1287	80417530 (2573, 2574)			UNCLASSIFIED	265011, 264602, 264766, 264687, 264769, 264689, 18108370, 264636, 18108385, 264563
1288	95338101 (2575, 2576)	Novel Protein sim. GBank gji5353510 (gb AAD42161.1 AF08891 - (AF088916) emilin precursor [Homo sapiens]	Contains protein domain (PF00386) - collagen C1q domain		35698052, 264107, 264508, 264509, 264805, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 33657402, 264595, 264758, 265011, 265019, 264760, 18108351, 264681, 264784, 264288, 264685, 264786, 264687, 264788, 264769, 265020, 265021, 264534, 264692, 18108370, 264628, 18108374, 35698423, 264555, 264556, 264557, 264558, 18108385, 264564, 264566, 264587, 264488, 18108391
1289	11813647 (2577, 2578)	Novel Protein sim. GBank gji1169995 (sp P46023 GPCR_LYMST - G-PROTEIN COUPLED RECEPTOR GRL101 PRECURSOR (Z95120) rhIE [Mycobacterium tuberculosis]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	UNCLASSIFIED	264637
1290	19526027 (2579, 2580)		Helicases conserved C-terminal domain	tm7	264563
1291	80470266 (2581, 2582)	Novel Protein sim. GBank gji2072674 (emb CAB08305  - (Z95120) rhIE [Mycobacterium tuberculosis]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	265007, 265008, 264769
1292	94723318 (2583, 2584)	Novel Protein sim. GBank gji1835755 (U86338) - zinc finger protein Png-1 [Mus musculus]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcript factor	264092, 264259, 29331822, 29331824, 264508, 264908, 264909, 264512, 265008, 265009, 264591, 265018, 264368, 264288, 264686, 264768, 264693, 18108374, 264632, 58182323, 264639, 83373044, 22279002, 264482, 264563
1293	80067536 (2585, 2586)	Novel Protein sim. GBank gji2129173 (pir JF64453 - oxaloacetate decarboxylase (EC 4.1.1.3) alpha subunit - Methanococcus jannaschii		UNCLASSIFIED	265006, 55812038, 264389, 264556
1294	82125908 (2587, 2588)	Novel Protein sim. GBank gji5441779 (emb CAB45803.1  - (AL096811) putative alcohol dehydrogenase (zinc-binding) [Streptomyces coelicolor A3(2)]	biolindp		264602, 264605, 264760, 18108351, 264689, 33657023, 264559
1295	11686651 (2589, 2590)		dehydrogenase		264689

1296	11687904 (2591, 2592)	Novel Protein sim. GBank gi 4982191 gb AAD36686.1 AE00180 - (AE001805) DNA- directed DNA polymerase I [Thermotoga maritima]	Contains protein domain (PF01367) - 5'-3' exonuclease	UNCLASSIFIED	264591, 264639 264693
1297	78639300 (2593, 2594)	Novel Protein sim. GBank gi 4982191 gb AAD36686.1 AE00180 - (AE001805) DNA- directed DNA polymerase I [Thermotoga maritima]			
1298	94239508 (2595, 2596)	Novel Protein sim. GBank gi 1943770 (U97181) - F53F10.1 gene product [Caenorhabditis elegans]		struct	18108348, 265017
1299	80255378 (2597, 2598)	Novel Protein sim. GBank gi 3445181 (AC005498) - R31685.2 [Homo sapiens]			
1300	80064867 (2599, 2600)	Novel Protein sim. GBank gi 4062973 dbj BAA36204.1  - (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264488, 264906, 264909, 22279002, 264586 264605
1301	17839614 (2601, 2602)	Novel Protein sim. GBank gi 4062973 dbj BAA36204.1  - (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]		UNCLASSIFIED	264906
1302	95416188 (2603, 2604)				85658542, 265020
1303	9684121 (2605, 2606)				264908
1304	79377196 (2607, 2608)			UNCLASSIFIED	264508
1305	19905899 (2609, 2610)				264586
1306	13089230 (2611, 2612)	Novel Protein sim. GBank gi 3242273 emb CAB07017  - (Z92669) hypothetical protein Rv0238c [Mycobacterium tuberculosis]		UNCLASSIFIED	264636
1307	82201028 (2613, 2614)	Novel Protein sim. GBank gi 1502421 (U59433) - 3-ketoacyl acyl carrier protein reductase [Bacillus subtilis]	Contains protein domain (PF00516) - Envelope glycoprotein GP120	UNCLASSIFIED	264907, 264592, 264764 264555
1308	21426814 (2615, 2616)	Novel Protein sim. GBank gi 95818 pir S16298 - ferric enterobactin transport protein fepC - Escherichia coli		transport	264906, 18108354
1309	79263011 (2617, 2618)	Novel Protein sim. GBank gi 5459220 emb CAB48893.1  - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264605
1310	20466319 (2619, 2620)				
1311	87613142 (2621, 2622)				35686286, 29331827, 264908, 265008, 264784, 264786, 264886, 21908767, 21908769, 35685917, 264691, 264693 22278995, 22278998, 22278999, 264805, 264908, 265011, 265017, 285019, 264687, 21908768, 265020, 265021, 33657023, 22279002, 264564
1312	88061720 (2623, 2624)	Novel Protein sim. GBank gi 4455118 gb AAD21084  - (AF125158) zinc finger DNA binding protein 99 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	22278995, 22278998, 22278999, 264805, 264908, 265011, 265017, 285019, 264687, 21908768, 265020, 265021, 33657023, 22279002, 264564
1313	91225458 (2625, 2626)	Novel Protein sim. GBank gi 4929733 gb AAD34127.1 AF15189 - (AF151890) CGI-132 protein [Homo sapiens]	Contains protein domain (PF00886) - Ribosomal protein S16	ribosomalprot	22278998, 22278999, 264259, 20281099, 29146498, 264508, 264908, 86712502, 60433356, 60433438, 265011, 265017, 264683, 264288, 21906765, 21906767, 29148627, 21906768, 35685917, 265021, 33657023, 33657109, 18108370, 18108377, 35685855, 60432113, 22279000, 264563, 18108390
1314	56926053 (2627, 2628)				264693
1315	84357192 (2629, 2630)	Novel Protein sim. GBank gi 2589223 (AF026565) - (ing finger protein [Mus musculus])	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	264691

1316	85381609 (2631, 2632)	Novel Protein sim. GBank gij5689407[dbj BAA82987.1] - (AB028958) KIAA1035 protein [Homo sapiens]		kinase	56182575, 56181886, 20281171, 29331822, 29331824, 60424288, 29331825, 35696052, 5264045, 264591, 60432229, 265018, 265019, 55811150, 56181562, 21906765, 21906767, 21906768, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 35695855, 18108387, 87168518, 60432113, 22279002, 264584
1317	88055167 (2633, 2634)	Novel Protein sim. GBank gij4836757[gb AAD30541.1]AF13491 - (AF134918) semaphorin subclass 4 member G [Mus musculus]		UNCLASSIFIED	264093, 264906, 264908, 264369, 264894
1318	85322893 (2635, 2636)	Novel Protein sim. GBank gij4680204[gb AAD27567.1]AF11417 - (AF114171) hypothetical protein [Sorghum bicolor]		UNCLASSIFIED	18108392, 18108348, 265011, 265017, 18108359, 18108382, 56182323, 18108385, 22278000
1319	94238546 (2637, 2638)				264908, 264909, 265006, 265008, 264592, 265019, 264766, 56181562, 18108388, 264628, 264629, 18108377, 264636
1320	86603567 (2639, 2640)	Novel Protein sim. GBank gij4240183[dbj BAA74870.1] - (AB020854) KIAA0847 protein [Homo sapiens]		UNCLASSIFIED	35696288, 55812038, 265018, 21906769, 265020, 263978, 22279002
1321	86676351 (2641, 2642)	Novel Protein sim. GBank gij4886505[embj CAB43377.1] - (AL050278) hypothetical protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	transcript factor	60432049, 29331828, 264907, 264808, 264909, 264910, 55812038, 264801, 284762, 264764, 264766, 264769, 264769, 264628, 18108374, 264634, 264635, 18108385
1322	87755272 (2643, 2644)	Novel Protein sim. GBank gij5262591[embj CAB45736.1] - (AL080143) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	29331828, 264908, 265020, 33657023, 264693, 264404
1323	94845931 (2645, 2646)	Novel Protein sim. GBank gij5459516[dbj BAA82407.1] - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 56994075, 264259, 29331822, 29331827, 264104, 56182435, 87168474, 18108351, 264288, 21906768, 21906767, 35695917, 265020, 264693, 65274791, 56182323, 18108387
1324	87737614 (2647, 2648)	Novel Protein sim. GBank gij5031717[ref NP_005704.1]pGPBP - goodpasture antigen-binding protein	Contains protein domain (PF01852) - START domain		22278996, 22278998, 29331828, 264905, 264907, 29331830, 264908, 264510, 265008, 264595, 264759, 21906754, 265018, 264288, 264768, 264769, 21906768, 265022, 18108376, 264631, 264632, 264634, 264636, 264638, 264583, 264584, 264585, 264586
1325	94847471 (2649, 2650)	Novel Protein sim. GBank gij3294501 (U64857) - similar to the DPT/Kunitz family of inhibitors, most similar to tissue factor pathway inhibitor precursor [Caenorhabditis elegans]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	protease	35696288, 264905, 264906, 264907, 264908, 264909, 264910, 264593, 33657402, 264758, 85658542, 264760, 264768, 264769, 264681, 35696423
1326	87316289 (2651, 2652)	Novel Protein sim. GBank gij1397275 (U61947) - C06G3.8 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264259, 66712502, 264682, 264683, 264635



1327	95322897 (2653, 2654)	Novel Protein sim. GBank gil728832 sp P39189 ALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY III	Contains protein domain (PF00279) - Plant lipid transfer protein family	UNCLASSIFIED	18108398, 22278996, 22278997, 22278999, 264091, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264105, 264905, 56182435, 264112, 265008, 265009, 21906754, 265010, 265011, 265017, 265019, 264681, 264448, 264764, 264684, 264288, 264685, 264768, 264688, 21906767, 21906769, 29148628, 265020, 264690, 264691, 264692, 264693, 263967, 33857109, 33857182, 27486282, 33857349, 18108370, 18108374, 55810764, 35895855, 264634, 56182323, 83373044, 87168518, 60432113, 22279000, 22279002, 264563, 264567, 264488, 22278997, 29331826, 264595, 18108351, 264766, 22279002, 264482, 264567
1328	87753493 (2655, 2656)			UNCLASSIFIED	22278996, 29331827, 264684, 264692, 33657109
1329	87755278 (2657, 2658)	Novel Protein sim. GBank gil467822 gb AAD26969.1 AC00713 - (AC007135) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264259, 29331825, 264512, 265019, 265021, 264555, 264558, 56528486
1330	87727737 (2659, 2660)	Novel Protein sim. GBank gil437310 (L23504) - nodulin [Medicago truncatula]		UNCLASSIFIED	264259, 29331826, 29331827, 35696052, 29331828, 60170831, 264448, 264686, 21906765, 55811957, 265020, 33657023, 33657109, 263973, 55811578, 35696423, 35695855, 56182323
1331	87376764 (2661, 2662)	Novel Protein sim. GBank gil4589586 db BAA76815.1  - (AB023188) KIAA0971 protein [Homo sapiens]		UNCLASSIFIED	65274572, 22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331826, 60432289, 29331827, 35696052, 52644045, 56182435, 264510, 21908754, 87168559, 265018, 265019, 264448, 264288, 264369, 264686, 21906765, 21908766, 21905767, 21906768, 265020, 265021, 52644150, 33657023, 56182323, 18108387, 60432113, 22279002
1332	94845937 (2663, 2664)	Novel Protein sim. GBank gil5459516 db BAA82407.1  - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]	Synthase		
1333	88098476 (2665, 2666)	Novel Protein sim. GBank gil5689527 db BAA83047.1  - (AB029018) KIAA1095 protein [Homo sapiens]		UNCLASSIFIED	60432289, 66712502, 264591, 60433356, 60433438, 55812038, 265010, 264639, 56526486
1334	87592388 (2667, 2668)	Novel Protein sim. GBank gil2662538 (AF036685) - Similar to protein-tyrosine phosphatase [Caenorhabditis elegans]	phosphatase		264905
1335	87644798 (2669, 2670)	Novel Protein sim. GBank gil4240285 db BAA74921.1  - (AB020705) KIAA0898 protein [Homo sapiens]	Contains protein domain (PF00843) - B-box zinc finger.	UNCLASSIFIED	22278998, 22278999, 29331827, 264509, 264511, 265007, 265008, 265009, 60433438, 21906754, 87168559, 265017, 264288, 21906765, 21906767, 21906768, 21906769, 265020, 33657109, 27486284, 18108374, 264556, 264638, 264557, 60170394, 264559, 18108385, 264563

1336	87787890 (2671, 2672)	Novel Protein sim. GBank gi465445 sp P33485 VNUA_PVK_A - PROBABLE NUCLEAR ANTIGEN				264509, 264905, 264512, 264784, 264893, 264635, 264837
1337	94312042 (2673, 2674)	Novel Protein sim. GBank (AB028980) KIAA1067 protein [Homo sapiens]			UNCLASSIFIED	56182575, 56894075, 22278988, 22278989, 264092, 264259, 60432289, 29331826, 264906, 264908, 264909, 264112, 265008, 265009, 60433356, 55812038, 33657084, 265011, 265017, 265018, 265019, 264682, 264448, 264683, 264389, 264688, 264688, 21908768, 21908769, 265020, 264691, 27488261, 20281069, 18108379, 55811578, 35895855, 56182323, 60432113, 22279002, 264567
1338	80366114 (2675, 2676)				UNCLASSIFIED	28331822, 265010, 264288, 264688, 18108370, 35895855
1339	80248231 (2677, 2678)	Novel Protein sim. GBank gi1176422 (U43194) - rhophilin [Mus musculus]			UNCLASSIFIED	35896052, 264909, 264688, 264556, 264558
1340	88316311 (2679, 2680)					264905, 264907, 87168559, 264764
1341	88101485 (2681, 2682)					264681, 264685, 264686, 264692
1342	80089017 (2683, 2684)	Novel Protein sim. GBank gi15019594 emb CAB44507.1  - (AL035542) dJ994E9.5 (hs6M1-17 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein)) [Homo sapiens]	Contains protein domain (PF000001) - 7 transmembrane receptor (rhodopsin family)	tm7		264629
1343	80082862 (2685, 2686)	Novel Protein sim. GBank gi4557543 ref NP_001384.1 pECM2 - extracellular matrix protein 2	Contains protein domain (PF00560) - Leucine Rich Repeat	struct		264810, 264686, 264534
1344	20562559 (2687, 2688)	Novel Protein sim. GBank gi2144101 pir  55210 - Irfcarboxylate carrier - rat (fragment)				263978
1345	91225548 (2689, 2690)	Novel Protein sim. GBank gi3881052 emb CAA19523  - (AL023843) predicted using GeneFINDER: similar to serine/threonine kinase; cDNA EST yk248a12.3 comes from this gene; cDNA EST yk358c10.5 comes from this gene; cDNA EST EMBL:M89047 comes from this gene; cDNA EST yk248a12.5 comes...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	glycoprotein		264808, 60170394
1346	80255717 (2691, 2692)				kinase	22278998, 264907, 264881, 264685, 264689, 265020, 264693, 22279000, 22279002, 264566
1347	80417393 (2693, 2694)	Novel Protein sim. GBank gi4504379 ref NP_003858.1 pHG38 - orphan G protein- coupled receptor HG38	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein		264806, 264908, 264908, 265006, 264910, 265011, 265017, 264764, 264768, 264767, 264769, 264631, 264634, 264638, 264587, 264486
1348	87352335 (2695, 2696)	Novel Protein sim. GBank gi3399720 dbj BAA32100  - (AB010999) peptidylarginine deiminase type IV [Rattus norvegicus]			UNCLASSIFIED	264488, 264489, 264508, 264509, 264510, 264511, 264512, 264591, 264592, 264601, 264684, 264685, 264769, 264532, 264534, 264555, 264556, 264557, 264558, 22278002, 264486

1349	91225548 (2697, 2698)	Novel Protein sim. GBank gl 2144101 pir  55210 - Irtcarboxylate carrier - rat (fragment)		UNCLASSIFIED	52646842, 35696286, 22278996, 22278998, 22278999, 264258, 29331822, 29331824, 35696052, 284509, 284905, 264906, 264907, 264908, 264909, 264511, 265008, 264512, 264910, 60170831, 284581, 60433438, 284757, 21906754, 265017, 265018, 264605, 264780, 264762, 264288, 264768, 264689, 21908765, 21908766, 21908767, 21908768, 55811957, 35695917, 265020, 264534, 264891, 264692, 33657023, 264693, 33657349, 18108374, 18108376, 35696423, 60170384, 22279000, 22279002, 264563, 264564
1350	87093136 (2699, 2700)			UNCLASSIFIED	52646842, 264259, 29331825, 264808, 264511, 264604, 264288, 21908769, 265020, 33657182, 33657349, 18108374, 35695855, 264555, 264558, 18108385, 22279002, 264488
1351	87361327 (2701, 2702)	Novel Protein sim. GBank gl 4887239 gb AAD32246.1  - (AF084564) BAW protein [Fugu rubripes]		UNCLASSIFIED	264806, 264907, 264638
1352	80076386 (2703, 2704)			UNCLASSIFIED	264693, 263981
1353	95345417 (2705, 2706)	Novel Protein sim. GBank gl 2144101 pir  55210 - Irtcarboxylate carrier - rat (fragment)			35696286, 60424269, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264758, 264596, 55811386, 265011, 264605, 55811150, 264782, 264784, 264766, 52644229, 56181562, 35695917, 265022, 33657023, 264693, 35695763, 60431528, 264629, 263978, 35696423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264568
1354	95350845 (2707, 2708)	Novel Protein sim. GBank gl 4889108 gb AAD27763.1 AF07703 - (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 29331826, 264906, 265008, 33657402, 21908754, 265011, 87168559, 264684, 264369, 264769, 264689, 21908765, 21908768, 52644150, 33657023, 264692, 264693, 18108374, 83373044, 87168518, 22279000
1355	88260186 (2709, 2710)	Novel Protein sim. GBank gl 1489199 db BAA08487  - (D50828) The KIAA0138 gene product is novel. [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278996, 22278997, 264259, 66714117, 264511, 21908754, 265010, 264769, 264689, 21908765, 21908768, 21908769, 264532, 27486262, 264629, 264638, 264556, 264638, 264639, 264482, 264484

1356	85313981 (2711, 2712)	Novel Protein sim. GBank gj113865 (U40342) - ninein [Mus musculus]		sinud	18108387, 22278995, 22278996, 22278998, 264094, 29331828, 264905, 265006, 265007, 265008, 265010, 265017, 265018, 265019, 264764, 18108354, 264689, 21906785, 265022, 18108384, 35698423, 83373044, 18108387
1357	86260268 (2713, 2714)	Novel Protein sim. GBank gj897693[embjCAA90330] - (Z50026) phosphatidylcholine transfer protein [Bos taurus]	Contains protein domain (PF01852) - START domain		264259, 29331822, 28331825, 264510, 87168559, 265018, 264448, 264288, 21906785, 21906786, 21906788, 285021, 264693, 18108376
1358	38719465 (2715, 2716)	Novel Protein sim. GBank gj556219 (L36831) - transcription regulator [Mus musculus]			264757
1359	87771643 (2717, 2718)			UNCLASSIFIED	264807, 264909, 264510, 264511, 264512, 18108351, 264764, 264534, 33657023, 18108374, 264634, 264635, 264638, 264639, 18108385, 264486, 264587
1360	87738272 (2719, 2720)	Novel Protein sim. GBank gj2598282[embjCAA75612] - (Y15417) acetate--CoA ligase [Coprinus cinereus]		synthase	60432289, 264603
1361	87593527 (2721, 2722)	Novel Protein sim. GBank gj5689443[dbjBAA83005.1] - (AB028976) KIAA1053 protein [Homo sapiens]	Contains protein domain (PF00536) - SAM domain (Sterile alpha motif)	UNCLASSIFIED	35696286, 22278997, 22278999, 284259, 29331828, 264508, 264509, 264905, 264907, 264908, 265007, 265009, 33109954, 21906754, 87168474, 265011, 264761, 264683, 264288, 264766, 264769, 264689, 21906768, 265020, 265021, 33657023, 55811576, 35698423, 264634, 60432113, 22279002, 264482, 264486
1362	95287861 (2723, 2724)	Novel Protein sim. GBank gj5689411[dbjBAA82989.1] - (AB028980) KIAA1037 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	eph	56182575, 56181886, 60432049, 284259, 29331822, 56182181, 29331827, 35696052, 29331828, 264905, 264906, 264908, 264595, 55812038, 85658542, 55811150, 264681, 264288, 264389, 56181562, 60431528, 55810784, 35698423, 60431850, 264558
1363	85758478 (2725, 2726)	Novel Protein sim. GBank gj1130494 (U35776) - ADP-ribosylation factor 1-directed GTPase activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	264488, 29331826, 264907, 264687, 264689, 264693
1364	88179488 (2727, 2728)				60432289, 60433358, 60433438, 87168559, 264603, 18108351, 21906788, 35698423, 60432113
1365	83003108 (2729, 2730)	Novel Protein sim. GBank gj4589562[dbjBAA76803.1] - (AB023176) KIAA0959 protein [Homo sapiens]		oncogene	264766
1366	87003262 (2731, 2732)	Novel Protein sim. GBank gj1084944[pirjS54495] - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	265007

1367	87721210 (2733, 2734)	Novel Protein sim. GBank gl 4884008 emb CAB43240.1  - (AL050018) hypothetical protein [Homo sapiens]	Contains protein domain (PF01342) - UNCLASSIFIED SAND domain	264488, 52646842, 52646365, 22278895, 56994075, 35696286, 22278996, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35696052, 264805, 264907, 264908, 264909, 264510, 265006, 265007, 264512, 264910, 285009, 60170831, 33657402, 55812038, 21908754, 265011, 87168559, 265017, 265019, 18108351, 264448, 264882, 264683, 264288, 264368, 264686, 264767, 264688, 21908765, 21908766, 21908768, 21908769, 55811957, 265020, 265021, 265022, 264534, 60170815, 264690, 264691, 18108362, 33657023, 33657109, 33657349, 264628, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264635, 264555, 264637, 264556, 52644332, 60170394, 264558, 18108381, 18108385, 56526486, 22279000, 264563, 264567
1368	94320078 (2735, 2736)	Novel Protein sim. GBank gl 464561 sp P35289 RB15_RAT RAS-RELATED PROTEIN RAB-15	Contains protein domain (PF00071) - oncogene Ras family	264259, 29331822, 29331826, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264908, 264909, 264510, 265007, 264910, 60433438, 264758, 85658542, 87168559, 264600, 264601, 264760, 264764, 264765, 264768, 52644229, 264689, 35695917, 265020, 265021, 264631, 264632, 264634, 264637, 52644332, 264558, 264639, 83373044, 264563, 264586, 264486, 264567, 265008, 60432229, 60433356, 33657084, 21906764, 21906769, 264555, 264638, 264559, 264567
1369	88634033 (2737, 2738)	Novel Protein sim. GBank gl 2062702 (U90550) - butyrophilin [Homo sapiens]	UNCLASSIFIED	22278996, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264908, 264807, 264908, 264909, 264510, 264511, 264512, 264758, 265011, 265018, 264764, 264766, 264768, 21906767, 35695917, 18108362, 35696423, 264632, 264635, 264636, 264555, 264638, 264556, 264639, 18108385, 65274727, 264404, 264563, 264566, 264486
1370	95316910 (2739, 2740)	Novel Protein sim. GBank gl 5031823 ref NP_005823.1 pKCNM - potassium large conductance calcium-activated channel, subfamily M, beta member 2	potassium_channel	22278996, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264805, 264509, 29331830, 66712502, 265008, 265009, 264758, 33657084, 85658542, 265010, 265018, 265019, 264762, 264448, 35695917, 33657109, 33657182, 33657349, 35695855, 264558, 22279002, 264563
1371	95336512 (2741, 2742)	Novel Protein sim. GBank gl 5032203 ref NP_005714.1 PTSPA - tetraspan 5	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins glycoprotein	22278996, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264805, 264509, 29331830, 66712502, 265008, 265009, 264758, 33657084, 85658542, 265010, 265018, 265019, 264762, 264448, 35695917, 33657109, 33657182, 33657349, 35695855, 264558, 22279002, 264563

1372	80248517 (2743, 2744)	Novel Protein sim. GBank gij1840708[jb][BAA09334] - (D50885) trans-sialidase [Trypanosoma cruzi]		collagen	263978
1373	80499421 (2745, 2746)			UNCLASSIFIED	264769, 21908765, 21908767, 22278988, 264691, 264910, 55812038, 265010, 264681, 264684
1374	95087036 (2747, 2748)	Novel Protein sim. GBank gij111876[pri][JC1241 - beta-interferon-induced protein - rat		interferon	264907, 264510, 265007, 264512, 265008, 60432229, 264689, 65274781, 264555, 264558, 264557, 83373044, 60432113
1375	84238942 (2749, 2750)	Novel Protein sim. GBank gij5649176[jb][AAD03500.2] - (AF051155) G beta-like protein GBL [Rattus norvegicus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52644507, 52645156, 52646842, 52646365, 56182575, 56181686, 22278988, 56964075, 35698288, 22278997, 22278988, 22278989, 264259, 29331822, 52645080, 29331824, 29331825, 60432229, 29331826, 29331827, 29331828, 35698052, 33658970, 264905, 264508, 264908, 264907, 264908, 29331830, 264909, 265008, 264511, 265007, 265008, 265009, 33657402, 60433356, 52646317, 33109854, 33657084, 52644286, 87188474, 87188559, 264600, 265017, 265018, 265019, 55811150, 18108351, 264448, 264764, 264288, 264389, 264768, 52644229, 21908765, 21908766, 21908767, 21908768, 21908768, 55811957, 35685917, 265020, 265021, 52644150, 33657023, 264693, 65274820, 52645129, 33657109, 27488261, 33657349, 27488265, 35695763, 18108376, 55810764, 35698423, 35695855, 264630, 264631, 264634, 264636, 264555, 264638, 18108385, 87188518, 60432113, 22279000, 22279002, 264563, 264564, 264566, 264567, 264768, 264769, 35695917, 22278997, 264691, 264259, 29331822, 264693, 35698052, 264508, 264509, 264905, 264906, 264628, 264908, 264629, 18108372, 264908, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 56526488, 265010, 265011, 264600, 264563, 264762, 264584, 264565, 264764, 264488, 264768
1376	87399050 (2751, 2752)	Novel Protein sim. GBank gij138350[sp][P28868][VGLX_HSVB - GLYCOPROTEIN X PRECURSOR		UNCLASSIFIED	264691, 264259, 29331822, 264693, 35698052, 264508, 264509, 264905, 264906, 264628, 264908, 264629, 18108372, 264908, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 56526488, 265010, 265011, 264600, 264563, 264762, 264584, 264565, 264764, 264488, 264768
1377	86864242 (2753, 2754)	Novel Protein sim. GBank gij1663648 (U75321) - chromaffin granule ATPase II homolog [Mus musculus]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase_associated	264691, 264259, 29331822, 264693, 35698052, 264508, 264509, 264905, 264906, 264628, 264908, 264629, 18108372, 264908, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 56526488, 265010, 265011, 264600, 264563, 264762, 264584, 264565, 264764, 264488, 264768

1378	87595071 (2755, 2766)	Novel Protein sim. GBank gi 4107015 dbj BAA36283  - (AB001772) PEM-5 [Ciona savignyi]			22278994, 22278998, 264093, 264094, 264259, 29331824, 29331827, 265009, 265018, 265019, 18108351, 264369, 264288, 29148627, 55811957, 264691, 18108368, 33657109, 18108388, 264635, 263981, 18108385
1379	85679344 (2757, 2758)	Novel Protein sim. GBank gi 3252872 (AF035620) - BRCA1-associated protein 2 [Homo sapiens]			265020
1380	87627862 (2759, 2760)	Novel Protein sim. GBank gi 4637737 gb AAD30662.1  - (AF096834) germ cell specific Y-box binding protein [Homo sapiens]		nuc_rept	284510, 264512, 265009, 264288, 264564
1381	88179856 (2761, 2762)	Novel Protein sim. GBank gi 4731580 gb AAD28508.1 AF12538 - (AF125384) L82A [Drosophila melanogaster]		UNCLASSIFIED	87168559, 285017, 264628, 22279002
1382	94847576 (2763, 2764)		Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	22278994, 22278997, 22278999, 29331822, 29331824, 29331826, 265007, 60432229, 60433356, 85658542, 265017, 265018, 264885, 264768, 21906788, 35695917, 33657023, 27486281, 27486282, 35695763, 35695855, 87168518, 22279002
1383	87860598 (2765, 2766)			UNCLASSIFIED	18108396, 264692
1384	86915895 (2767, 2768)			UNCLASSIFIED	264488, 264508, 264509, 264905, 264906, 264908, 264909, 264511, 264512, 264910, 264760, 18108351, 264766, 264769, 35695855, 264630, 264636, 264555, 264638, 264483, 264564, 264486
1385	86378788 (2769, 2770)	Novel Protein sim. GBank gi 2384732 (AF015911) - NAC-1 protein [Rattus norvegicus]		UNCLASSIFIED	35696052, 55811386, 264688, 21906765, 265020, 33657023, 18108385
1386	91013049 (2771, 2772)	Novel Protein sim. GBank gi 2384910 (AF022982) - contains similarity to the A-type potassium current class of channel proteins [Caenorhabditis elegans]		Inf	60432289, 29331828, 264908, 264807, 56182435, 265011, 264681, 60170615, 33657023, 83373044, 264588
1387	87797958 (2773, 2774)	Novel Protein sim. GBank gi 4160304 emb CAA10600  - (AJ132192) HS1 binding protein 3 [Mus musculus]		UNCLASSIFIED	264591
1388	85101652 (2775, 2776)	Novel Protein sim. GBank gi 4895164 gb AAD32753.1 AC007231 - (AC007231) putative disease resistance protein [Arabidopsis thaliana]		glycoprotein	85274572, 22278999, 264259, 29331826, 29331827, 35696052, 264509, 264907, 264908, 264909, 265006, 265008, 60170831, 33657402, 60433438, 264596, 21906754, 87168559, 264600, 265017, 264683, 18108354, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 264682, 33657023, 33657109, 35695855, 264558, 60170394, 83373044, 22279000

1388	91256016 (2777, 2778)	Novel Protein sim. GBank gi 5689387 dbj BAA82977.1  - (AB028948) KIAA 1025 protein [Homo sapiens]	Contains protein domain (PF00841) - Zn-finger in Ran binding protein and others.	UNCLASSIFIED	65274572, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29146499, 264908, 68712502, 55812038, 285017, 265018, 265019, 18108351, 264369, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 284692, 33657023, 33657349, 18108370, 18108374, 55811576, 284555, 264556, 284557, 60170394, 83373044, 22279000, 264563, 284564
1389	94111916 (2779, 2780)	Novel Protein sim. GBank gi 3702295 (AC005783) - R33083_1 [Homo sapiens]	peptidase		52645156, 52646365, 264259, 52645080, 29331825, 29331826, 284806, 52644045, 265009, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 264760, 264682, 264288, 264686, 264687, 56181562, 52644229, 21906765, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 27486281, 27486284, 85274791, 264631, 264555, 52644332, 87168518, 22279000, 264587
1391	91227345 (2781, 2782)	Novel Protein sim. GBank gi 1346910 sp P28650 PUA1, MOUSE - ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (IMP--ASPARTATE LIGASE)	Contains protein domain (PF00709) - Adenylosuccinate synthetase		29331826, 29331828, 29331830, 264448, 264288, 33657023, 18108365, 264555, 264556, 83373044
1392	94311087 (2783, 2784)	Novel Protein sim. GBank gi 726286 (U22394) - mSin3A [Mus musculus]			52646842, 65274572, 22278994, 22278995, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35696052, 29331828, 33656870, 284907, 52644045, 265006, 265007, 265008, 60431735, 60433356, 52646317, 55811386, 52644296, 265010, 87168559, 265017, 284604, 265018, 265019, 264448, 264288, 264369, 264766, 21906764, 21906767, 35695917, 265020, 265021, 33657109, 52645129, 27486261, 27486282, 27486265, 33657349, 35695763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264636, 52644332, 18108382, 18108385, 87168518, 60432113, 22279000, 264484, 264586, 18108391
1393	80409472 (2785, 2786)		Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264763, 264631
1394	15028819 (2787, 2788)			UNCLASSIFIED	264629
1395	95361471 (2789, 2790)	Novel Protein sim. GBank gi 2274845 dbj BAA21534  - (D88461) N-WASP [Rattus rattus]		UNCLASSIFIED	265009, 18108381



1396	95363263 (2791, 2792)	Novel Protein sim. GBank gij2135904 p j 54810 - pHLEIF1 - human			22278997, 22278999, 264259, 29331825, 60432289, 29331828, 29146498, 29146499, 284907, 264908, 29331830, 264909, 265006, 265007, 265008, 265009, 60433356, 265010, 264602, 265017, 265018, 265019, 18108354, 52644228, 18108358, 21906767, 29148627, 21908768, 21908769, 29148629, 29148784, 265021, 265022, 18108368, 18108374, 56182323, 18108385, 264563, 264567
1397	87631317 (2793, 2794)			UNCLASSIFIED	35696286, 264907, 66712502, 264510, 35695917, 264692, 264693, 35696423
1398	91233667 (2795, 2796)	Novel Protein sim. GBank gij5420389 emb CAB46680.1  - (AJ243460) proteophosphoglycan [Leishmania major]			264259, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 87168474, 265018, 265019, 264682, 264768, 21906767, 265020, 33657023, 27488261, 55811576, 284632, 264639, 83373044, 87168518, 22279002
1399	87631076 (2797, 2798)	Novel Protein sim. GBank gij2496887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	264768, 18108370, 264555, 264557
1400	95418064 (2799, 2800)	Novel Protein sim. GBank gij283920 p j S27939 - tensin - chicken	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	56182575, 22278994, 22278997, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264908, 56182435, 264112, 265009, 265011, 265017, 265018, 265019, 264760, 264762, 264765, 264288, 264685, 264687, 56181562, 264769, 21906768, 21908767, 55811957, 264691, 264692, 264628, 264629, 55811576, 264634, 264555, 264637, 264557, 264638, 18108381, 264558, 18108384, 60432113, 22279000
1401	91226378 (2801, 2802)	Novel Protein sim. GBank gij325618 emb CAA15485  - (AL008635) dJ510H16.1 [Homo sapiens]	Contains protein domain (PF00780) - VHS domain	UNCLASSIFIED	65274572, 60432289, 264909, 264758, 264768, 21906769, 22279002
1402	95361475 (2803, 2804)	Novel Protein sim. GBank gij1515427 (U57523) - nel homolog [Homo sapiens]	Contains protein domain (PF00009) - Igf EGF-like domain	igf	264905, 264907, 264908, 264909, 264112, 264693, 33657109, 264634
1403	94147933 (2805, 2806)	Novel Protein sim. GBank gij5262615 emb CAB45747.1  - (AL080156) hypothetical protein [Homo sapiens]			65274572, 66712502, 265017, 264448, 264288, 21906765, 21906769, 264693, 55811576, 65274791, 60432113
1404	90835393 (2807, 2808)			UNCLASSIFIED	65274572, 22278998, 29331822, 29331828, 66712502, 265008, 60433438, 265017, 264693, 18108385

1405	95095068 (2809, 2810)	Novel Protein sim. GBank gij854065[emb CAA58337] - (X83413) U88 [Human herpesvirus 6]			264488, 56994075, 35696286, 29331822, 29331824, 29331826, 29331828, 35696052, 264508, 264908, 264907, 264908, 264510, 264511, 264910, 33657402, 264594, 264758, 264600, 264604, 264762, 18108351, 264764, 33657023, 33657109, 264628, 264634, 83373044, 22279002, 264563, 264482, 264486, 264587
1406	87612369 (2811, 2812)	Novel Protein sim. GBank gij624076[gijAAC96425.1] - (U42580) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (8X), similar to soybean pro-rich cell wall protein, corresponds to Swiss-Prot Accession Number P13993 [Paramedum bursaria Chlorella virus 1]	collagen		264907, 264605
1407	94129872 (2813, 2814)	Novel Protein sim. GBank gij2827886 (AF015037) - endonucleopeptidase A related protein; EOPA related protein [Oryctolagus cuniculus]	UNCLASSIFIED		35696286, 22278999, 264094, 264259, 66714117, 29331826, 29331827, 29331828, 29146498, 264107, 264908, 265008, 265008, 264910, 60433438, 265011, 265017, 18108351, 264448, 264288, 264686, 21908765, 21908769, 264692, 33657109, 18108370, 264628, 263972, 18108374, 35696423, 55811576, 264631, 264557, 264558, 83373044, 18108365, 87168518, 80432113, 22279002
1408	95361477 (2815, 2816)	Novel Protein sim. GBank gij2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF000008) - EGF-like domain	oncogene	264488, 264489, 35696286, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 264908, 265008, 265009, 264910, 33657402, 264757, 264758, 265011, 264601, 265017, 264760, 264762, 264683, 264685, 264766, 264687, 264689, 21908767, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264638, 264637, 264638, 56182323, 264639, 264563, 264564, 264565, 264566, 264567
1409	86644385 (2817, 2818)	Novel Protein sim. GBank gij2662165[dj BAA23714] - (AB007802) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]			264693
1410	86612587 (2819, 2820)	Novel Protein sim. GBank gij2493780[sp Q60994 ACR3_MOUSE - 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ)]	Contains protein domain (PF003368) - C1q domain	complement	29331826, 264112, 264512, 265008, 265010, 264601, 264686, 264769, 21906767, 263974, 264631, 264566

1411	87818641 (2821, 2822)	Novel Protein sim. GBank gi 3123155 sp P91343 YM3M_CAEEL - HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	22278995, 22278997, 22278998, 29331822, 60432289, 29331828, 284907, 265017, 265018, 264682, 21906767, 21906768, 21906769, 265020, 264690, 264691, 33657023, 33657109, 27486284, 264628, 263972, 264634, 264558, 18108385 264737
1412	84390919 (2823, 2824)			UNCLASSIFIED	
1413	95416559 (2825, 2826)	Novel Protein sim. GBank gi 387912 emb CAA94370  - (Z70310) predicted using GeneFinder. Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:TO1923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	homeobox	56994075, 29331822, 35696052, 29331828, 29331830, 264909, 52644045, 264510, 52644296, 85658542, 87168474, 265017, 265018, 264681, 264687, 21906768, 35695917, 265020, 52644150, 264692, 263987, 27486284, 35695763, 264639, 18108387, 264566
1414	94675860 (2827, 2828)	Novel Protein sim. GBank gi 3252981  (AF068921) - Ras- binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264682, 264683, 265022, 264636
1415	94326948 (2829, 2830)	Novel Protein sim. GBank gi 1871187  (U90439) - unknown protein [Arabidopsis thaliana]			52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 66712502, 29331830, 52644045, 264413, 264511, 33657402, 264757, 21906754, 55811386, 265017, 265018, 265019, 264761, 264683, 264368, 264288, 264686, 264689, 21906766, 21906767, 29148627, 21906769, 55811957, 265020, 265021, 264690, 33657023, 65274620, 52645128, 27486262, 27486284, 60431528, 264629, 35695855, 56182323, 264559, 60432113, 264404, 22279002, 264482

1416	94325977 (2831, 2832)	Novel Protein sim. GBank gi 5106557 gb AAD39749.1 AF123052 MLL sepin-like fusion protein [Homo sapiens]	Contains protein domain (PF00735) - Cell division protein	- struct	18108392, 18108394, 18108397, 18108398, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 29331822, 35696052, 29331828, 29146498, 264905, 264907, 264908, 264828, 264909, 264113, 265006, 265007, 265008, 265009, 60170831, 264595, 18108348, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264762, 18108351, 264681, 264763, 264682, 264683, 264766, 52844229, 264688, 264689, 21906765, 21906768, 21906767, 29148827, 21906768, 55811957, 29148629, 265020, 52844150, 18108361, 33657023, 18108362, 18108368, 264628, 18108370, 264629, 18108374, 18108379, 55811576, 65274791, 264634, 264636, 56182323, 18108381, 60170394, 18108385, 56526486, 87168518, 22279000
1417	87826663 (2833, 2834)	Novel Protein sim. GBank gi 4958935 dbj BAA78095.1  - (AB027570) suppressor of potassium transport defect 3 [Rattus norvegicus]		ATPase_associated	264107, 264448
1418	87594276 (2835, 2836)			UNCLASSIFIED	264259, 264808, 265010, 52644229, 21906764, 21906768, 264690, 264639, 18108388
1419	87757168 (2837, 2838)	Novel Protein sim. GBank gi 2072294 (U95097) - mitotic phosphoprotein 43 [Xenopus laevis]		struct	264259, 60432289, 265006, 87168474, 264288
1420	87288628 (2839, 2840)	Novel Protein sim. GBank gi 5174421 ref NP_008023.1 pCPNE - copine VI (neuronal) (Z69635) Similarity to Yeast uridine Kinase		ATPase_associated	28331824, 265007, 264563
1421	94746986 (2841, 2842)	Novel Protein sim. GBank gi 3876090 emb CAA93459.1  - (SWLURK1_YEAST): cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this gene...		kinase	18108358, 18108396, 18108397, 21906766, 18108398, 21906767, 56182575, 21906768, 21906769, 56181886, 55811957, 35695917, 35696286, 22278996, 22278997, 22278998, 22278999, 265021, 265022, 60170815, 264259, 33657023, 29331822, 56182181, 29331824, 66714117, 29331825, 33657109, 29331826, 27486261, 29331828, 35696052, 33657348, 264905, 264509, 20281149, 18108370, 264907, 60431528, 66712502, 263972, 55811576, 35696423, 35695855, 264512, 265007, 60431850, 60432229, 60431735, 56182323, 264558, 60170394, 83373044, 55812038, 264758, 18108385, 21906754, 55811386, 87168518, 87168559, 60432113, 265017, 265018, 265019, 22279002, 55811150, 264563, 264682, 264763, 264448, 264566, 264486, 18108391

1422	88178777 (2843, 2844)	Novel Protein sim. GBank gij4505939(jfjNP_000928.1)pPOLR - polymerase (RNA) II (DNA directed) polypeptide A (220kD)		inapolymerase	56994075, 35698286, 87168559, 55811957, 55811576, 264555, 264557, 87168518
1423	86997762 (2845, 2846)			UNCLASSIFIED	264686, 264489, 264692, 264594, 264603, 265018, 264908
1424	95201610 (2847, 2848)	Novel Protein sim. GBank gij437181 (U02289) - GTPase- activating protein [Caenorhabditis elegans]	Contains protein domain (PF00620) - RhoGAP domain	struct	29331822, 29331825, 29331827, 29146498, 264905, 264908, 264908, 264909, 265007, 264910, 265009, 33109954, 265010, 87168559, 265019, 264766, 264687, 21906765, 21906766, 21906767, 21906768, 29148627, 55811957, 29148629, 265021, 264691, 264692, 56526486, 22279002, 264583
1425	21662314 (2849, 2850)	Novel Protein sim. GBank gij100788(priJ)S14959 - proline- rich protein - wheat		UNCLASSIFIED	265007, 264558
1426	94322115 (2851, 2852)	Novel Protein sim. GBank gij2078441 (U56964) - weak similarity to S. cerevisiae intracellular protein transport protein US1 (SP:P25386) [Caenorhabditis elegans]		UNCLASSIFIED	264488, 80424178, 35698286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331827, 56182435, 264910, 60433356, 60433438, 21906764, 265018, 264288, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 33657109, 18108370, 18108376, 264558, 83373044, 18108385, 56526486, 22279002, 264482
1427	91272510 (2853, 2854)	Novel Protein sim. GBank gij5616074(gbIAAD45616.1)AF06194 - (AF061943) prolase- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278994, 56694075, 22278997, 29331828, 29331830, 264828, 265006, 265007, 265008, 265009, 264683, 264288, 18108354, 21906765, 21906768, 29148629, 33657023, 18108374, 35698555, 83373044, 22279002, 264564
1428	94323008 (2855, 2856)	Novel Protein sim. GBank gij138350(spP28968)GLX_HSVB - GLYCOPROTEIN X PRECURSOR		glycoprotein	56181686, 264259, 264907, 265007, 265009, 264595, 265010, 264688, 65274620, 264629, 65274791, 22279002, 264568
1429	87888689 (2857, 2858)			UNCLASSIFIED	264112, 264595, 265017, 265019, 21906765, 263977, 264555
1430	94735021 (2859, 2860)	Novel Protein sim. GBank gij1181619(dbj)BAA11565] - (D82364) a variant of TSC-22 [Gallus gallus]			264094, 29331824, 264591, 264593, 265018, 264681, 21906765, 21906767, 65274620, 55811576, 264639, 87168518, 22279002
1431	80429081 (2861, 2862)	Novel Protein sim. GBank gij5420389(jemb)CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264768, 265020, 264691, 264693, 264638
1432	87463004 (2863, 2864)	Novel Protein sim. GBank gij414797 (L18966) - pyruvate dehydrogenase phosphatase [Bos taurus]		phosphatase	18108394, 26146498, 265007, 60433438, 264763, 29148629, 263989
1433	87605403 (2865, 2866)	Novel Protein sim. GBank gij2460316 (AF022147) - uterus- ovary specific putative transmembrane protein [Rattus norvegicus]	Contains protein domain (PF00100) - Zona pellucida-like domain	UNCLASSIFIED	264259, 264510, 264591, 264603, 264565
1434	85713730 (2867, 2868)			UNCLASSIFIED	264682, 264691

1435	84708213 (2869, 2870)	Novel Protein sim. GBank gij3970850[dbj BAA34789.1] - (AB015330) HRIHFB2007 [Homo sapiens]		transcriptfactor	22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 33656970, 264508, 264905, 66712502, 29331830, 264909, 265007, 265008, 264910, 265009, 60433356, 60433438, 264598, 21906754, 265010, 265017, 265018, 265019, 18108351, 264762, 264448, 264288, 264769, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264690, 264691, 33657109, 264628, 18108374, 18108378, 55811576, 264636, 60170394, 56182323, 264558, 83373044, 87168518, 60432113, 22279000, 22279002, 264563, 264482, 264565
1436	86635024 (2871, 2872)	Novel Protein sim. GBank gij3183977[emb CAA39515] - (X59044) protein sim. GBank		UNCLASSIFIED	263978, 264557, 264559
1437	87631082 (2873, 2874)	gij2496887[sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C08F5.2 IN CHROMOSOME III		UNCLASSIFIED	22278997, 66714117, 29331826, 264907, 56182435, 265009, 18108351, 264692, 264693
1438	85544280 (2875, 2876)	Novel Protein sim. GBank gij1905908 (AD000092) - hypothetical human serine-threonine protein kinase R31240.1 [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	kinase	264488, 264508, 264906, 264909, 264757, 264800, 264601, 264605, 264768, 264769, 264890, 35898423, 264558, 264563, 264566
1439	91231894 (2877, 2878)	Novel Protein sim. GBank gij3876269[emb CAA94892] - (Z71180) similar to BPTIKUNITZ inhibitor domain; cDNA EST EMBL:D88293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabdi...	Contains protein domain (PF00450) - Serine carboxypeptidase	calhepsin	264489, 18108394, 65274572, 56182575, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 264107, 264508, 264509, 264907, 66712502, 29331830, 56182435, 264511, 265006, 265007, 265009, 60432229, 60433438, 264595, 55812038, 55811388, 265011, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 18108355, 264767, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 264638, 56182323, 83373044, 18108387, 87168518, 60432113, 22279000, 264486
1440	87423843 (2879, 2880)	Novel Protein sim. GBank gij2662165[dbj BAA23714] - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]		UNCLASSIFIED	264887, 264259, 264906, 264907, 264908, 264909, 265008, 265010, 265017, 265018, 265019, 18108351, 264369, 265020, 33657023, 33657109, 60431528, 55811576, 264635

1441	95317662 (2881, 2882)	Novel Protein sim. GBank gi4493956[embjCAB1123.2] - (Z98551) predicted using hexExon; MAL3P6.28 (PF00845c). Hypothetical protein; len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe), C.elegans protein ZK287.5 (TR....	Contains protein domain (PF00846) - F-box domain.	helicase	18108392, 264488, 263994, 264489, 56182575, 22278994, 22278995, 56994075, 35986286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 56182181, 66714117, 29331826, 29331827, 29331828, 35698052, 29146498, 264508, 264905, 264509, 264908, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264910, 264592, 264593, 33657402, 60433438, 264595, 264758, 21906754, 85858542, 87168474, 265010, 87168559, 264600, 264602, 265017, 264604, 265018, 264605, 265019, 264760, 264761, 264762, 264681, 264448, 264764, 264683, 264288, 264766, 264768, 264769, 52644229, 264689, 21908765, 21906766, 21906767, 21906788, 21906789, 55811957, 35695917, 265020, 265021, 60170815, 52844150, 264681, 264692, 33657023, 85274620, 33657109, 35695763, 264628, 18108370, 264629, 18108374, 55811576, 35696423, 65274791, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 56182323, 264558, 60170394, 264638, 264559, 83373044, 18108385, 18108388, 56526486, 22279000, 22279002, 264563, 264483, 264564, 264566, 264567, 264486
1442	83367491 (2883, 2884)	Novel Protein sim. GBank gi5103027[dbjBAA78765.1] - (AB023419) mSox7 [Mus musculus]		transcript factor	264806, 265007, 264693, 264558
1443	87109935 (2885, 2886)	Novel Protein sim. GBank gi4887229[gbjAAD32244.1]AF150755 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	struct	52645080, 264691, 264628, 264555
1444	87620478 (2887, 2888)	Novel Protein sim. GBank gi3874447[embjCAB02772] - (Z81039) predicted using Genefinder; cDNA EST EMBL: T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...		UNCLASSIFIED	264259, 29331822, 29331824, 66714117, 29331828, 264288, 35695917, 33657023, 264635, 60170394
1445	94990470 (2889, 2890)	Novel Protein sim. GBank gi2959866[embjCAA11022] - (AJ222968) L-periaxin [Mus musculus]		UNCLASSIFIED	264369
1446	85079268 (2891, 2892)	Novel Protein sim. GBank gi5081610[gbjAAD39484.1]AF13544 - (AF135440) huntington yeast partner C [Mus musculus]	Contains protein domain (PF01846) - FF domain		264369
1447	86945382 (2893, 2894)				18108386, 35696286, 22278997, 66714117, 29331828, 265009, 264758, 265018, 264288, 21906766, 21906767, 264692, 264634, 264566
1448	94990477 (2895, 2896)	Novel Protein sim. GBank gi3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]	Contains protein domain (PF00439) - Bromodomain		29331827, 264508, 264908, 265008, 264595, 18108357, 18108385, 264568, 264486

1449	87860859 (2897, 2898)			UNCLASSIFIED	66714117, 284908, 284908, 284591, 284601, 284764, 284632
1450	87458686 (2899, 2900)	Novel Protein sim. GBank gij1707074 (U80450) - M01E11.2 [Caenorhabditis elegans]		UNCLASSIFIED	35696286, 35696052, 265008, 265009, 60170831, 33109854, 264683, 264689, 35696423, 35695855, 56526488
1451	87787970 (2901, 2902)	Novel Protein sim. GBank gij4160304[emb]CAA10600] - (AJ132182) HS1 binding protein 3 [Mus musculus]		UNCLASSIFIED	29331826, 284683, 284683, 263978, 264630
1452	85682898 (2903, 2904)	Novel Protein sim. GBank gij2832906[dbj]BAA24608.1] - (D89340) dipeptidyl peptidase III [Rattus norvegicus]		peptidase	264681, 33657023, 284629
1453	86130434 (2905, 2906)	Novel Protein sim. GBank gij28831[sp]P39188[ALU1_HUMAN - III] ALU SUBFAMILY J WARNING ENTRY IIII		kinase	284510, 284768
1454	11204898 (2907, 2908)				264556
1455	87787898 (2908, 2910)			UNCLASSIFIED	29331822, 66714117, 29331825, 264905, 29331830, 265008, 265008, 265009, 265011, 265019, 18108351, 21908768, 33657109, 18108376, 284632, 56182323, 87168518
1456	86320218 (2911, 2912)	Novel Protein sim. GBank gij729230[sp]P41004[CUT3_SCHPO - CHROMOSOME SEGREGATION PROTEIN CUT3]		transport	22278995, 22278996, 22278997, 22278998, 22278999, 29331827, 264107, 265017, 21908765, 21908766, 21908767, 21908769, 29148629, 18108370, 22279000
1457	80076900 (2913, 2914)			UNCLASSIFIED	264107, 264566
1458	87800460 (2915, 2916)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		transport	56182575, 22278999, 60432049, 264259, 29331826, 29331827, 29331828, 265017, 265018, 264107, 264110, 265009, 60432229, 265019, 265020, 263972, 263976, 264635, 22279002, 264566
1459	95360920 (2917, 2918)	Novel Protein sim. GBank gij5524667[gb]AAD4333.1[AF15935 - (AF159356) Munc13-4 protein [Rattus norvegicus]	Contains protein domain (PF00168) - C2 domain	kinase	22278997, 264259, 29331824, 29331826, 29331827, 29331828, 265017, 265018, 264760, 264682, 264448, 264288, 264766, 265021, 264692, 33657023, 33657109, 35695855, 284566
1460	95354602 (2919, 2920)			UNCLASSIFIED	29331822, 264591, 55811957, 264691, 264693, 65274620
1461	84741513 (2921, 2922)	Novel Protein sim. GBank gij1707274 (U80931) - strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases [Caenorhabditis elegans]	Contains protein domain (PF00202) - gaba Aminotransferases class-III pyridoxal phosphate	gaba	22278997, 29331822, 35696052, 265009, 264758, 265017, 265018, 265019, 264760, 264369, 264687, 21908765, 21908768, 265022, 33657109, 27486261, 284555, 83373044
1462	87732018 (2923, 2924)			UNCLASSIFIED	264555, 284556
1463	88090805 (2925, 2926)	Novel Protein sim. GBank gij1770466[emb]CAA66912] - (X98259) M-phase phosphoprotein 8 [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHR)romatin Organization Modifier domain	struct	60432049, 264259, 28146499, 264908, 264907, 264512, 265017, 264763, 264768, 18108370, 18108374, 264636, 18108385, 18108388



1464	87620482 (2927, 2928)	Novel Protein sim. GBank gl 3874447 emb CAB02772  - (Z81039) predicted using Genefinder; cDNA EST EMBL: T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...		UNCLASSIFIED	264569, 22278995, 22278996, 22278997, 22278998, 29331822, 29331824, 29331825, 35696052, 20281100, 264905, 29331830, 264909, 265007, 33657402, 21908754, 265017, 265018, 264682, 264684, 264368, 264288, 264766, 21908765, 21908766, 21908767, 21908769, 35695917, 264691, 33657023, 264692, 35696423, 35695855, 264630, 264631, 264639, 264565
1465	87425182 (2928, 2930)	Novel Protein sim. GBank gl 4595958 db BAA76821.1  - (AB023194) KIAA0977 protein [Homo sapiens]		glucoamylase	264488, 22278994, 56984075, 60432049, 264259, 56182181, 60432289, 29331827, 52844045, 264511, 265007, 265008, 264598, 55812038, 55811386, 264600, 264602, 265017, 265018, 264604, 265019, 18108351, 18108354, 56181562, 21908769, 265021, 33657023, 33857182, 55811576, 264557, 18108382, 60432113
1466	87606227 (2931, 2932)	Novel Protein sim. GBank gl 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	264512, 265017, 264689, 264558
1467	87614328 (2933, 2934)			struc	264683, 264636
1468	95342862 (2935, 2936)	Novel Protein sim. GBank gl 4507241 ref NP_003137.1 pSSRP - structure specific recognition protein 1			
1469	78236174 (2937, 2938)	Novel Protein sim. GBank gl 1906586 (U81788) - kinesin-73 [Drosophila melanogaster]		struc	22278998, 264758, 265018, 265019, 21906768, 265020, 33857109, 22279002
1470	94890482 (2939, 2940)	Novel Protein sim. GBank gl 5849170 gb AAD43131.2 AF15909 - (AF159092) syd709613 protein [Homo sapiens]		UNCLASSIFIED	18108394, 18108397, 18108398, 35696052, 29146499, 265007, 265008, 265009, 265010, 265011, 18108354, 18108365, 18108368, 18108374, 18108381, 18108382, 18108384, 18108388
1471	87826842 (2941, 2942)	Novel Protein sim. GBank gl 3876146 emb CAB01750  - (Z78542) similar to Mitochondrial carrier proteins; cDNA EST EMBL: T01651 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	18108394, 18108398, 56182575, 264259, 29331822, 29331824, 29331825, 60432289, 264907, 264909, 265007, 264910, 265009, 264591, 60432229, 60433356, 264595, 60433438, 264758, 33109954, 265010, 265011, 265018, 264760, 264448, 264764, 264288, 264368, 18108357, 264769, 18108358, 21906767, 21906769, 55811857, 265021, 18108361, 264691, 18108362, 18108365, 18108368, 264628, 18108379, 264637, 264557, 18108381, 56182323, 18108382, 83373044, 18108384, 18108388, 87166518, 60432113, 264404, 22279002, 264482, 264567, 264487
					29331822, 29331824, 29331825, 264828, 264603, 264688, 264693, 18108374, 55811576

1472	87756616 (2043, 2044)	Novel Protein sim. GBank gi 4680707 gb AAD27743.1 AF13296 - (AF132968) CGI-34 protein [Homo sapiens]		UNCLASSIFIED	264905, 18108351, 21906765, 264486
1473	87791609 (2045, 2046)	Novel Protein sim. GBank gi 3688780 (AF042180) - testis-specific Y-encoded-like protein [Mus musculus]	Contains protein domain (PF00956) - Nucleosome assembly protein (NAP)	MHC	18108394, 22278995, 56994075, 22278999, 29331822, 29331824, 66714117, 29331825, 29331826, 35686052, 264908, 264907, 56182435, 265007, 264758, 265018, 265019, 264760, 264764, 264288, 264685, 264686, 264768, 21906768, 55811957, 265021, 264681, 264693, 264629, 55811578, 264634, 264638, 56182323, 22278002, 264566, 264486
1474	85800989 (2047, 2048)	Novel Protein sim. GBank gi 2494890 sp Q92176 CORO_BOVIN - CORONIN-LIKE PROTEIN P57	Contains protein domain (PF00400) - WD domain, G-beta repeat	struct	264488, 35695917, 35686286, 264692, 33657023, 264693, 33657109, 35696052, 264508, 264905, 264906, 264907, 264629, 264908, 264909, 35696423, 35695855, 264511, 264910, 264632, 264634, 264635, 264636, 264637, 264556, 264557, 264638, 264758, 60432113, 264604, 264605, 264565, 264566, 264764, 264488, 264885, 264766
1475	86871835 (2049, 2050)		Contains protein domain (PF00041) - Fibronectin type III domain	UNCLASSIFIED	264681, 264682, 264288, 264566
1476	87548855 (2051, 2052)	Novel Protein sim. GBank gi 4757752 ref NP_004664.1 PANGP - angiotensin 3	Contains protein domain (PF00147) - Fibrinogen beta and gamma chains, C-terminal globular domain	glycoprotein	60424179, 56181686, 29331824, 60424269, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264512, 265007, 265008, 265009, 264910, 33657402, 264595, 264596, 55812038, 265011, 264801, 264762, 18108351, 264288, 264369, 264685, 264766, 264689, 55811957, 264691, 264692, 264693, 18108370, 60431528, 18108374, 35696423, 264634, 264635, 264636, 60431850, 264555, 264638, 264557, 264639, 18108382, 18108388, 60432113, 22278002
1477	87774278 (2053, 2054)	Novel Protein sim. GBank gi 2498308 sp Q80870 DP1_MOUSE - POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)		UNCLASSIFIED	264259, 264107, 264905, 265008, 265010, 265011, 264682, 264288, 265020, 265021, 263974
1478	11754412 (2055, 2056)				264686

1479	91640140 (2857, 2858)	Novel Protein sim. GBank gi 5499741 gb AAD43978.1 AF15296 - (AF15296) chromatin-specific transcription elongation factor FACT 140 kDa subunit [Homo sapiens]		peptidase	56182575, 22278995, 22278996, 22278998, 22278999, 29331822, 29331824, 68714117, 284908, 264907, 56182435, 265006, 60170831, 33657402, 264758, 33108954, 21906754, 265017, 285018, 264448, 264288, 264767, 264687, 52644229, 21906764, 264688, 21906765, 21906768, 21906769, 285020, 265021, 60170815, 264691, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 18108370, 60431528, 263976, 55811576, 264556, 264557, 60170394, 87168518, 264404, 22278000, 22279002, 264563, 264482
1480	94312412 (2859, 2860)	Novel Protein sim. GBank gi 3550456 emb CAA06329.1  - (AJ005073) Alix [Mus musculus]		UNCLASSIFIED	18108394, 65274572, 56182575, 22278995, 35698286, 56994075, 22278996, 22278997, 22278998, 22278999, 264091, 264259, 35696052, 26146499, 264103, 264105, 264108, 264907, 52644045, 264112, 265007, 265008, 265009, 60433358, 60433438, 264598, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264448, 264682, 264683, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657109, 33657182, 263972, 35698585, 264557, 263981, 83373044, 18108385, 87168518, 264566, 264089, 264486
1481	87021442 (2861, 2862)	Novel Protein sim. GBank gi 4836807 gb AAD30566.1 AF14679 - (AF146793) PFT27 [Mus musculus]		MHC	265008, 265007, 265010, 18108374
1482	85320442 (2863, 2864)	Novel Protein sim. GBank gi 4585372 gb AAD25403.1 AF12292 - (AF122923) Wnt inhibitory factor-1 [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	284908, 264910, 264758
1483	94115503 (2865, 2866)	Novel Protein sim. GBank gi 535428 (U13736) - calmodulin- like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	struct	264259, 29331822, 52645080, 29331825, 29331826, 33656970, 29331830, 265007, 55812038, 33109954, 285017, 264288, 21906768, 21906769, 264638, 18108380, 87168518, 22279000
1484	94131544 (2867, 2868)	Novel Protein sim. GBank gi 1911774 bbs 180090 - (S83364) putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]		UNCLASSIFIED	264489, 35696286, 264259, 264107, 264908, 265008, 60433356, 33657402, 60433438, 264288, 21906765, 21906768, 29148627, 33657023, 27486262, 18108374, 35696423, 83373044, 60432113
1485	80194441 (2869, 2970)	Novel Protein sim. GBank gi 5360129 gb AAD42863.1 AF15511 - (AF155117) NY-REN 62 antigen [Homo sapiens]	Contains protein domain (PF00225) - Kinesin motor domain	struct	264369, 265020, 18108374

1486	94125066 (2971, 2972)	Novel Protein sim. GBank gi 4589516 dbj BAA76780.1  - (AB023153) KIAA0936 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	56182575, 22278999, 264906, 264907, 21908754, 87168474, 265017, 265019, 18108351, 264288, 265020, 264566, 21908754, 264486
1487	86452711 (2973, 2974)	Novel Protein sim. GBank gi 5019275 emb CAB44431.1  - form XL-III [Bos taurus]		synthase	
1488	87732026 (2975, 2976)	Novel Protein sim. GBank gi 5712131 gb AAD47379.1  (AF120499) DEM1 protein [Homo sapiens]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	tgf	264686, 264769, 264689, 264692, 264693, 264509, 264908, 264907, 18108370, 264908, 264629, 264909, 264510, 265006, 264512, 265007, 265008, 265009, 264555, 264556, 264557, 264558, 264762, 264564, 264692
1489	95104277 (2977, 2978)	Novel Protein sim. GBank gi 2497303 sp Q82766 FPRP_RAT - PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN)	Contains protein domain (PF00047) - Immunoglobulin domain	prostaglandin	21908767, 22278999, 265022, 264259, 264693, 29331824, 29331825, 29331826, 29331827, 29331828, 264103, 263972, 66712502, 35896423, 35898555, 265007, 265008, 265009, 83373044, 21908754, 56526486, 265017, 264563, 18108351, 264564, 264566, 264369, 264288
1490	87390127 (2978, 2980)			UNCLASSIFIED	56182575, 264259, 29331822, 29331824, 66714117, 29331827, 29331828, 264508, 264905, 66712502, 265007, 265008, 264594, 33657402, 55812038, 87168474, 265018, 18108351, 264369, 264288, 264769, 264689, 21908767, 21908768, 55811957, 60170615, 33657109, 35695855, 264635, 60170394, 56526486, 22279002, 264563
1491	83584305 (2981, 2982)	Novel Protein sim. GBank gi 295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]		UNCLASSIFIED	265007, 264448, 18108372, 264558, 56182323
1492	85805363 (2983, 2984)	Novel Protein sim. GBank gi 1656005 (U71205) - rit [Mus musculus]	Contains protein domain (PF00071) - Res family	oncogene	22278997, 22278998, 29331822, 264907, 66712502

1493	91677215 (2985, 2986)	Novel Protein sim. GBank gij5689515dbj[BAA83041.1] - (AB029012) KIAA1089 protein [Homo sapiens]		UNCLASSIFIED	264488, 52646365, 65274572, 56182575, 22278994, 35696286, 58994075, 22278999, 60432049, 29331824, 29331820, 35696052, 264508, 264805, 264906, 52844045, 264909, 56182435, 265008, 265008, 265009, 60170831, 33657402, 55812038, 265010, 265011, 265017, 265018, 265019, 55811150, 264448, 264682, 264685, 264686, 52844229, 21906765, 21906768, 21906769, 265020, 265021, 60170815, 52844150, 33657023, 18108364, 18108365, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108370, 264629, 18108374, 52844332, 56182323, 87168518, 22279002, 264564, 264566, 264567
1494	87605265 (2987, 2988)	Novel Protein sim. GBank gij728832spjP39189[ALU2_HUMAN - III] ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF01352) - KRAAB box	kinase	264807, 265009, 264768, 18108370, 55811576, 264639, 264565, 264488
1495	87605267 (2989, 2990)	Novel Protein sim. GBank gij4589588jdbj[BAA76816.1] - (AB023189) KIAA0972 protein [Homo sapiens]	Contains protein domain (PF01352) - KRAAB box	transcriptifactor	22278997, 264259, 264806, 264907, 265009, 264594, 33657084, 265017, 264760, 264448, 33657109, 264630, 264634, 56526486, 264563, 264565, 264566, 264488, 264567
1496	87784322 (2991, 2992)	Novel Protein sim. GBank gij542038jembj[CAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	35696288, 264906, 265019, 264693
1497	81695428 (2993, 2994)	Novel Protein sim. GBank gij3874925jembj[CA92591] - (Z66296) Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE); cDNA EST EMBL:D27610 comes from this gene; cDNA EST EMBL:TO1018 comes from this gene; cDNA EST EMBL:D33256 comes from this gene...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264910, 264758, 265011, 264764, 264288, 264690, 264634, 264635, 56526486
1498	80834838 (2995, 2996)	Novel Protein sim. GBank gij728836spjP39183[ALU6_HUMAN - III] ALU SUBFAMILY Y SP WARNING ENTRY IIII		oncogene	264488, 65274572, 29331822, 265017, 265018, 21906765, 29148627, 29148629, 18108374, 264637, 264638, 264567
1499	86451569 (2997, 2998)	Novel Protein sim. GBank gij2570198 (U54556) - microfilament sheath protein SHP3 [Lilomiosoides sigmodontis]		glucoamylase	263978, 264566
1500	80489386 (2999, 3000)	Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycopeptide AFGP polypeptide precursor [Boreogadus saida]		UNCLASSIFIED	22278999, 264769, 18108379
1501	85795297 (3001, 3002)	Novel Protein sim. GBank gij3900855 (AC004874) - similar to N-acetylglucosaminyltransferase; similar to Q07537 (PID.g1171989) [Homo sapiens]	Contains protein domain (PF00535) - Glycosyl transferases	UNCLASSIFIED	264559
1502	80206141 (3003, 3004)				264508, 264112, 264604, 264684, 52844150, 55811576, 264632, 264556, 264638, 56182323, 264563, 264486
1503	87012701 (3005, 3006)			transferase	29331822, 265007, 264369

1504	76640051 (3007, 3008)		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264893
1505	86102872 (3009, 3010)	Novel Protein sim. GBank gll4753775jmbjCAB41970.1] - (AJ132546) protein kinase [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	29331826, 35686052, 264509, 264908, 264907, 264908, 264909, 264511, 264910, 55612038, 264759, 264763, 264764, 264689, 35695917, 265022, 33657109, 18108374, 264631, 264635, 264638, 264566
1508	94143219 (3011, 3012)	Novel Protein sim. GBank gll1304201dbjBAA06170] - (D29766) alternatively spliced product [Rattus norvegicus]	Contains protein domain (PF00018) - SH3 domain	glycoprotein	65274572, 56182575, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 60432049, 264259, 52645080, 29331822, 29331827, 264108, 29331830, 264908, 56182435, 264110, 264511, 264512, 55612038, 21906754, 87168559, 264600, 265017, 265018, 264681, 18108354, 264369, 264687, 264689, 21906765, 29148627, 21906768, 21906769, 29148829, 52644150, 33657023, 18108376, 65274781, 56182323, 264558, 264559, 18108385, 87168518, 60432113, 22279000, 264565
1507	83738250 (3013, 3014)	Novel Protein sim. GBank gll5689513dbjBAA83040.1] - (AB029011) KIAA1088 protein [Homo sapiens]		helicase	264639
1508	11618758 (3015, 3016)	Novel Protein sim. GBank gll5031975refjNP_005875.1]pPAK4 - protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264593
1509	87318451 (3017, 3018)	Novel Protein sim. GBank gll113161]spP28614]ACOR_ALCEU - ACETOIN CATABOLISM REGULATORY PROTEIN		UNCLASSIFIED	264259, 29331822, 265007, 18108374, 264556
1510	85362643 (3019, 3020)	Novel Protein sim. GBank gll728831]spP39188]ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	264259, 29331822, 29331824, 29331827, 264509, 264907, 264510, 264511, 265007, 264512, 265008, 87168559, 264288, 265022, 33657023, 35695855, 264637, 264638, 264563
1511	88318073 (3021, 3022)	Novel Protein sim. GBank gll728831]spP39188]ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	264259, 29331822, 29331824, 29331827, 264509, 264907, 264510, 264511, 265007, 264512, 265008, 87168559, 264288, 265022, 33657023, 35695855, 264637, 264638, 264563
1512	95345390 (3023, 3024)	Novel Protein sim. GBank gll4559353]gbjAAD23014.1]AC00658 - (AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01183) - RIO1/ZK632.3/MJ0444 family		52645156, 18108396, 56994075, 60432289, 265008, 60433356, 60433438, 21906754, 87168474, 87168559, 265018, 264762, 264763, 264687, 21906765, 21906769, 27486262, 35695763, 18108374, 35696423, 264555, 18108385, 18108387, 18108388, 87168518, 264482
1513	87436228 (3025, 3026)	Novel Protein sim. GBank gll1330394 (U58761) - C01F1.6 gene product [Caenorhabditis elegans]			35696052, 264905, 264806, 264907, 264908, 264909, 264910, 264591, 264766, 264689, 264692, 264629, 264636

1514	95345392 (3027, 3028)	Novel Protein sim. GBank gi4559353 gb AAD23014.1 AC00658  putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family	UNCLASSIFIED	52644507, 52645156, 52646365, 52646842, 65274572, 22278994, 35698286, 56994075, 264259, 52645080, 29331822, 29331825, 35698052, 29331830, 52644045, 59182435, 265006, 60433358, 60433438, 55812038, 21908754, 52646317, 52644296, 87168474, 87168559, 264448, 52644229, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 33657023, 52645129, 33657108, 33657182, 27486261, 27486262, 27486264, 27486265, 35695763, 18108376, 35696423, 35695855, 52644332, 18108385, 18108387, 87168518, 60432113 265020, 264639
1515	79163536 (3029, 3030)	Novel Protein sim. GBank gi3879501 emb CAA87795  - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...	ubiquitin		
1516	88073538 (3031, 3032)	Novel Protein sim. GBank gi498015 (L27479) - X123 [Homo sapiens]	UNCLASSIFIED	265008, 56182323, 22278002	
1517	87783325 (3033, 3034)	Novel Protein sim. GBank gi3415134 (AF082024) - Phyb1 [Pimpinella brachycarpa]		264081, 18108370, 264404	
1518	87350697 (3035, 3036)	Novel Protein sim. GBank gi728838 sp P39195 ALU8_HUMAN - IIII ALU SUBFAMILY SX WARNING ENTRY IIII	Im7	66714117, 264508, 264509, 264905, 264510, 264810, 264591, 264595, 264288, 264768, 264769, 18108374, 264636, 264638, 264486 264569, 264489, 60432049, 265008,	
1519	94328688 (3037, 3038)	Novel Protein sim. GBank gi5262681 emb CAB45771.1  - (AL080198) hypothetical protein [Homo sapiens]		33657402, 264598, 21906754, 265019, 264369, 21908785, 21906768, 21906769, 264691, 65274620, 33657182, 27486261, 18108374, 264557, 264639, 87168518, 22278002	
1520	87592855 (3039, 3040)	Novel Protein sim. GBank gi2662161 db BAA23712  - (AB007900) HH0452 cDNA clone for KIAA0440 has a 438- bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]	UNCLASSIFIED	18108392, 60432049, 264259, 29331824, 265007, 60433356, 265010, 21906768, 264636	
1521	86970696 (3041, 3042)	Novel Protein sim. GBank gi5052351 gb AAD38516.1 AF13542 - (AF135421) GDP- mannose pyrophosphorylase B [Homo sapiens]	Contains protein domain (PF00483) - Nucleotidyl transferase	18108394, 264259, 66714117, 265011, 264803, 265019, 18108364, 35698423, 264557, 264558, 18108388	
1522	78660687 (3043, 3044)	Novel Protein sim. GBank gi3776567 (AC005388) - Strong similarity to F21B7.33 gi2809264 from A. thaliana BAC gp AC002560. EST gb N65119 comes from this gene. [Arabidopsis thaliana]	UNCLASSIFIED	29331824, 265018, 265020, 265021	
1523	91005151 (3045, 3046)	Novel Protein sim. GBank gi3776567 (AC005388) - Strong similarity to F21B7.33 gi2809264 from A. thaliana BAC gp AC002560. EST gb N65119 comes from this gene. [Arabidopsis thaliana]	UNCLASSIFIED	65274572, 21906768, 264693	
1524	80203723 (3047, 3048)	Novel Protein sim. GBank	UNCLASSIFIED	264112, 21906754, 263974	
1525	87799867 (3049, 3050)	Novel Protein sim. GBank gi4759040 ref NP_004283.1 pRIN1 - ras inhibitor	UNCLASSIFIED	264883, 264687, 264688, 264690, 264692, 264693	

1528	95105344 (3051, 3052)	Novel Protein sim. GBank gij728650 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		glycoprotein	35696286, 56182181, 60431735, 264595, 55912038, 264605, 264683, 21906765, 55811957, 265020, 65274791, 264555, 264556, 264557, 264558, 264559, 83373044
1527	88262512 (3053, 3054)	Novel Protein sim. GBank gij2792496 (AF041107) - tulip 2 [Rattus norvegicus]			56182575, 264259, 60432049, 29331822, 60432289, 264908, 86712502, 60433438, 87168559, 265017, 264288, 21906768, 21906769, 263977, 55811576, 56182323, 18108381
1528	94130918 (3055, 3056)			UNCLASSIFIED	22278895, 22278897, 264259, 66712502, 264598, 265017, 265019, 264682, 264448, 264683, 264764, 264685, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 264693, 83373044, 18108385
1529	94120793 (3057, 3058)	Novel Protein sim. GBank gij4406663 gb AAD20053] - (AF131826) Unknown [Homo sapiens]		UNCLASSIFIED	264488, 263994, 56182575, 22278895, 35696286, 22278897, 264259, 29331822, 60432289, 29331827, 35698052, 264509, 264906, 264907, 264908, 264909, 52644045, 56182435, 264511, 265009, 264910, 60433356, 60433438, 265017, 265018, 264760, 264448, 264764, 264369, 264288, 264766, 18108357, 264768, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 52644150, 33657109, 264629, 35695855, 60432113, 22278002, 264563, 264564, 264486, 264567
1530	85012765 (3059, 3060)	Novel Protein sim. GBank gij2828710 (AF043842) - maltrin cyclophilin [Rattus norvegicus]			264488, 264489, 35696286, 29331825, 35696052, 264508, 264905, 264906, 264907, 264908, 264510, 264511, 264512, 264910, 264592, 264595, 18108351, 264764, 264683, 264694, 264766, 264768, 18108357, 264769, 35695917, 264628, 264629, 18108374, 35695855, 264630, 264631, 264634, 264555, 264636, 264637, 264404, 264563, 264566, 264486
1531	95418351 (3061, 3062)	Novel Protein sim. GBank gij1905874 (U90878) - carboxyl terminal LIM domain protein [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	56182575, 35696286, 264097, 264259, 29331822, 29331825, 29331826, 29331827, 35696052, 264509, 56182435, 264510, 264511, 265007, 60433356, 55811388, 264681, 264369, 264288, 264766, 264687, 55811957, 35695917, 33657023, 35695763, 55810764, 35696423, 55811576, 263981, 60170394, 56182323, 83373044, 60432113, 264568



1532	85718224 (3063, 3064)	Novel Protein sim. GBank gll3874716[emb]CAA91265] - (Z66494) cDNA EST EMBL:D65271 comes from this gene; cDNA EST EMBL:D64845 comes from this gene; cDNA EST EMBL:D64449 comes from this gene; cDNA EST EMBL:D67438 comes from this gene; cDNA EST EMBL:D68087 comes from this gene; cDN...			UNCLASSIFIED	264689
1533	94239830 (3065, 3066)	Novel Protein sim. GBank gll1480324[emb]CAB01543] - (Z78141) unknown [Mus musculus]			struct	29331824, 29146499, 264807, 264112, 265008, 265011, 265017, 265018, 264762, 18108351, 263967, 20281149, 18108374, 263981, 264568
1534	95343941 (3067, 3068)	Novel Protein sim. GBank gll81286[pir]S22697 - extensin - Volvox carterl (fragment)			UNCLASSIFIED	264905, 264807, 264766, 264637
1535	90938732 (3069, 3070)					65274572, 22278997, 264259, 60432049, 29331822, 60432289, 29331827, 28146489, 265008, 265008, 60170831, 60433438, 33109854, 87188559, 265018, 18108357, 21908768, 29148629, 265021, 265022, 18108377, 58182323, 60432113, 22279000, 22279002
1536	87602656 (3071, 3072)	Novel Protein sim. GBank gll106024[pir]B32891 - finger protein 2, placental - human	Contains protein domain (PF00098) - Zinc finger, C2H2 type		transcript/factor	264686, 18108357, 18108394, 21906767, 21908768, 29148629, 35698286, 265020, 265021, 52844150, 264693, 86714117, 29331825, 29331826, 264508, 264905, 20281149, 264909, 18108374, 35696423, 35895855, 265009, 264634, 264636, 264638, 18108385, 56526486, 265017, 265018, 264563, 264762, 18108351, 264448, 264369, 264766
1537	95354556 (3073, 3074)	Novel Protein sim. GBank gll3876332[emb]CAB02096] - (Z78754) cDNA EST EMBL:T01054 comes from this gene; cDNA EST EMBL:D73600 comes from this gene; cDNA EST yk426112.5 comes from this gene; cDNA EST yk342110.5 comes from this gene; cDNA EST yk475c5.5 comes from this gene; cDNA ES...				65274572, 56182575, 60432049, 264259, 29331826, 265006, 265007, 60433356, 60433438, 264601, 18108351, 264448, 264369, 264288, 33657023, 65274620, 33657109, 60432113
1538	85724628 (3075, 3076)	Novel Protein sim. GBank gll403440 (M81787) - [Gallus domesticus skeletal muscle mRNA, partial cds.] gene product [Gallus gallus]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain		kinase	18108394, 18108397, 264909, 265008, 265009, 265010, 18108351, 264638, 18108382, 18108385, 18108388

1539	95337628 (3077, 3078)	Novel Protein sim. GBank gij3218411[emb CAA19575.1] - (AL023859) SPBC19C7.07c, putative tRNA splicing endonuclease gamma subunit, len:284aa, similar eg. to YAR008W, YAH8_YEAST, P39707, YAR008W, tRNA splicing endonuclease gamma subunit, (273aa), fasta scores, opt:269, E(16.4e-2...	nuclease	22278994, 22278996, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60424269, 29331825, 60432289, 29331828, 29331827, 29331828, 35696052, 33656870, 56182435, 265009, 33657402, 60433356, 60433438, 55812038, 21906754, 87168558, 265017, 265018, 265019, 18108351, 264288, 52644229, 18108359, 21906764, 21906767, 21906768, 35695917, 265020, 265021, 52644150, 33657023, 33657109, 27486281, 18108370, 18108376, 35696423, 55811576, 65274791, 264558, 56182323, 60170394, 83373044, 87168518, 60432113, 22278000, 22279002, 264568
1540	95352858 (3079, 3080)	Novel Protein sim. GBank gij5052634[gb AAD38647.1 AF14567 - (AF145672) BcDNA.GH12174 [Drosophila melanogaster]	UNCLASSIFIED	264368, 264681, 263978
1541	95317948 (3081, 3082)	Novel Protein sim. GBank gij5052349[gb AAD38515.1 AF13501 - (AF135016) protein phosphatase 2A 48 kDa regulatory subunit [Homo sapiens]	phosphatase	264488, 264489, 22278999, 264259, 29331822, 35696052, 264508, 264509, 264905, 264907, 264908, 264511, 264512, 264910, 264592, 264761, 264762, 264448, 264764, 264288, 264687, 21906769, 55811957, 35695917, 265020, 264691, 33657023, 264692, 33657109, 264628, 18108374, 264632, 264634, 264635, 264639, 18108385, 264563, 264564, 264565, 264568, 264488
1542	90937549 (3083, 3084)	Novel Protein sim. GBank gij5305702[gb AAD41778.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]	calhepsin	18108392, 18108394, 65274572, 29331822, 264508, 265007, 265008, 265009, 265011, 264682, 18108354, 18108355, 52644150, 18108358, 264636, 18108381, 18108382, 264106, 33109854, 265019, 264683, 35695917, 264690, 264692, 33657109
1543	84348768 (3085, 3086)	Novel Protein sim. GBank gij728832[sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	nuclease	
1544	87757295 (3087, 3088)	Novel Protein sim. GBank gij3493162 (AF084259) - bromodomain-containing protein BP75 [Mus musculus]	nuc_l_recpt	35696286, 56994075, 22278999, 35696052, 60433356, 60433438, 265011, 264683, 33657109, 35696423, 264631, 87168518, 22279000
1545	85757973 (3089, 3090)	Novel Protein sim. GBank gij1086591 (U41007) - similar to S. carvislae nuclear protein SNF2 (SP:P22082) in a region of gly-arg repeats [Caenorhabditis elegans]	UNCLASSIFIED	264112, 264692, 264693, 55811576
1546	79476589 (3091, 3092)		UNCLASSIFIED	264905, 264686
1547	86999504 (3093, 3094)	Novel Protein sim. GBank gij2661132 (AF035683) - p21 [Mus musculus]	UNCLASSIFIED	264259, 29331822, 66714117, 265007, 55811386, 265010, 264600, 265017, 265019, 264288, 264768, 265020, 265022, 55811576, 18108380, 264563

1548	94233065 (3095, 3096)	Novel Protein sim. GBank glij3043692[dbj BAA25510] - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	29331824, 60431528, 264639, 56182323
1549	95330048 (3097, 3098)	Novel Protein sim. GBank glij5689519[dbj BAA83043.1] - (AB029014) KIAA1091 protein [Homo sapiens]		eph	60424178, 22278995, 35696286, 22278998, 22278999, 264092, 264094, 29331822, 56182181, 29331824, 35696052, 264905, 264906, 264908, 264909, 265006, 264511, 265008, 60431735, 60433356, 21808754, 55811386, 87168559, 265017, 265018, 265019, 55811150, 264682, 264288, 264368, 56181562, 264769, 21906765, 21906768, 21906769, 55811957, 265020, 264691, 33657109, 60431528, 35695855, 56526486, 60432113, 22279002, 264563, 264566
1550	95201907 (3099, 3100)	Novel Protein sim. GBank glij544483[sp P35350 GUSB_BOVIN - POSSIBLE GUSTATORY RECEPTOR TYPE B (PPRT PROTEIN)]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	lm7	65274572, 60432289, 265008, 264910, 265011, 265017, 265019, 264768, 56182323
1551	88077111 (3101, 3102)	Novel Protein sim. GBank glij4758566[ref NP_004798.1 pH56S - heparan-sulfate 6-sulfotransferase		UNCLASSIFIED	22278999, 29331822, 264508, 264509, 264906, 264907, 264909, 265007, 264512, 264910, 21808754, 265018, 265019, 264681, 264764, 264766, 264688, 264769, 21906769, 264692, 35695763, 264635, 264555, 264556, 264557, 264638, 264558, 264563
1552	87617114 (3103, 3104)			UNCLASSIFIED	264259, 29331828, 66712502, 264764, 264288, 264686, 33657109, 264556
1553	94725512 (3105, 3106)	Novel Protein sim. GBank glij4589570[dbj BAA76807.1] - (AB023180) KIAA0983 protein [Homo sapiens]	Contains protein domain (PF00304) - Gamma-thionins family	- dehydrogenase	56182575, 35696286, 29146499, 264509, 264907, 264908, 264909, 56182435, 265006, 265008, 265009, 264910, 264757, 264758, 265017, 55811150, 18108351, 264764, 56181562, 35695917, 264693, 33657109, 18108374, 35696423, 65274791, 35695855, 264635, 264555, 56182323, 18108382, 83373044, 22279000
1554	94233069 (3107, 3108)	Novel Protein sim. GBank glij3043692[dbj BAA25510] - (AB011156) KIAA0584 protein [Homo sapiens]	Contains protein domain (PF00446) - Gonadotropin-releasing hormones	- transferase	35696286, 22278997, 264259, 29331822, 29331824, 29331825, 29331828, 265007, 265008, 60432229, 33657402, 55812038, 265011, 265018, 264681, 264369, 264686, 264767, 264768, 21906765, 21906769, 35695917, 264693, 18108370, 60431528, 55811576, 264631, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002

1555	87332970 (3109, 3110)	Novel Protein sim. GBank gj12257495[dbjBAA21392] - (AB004534) p1015 [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264259, 29331828, 35696052, 264508, 264805, 264906, 264907, 264908, 52644045, 264909, 264910, 60432228, 60433356, 55812038, 264758, 264759, 33657094, 265011, 87168559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21908765, 35695917, 265022, 264691, 33657023, 35698423, 35698555, 264635, 264555, 264636, 264638, 264639, 18108385, 56528488
1556	81229268 (3111, 3112)			UNCLASSIFIED	83373044, 264758, 265022, 264600, 35696052, 264630, 35698423, 265018, 264632, 264682, 29331822, 265020, 265011
1557	87840609 (3113, 3114)	Novel Protein sim. GBank gj13329611 (AF078783) - contains similarity to C3HC4-type zinc fingers (Pfam; zf-C3HC4.hmm, score: 34.08); most similar to drosophila goliath protein (SW: Q06003) [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	60432289, 264509, 264906, 264907, 264908, 264909, 264910, 264758, 55811386, 264761, 264762, 264766, 264769, 264690, 263978, 264634, 264635, 264639, 264564, 264486
1558	84840376 (3115, 3116)	Novel Protein sim. GBank gj15360105[gibAADA2871.1]AF155105 - (AF155105) putative zinc finger protein NY-REN-34 antigen [Homo sapiens]			22278994, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21908754, 265017, 265018, 264448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811578, 83373044, 87168518, 22279000, 22279002
1559	86224865 (3117, 3118)	Novel Protein sim. GBank gj112908[spIP02750]A2GL_HUMAN - LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264259, 29331822, 60432289, 35696052, 264107, 264110, 21906754, 33109854, 87168559, 264760, 264763, 21906764, 21908765, 21908769, 265021, 264690, 35695955
1560	84580675 (3119, 3120)	Novel Protein sim. GBank gj13880146[emb]CAA92704] - (Z68319) Similarity to Human hnRNP F protein (PIR Acc. No. S43484); cDNA EST EMBL:D34218 comes from this gene; cDNA EST EMBL:D37248 comes from this gene; cDNA EST EMBL:D71817 comes from this gene; cDNA EST EMBL:D74531 comes from...		UNCLASSIFIED	264908, 264603, 264638
1561	86608159 (3121, 3122)				264510, 264594
1562	83359682 (3123, 3124)			UNCLASSIFIED	263967
1563	85508694 (3125, 3126)			UNCLASSIFIED	264910, 264764, 264768
1564	87766371 (3127, 3128)	Novel Protein sim. GBank gj1168287[spIP45953]ACDV_RAT - ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD)	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	18108394, 35698286, 264259, 29331822, 60432289, 35696052, 29331828, 264508, 66712502, 264908, 56182435, 265007, 264910, 60170831, 21908754, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 21906765, 21906768, 265021, 60170615, 264692, 35698423, 35698555, 264557, 56182323, 60432113, 22279002, 264482

1565	87783381 (3129, 3130)	Novel Protein sim. GBank gji128726[sp]p05307[PD] BOVIN - PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P65)		isomerase	264488, 264689, 18108398, 55811957, 264534, 264259, 264508, 264905, 264509, 264908, 18108372, 264510, 264511, 264512, 265008, 264630, 265009, 264910, 264635, 264636, 264591, 264555, 264592, 264637, 264593, 264594, 264595, 264596, 265011, 264603, 22278002, 18108351, 264762, 264585, 264587
1566	87424749 (3131, 3132)	Novel Protein sim. GBank gji388044[semb]CAA20329] - (AL031268) VM106R.1 [Caenorhabditis elegans]		inf	22278996, 22278999, 264259, 29331822, 29331824, 60432288, 29331827, 66712502, 264908, 265008, 18108351, 52644229, 21906765, 21906767, 21908768, 21906769, 33557109, 264555, 264639, 264482, 56182575, 21906768, 264692
1567	84999006 (3133, 3134)	Novel Protein sim. GBank gji4929899[gb]AAD34110.1[AF15187] - (AF151873) CGI-115 protein [Homo sapiens]		UNCLASSIFIED	
1568	87648761 (3135, 3136)	Novel Protein sim. GBank gji4827063[ref]NP_005072.1[pZNF1 - zinc finger protein 142 (clone pHZ-49)]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	transcript factor	28331827, 28331830, 264511, 265009, 264758, 21906767, 21906768, 264691, 264693, 22279000, 22279002
1569	90836668 (3137, 3138)	Novel Protein sim. GBank gji5689451[dbj]BAA83009.1] - (AB028880) KIAA1057 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	65274572, 29331822, 29331824, 29331828, 284905, 56182435, 265007, 265019, 264764, 21906765, 21906769, 55811957, 60170615, 52644150, 264692, 33657023, 33657109, 18108377, 264563, 264567, 264595, 264682, 265021
1570	86943981 (3139, 3140)	Novel Protein sim. GBank gji1255430 (U53155) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	
1571	91210340 (3141, 3142)	Novel Protein sim. GBank gji4507731[ref]NP_001061.1[pTUBG - tubulin, gamma polypeptide]	Contains protein domain (PF00091) - Tubulin/Fisz family	tubulin	22278996, 35696286, 22278997, 264091, 264259, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 56182435, 264510, 265007, 264758, 265011, 18108351, 264448, 264288, 264368, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 264693, 18108370, 18108377, 35696423, 35695855, 264634, 264555, 264558, 18108384, 35696052, 264905, 264908, 264908, 264910, 264758, 264766, 35695917, 264637, 263972
1572	81201864 (3143, 3144)			UNCLASSIFIED	
1573	80207068 (3145, 3146)			UNCLASSIFIED	

1574	94216142 (3147, 3148)	Novel Protein sim. GBank gi 4758334 ref NP_004256.1 pFADS - delta-6 fatty acid desaturase	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	Cytochrome	18108394, 264887, 18108397, 18108398, 22278996, 22278997, 22278999, 264259, 29331825, 29331827, 29146498, 29146499, 264107, 264907, 264909, 52644045, 264511, 265008, 264910, 285009, 264591, 21906754, 265011, 265019, 18108351, 264682, 264763, 264764, 18108354, 264369, 264288, 264685, 264768, 264686, 264768, 264688, 21906765, 21906768, 21906767, 21906768, 21906769, 29148629, 264680, 264691, 264693, 20281069, 18108370, 18108374, 18108378, 35695855, 264634, 18108384, 18108385, 22279002, 264563, 264566
1575	95340019 (3149, 3150)	Novel Protein sim. GBank gi 3881810 emb CAA94856  - (Z70783) similar to EF-hand calcium binding protein; cDNA EST EMBL: C08700 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00036) - EF hand	phosphatase	56994075, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 264909, 265006, 265008, 265009, 265010, 87168559, 55811150, 264448, 18108354, 264369, 264288, 18108357, 55811857, 265020, 265021, 60170615, 264691, 33657023, 33657109, 60431528, 65274781, 35695855, 18108385, 60432113, 22279002, 264482
1576	95314019 (3151, 3152)	Novel Protein sim. GBank gi 2773195 (AF039711) - contains similarity to Physcomitrella patens glyceraldehyde 3-phosphate dehydrogenase (GB:X72381) [Caenorhabditis elegans]		UNCLASSIFIED	264569, 264092, 264084, 264095, 264259, 264508, 264905, 264509, 264907, 264909, 264510, 264511, 265006, 264910, 21906754, 265010, 265011, 87168559, 264761, 264762, 264288, 264766, 264769, 264691, 264693, 35695855, 264632, 264634, 264635, 264638, 83373044, 264486
1577	87613800 (3153, 3154)	Novel Protein sim. GBank gi 2499130 sp P70315 WASP_MOUSE - WISKOTT- ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)		UNCLASSIFIED	264511, 265011, 264681, 264369, 264686, 264689, 264628, 264555, 264558, 264559
1578	87123138 (3155, 3156)				264259, 29331826, 265017, 264689, 264693, 60432113
1579	88085141 (3157, 3158)	Novel Protein sim. GBank gi 2978255 db BAA25190  - (AB007407) myeloid zinc finger protein-2 [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	35698286, 264908, 264909, 60433438, 55811386, 264369, 264685, 33657023, 264555, 264556, 264557, 87168518
1580	87255702 (3159, 3160)	Novel Protein sim. GBank gi 4324682 gb AAD16986  - (AF108674) late gestation lung protein 1 [Rattus norvegicus]	Contains protein domain (PF00188) - SCP-like extracellular protein	glycoprotein	22278999, 35696052, 29331830, 52644045, 55812038, 87168474, 265018, 264448, 265022, 264638, 56526486, 22279000
1581	95087431 (3161, 3162)	Novel Protein sim. GBank gi 2088838 (AF003386) - F59E12.4 gene product [Caenorhabditis elegans]			22278995, 29331822, 29331824, 29331826, 56182435, 264595, 55812038, 87168559, 265017, 264288, 21908764, 55811957, 35695917, 264692, 55811578, 264637, 56182323, 264559, 83373044, 60432113

1582	95358052 (3163, 3164)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (A)243459) proteophosphoglycan [Leishmania major]	phosphatase	264259, 60432289, 29331827, 264509, 264905, 264906, 264907, 264909, 264910, 264762, 264288, 264768, 264769, 264632, 264555, 264639, 56526486, 22278000
1583	87022715 (3165, 3166)	Novel Protein sim. GBank gij5578959[emb]CAB51351.1] - (AL050306) dJ475B7.2 (novel protein) [Homo sapiens]	UNCLASSIFIED	60170831, 33657402, 264682, 21906766, 35695855, 264563
1584	95337722 (3167, 3168)	Novel Protein sim. GBank gij5531815[gb]AAD44482.1] - (AF078850) steroid dehydrogenase homolog [Homo sapiens]	Contains protein domain (PF00108) - short chain dehydrogenase	60424179, 52646842, 65274572, 56182575, 22278995, 35696286, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 60424269, 60432289, 29331827, 29331828, 35696052, 29146498, 66712502, 29331830, 52644045, 56182435, 264510, 264512, 265008, 60433356, 33657402, 60433438, 55812038, 21906754, 55811386, 52644296, 87168474, 87168559, 265018, 265019, 264448, 264369, 264288, 18108358, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108374, 55810784, 55811576, 35696423, 65274781, 35695855, 56182323, 83373044, 18108387, 87168518, 60432113, 22278002
1585	87626117 (3169, 3170)	Novel Protein sim. GBank gij4240132[db]BAA74846.1] - (AB020630) KIAA0823 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	35696286, 22278998, 264259, 29331822, 29331824, 29331825, 264905, 265006, 265007, 265008, 60433356, 33108954, 87168474, 265011, 265017, 264604, 264369, 264288, 264685, 264769, 18108359, 21906765, 18108364, 18108370, 264829, 263972, 18108383, 18108388, 264482, 264564
1586	88067081 (3171, 3172)	Novel Protein sim. GBank gij3786494 (AF098993) - No definition line found [Caenorhabditis elegans]	phosphatase	285017, 265018, 264689, 33657023, 263978, 264636, 264563
1587	87617126 (3173, 3174)	Novel Protein sim. GBank gij3253159 (AF005355) - [translation initiation factor eIF2C [Oryctolagus cuniculus]	UNCLASSIFIED	264907, 264908, 264511, 264910, 264591, 264594, 264628, 264631, 264563, 264483, 264567
1588	87802536 (3175, 3176)	Novel Protein sim. GBank gij1077573[pir]S52680 - probable ribosomal protein L34, mitochondrial - yeast [Saccharomyces cerevisiae]	UNCLASSIFIED	264259, 29331828, 264905, 265006, 264758, 21906754, 264761, 284762, 21906765, 21906769, 60170615, 52644150, 33657109, 35695855, 56182323, 18108385
1589	90980653 (3177, 3178)	Novel Protein sim. GBank gij2137756[pir]I48746 - semaphorin C - mouse (fragment)	UNCLASSIFIED	65274572, 264490, 29331822, 66714117, 29331827, 29331828, 56182435, 265008, 60170831, 264595, 264758, 264586, 265011, 264686, 21908766, 21906768, 55811957, 27486265, 264639, 18108385, 56526486, 60432113

1590	85319825 (3179, 3180)			UNCLASSIFIED	264489, 22278986, 264259, 29331824, 29331825, 29331826, 29331827, 285006, 60433356, 21906754, 265017, 265018, 265019, 264448, 264765, 264288, 52844228, 21906765, 21906767, 21906768, 21906769, 265021, 264692, 27486285, 35695763, 56526486, 60432113, 22278000, 22279002, 264564
1591	86877160 (3181, 3182)	Novel Protein sim. GBank		MHC	264259, 264805, 26331830, 264595, 265017, 264448, 264288, 264690, 264629, 87168518
1592	87882533 (3183, 3184)	gi 4557749 ref NP_000237.1 pMHC2 - MHC class II transactivator			65274572, 60432049, 264509, 60433356, 21908754, 21908767, 21908768, 18108370, 35696423, 22279000, 264565, 264567
1593	94891661 (3185, 3186)			UNCLASSIFIED	264488, 29331827, 264905, 264906, 264907, 264908, 264909, 264910, 264592, 264593, 264757, 264602, 264604, 264760, 264681, 264288, 264766, 264768, 29148629, 35695917, 264692, 264628, 264629, 264630, 264632, 264634, 264635, 264636, 264639, 264583, 264584, 264586
1594	87773752 (3187, 3188)	Novel Protein sim. GBank gi 3677072 emb CAA87060  - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]		UNCLASSIFIED	29331826, 264908, 55811957
1595	78918425 (3189, 3190)	Novel Protein sim. GBank gi 3152703 (AF065389) - tetraspan NET-4 [Homo sapiens]	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	UNCLASSIFIED	
1596	79933928 (3191, 3192)			UNCLASSIFIED	29146498, 264758, 263967
1597	86971857 (3193, 3194)	Novel Protein sim. GBank gi 5257114 gb AAD41244.1 AF094448 - (AF094480) cholesterol 24-hydroxylase [Homo sapiens]	Contains protein domain (PF00067) - Cytochrome P450	cyto450 -	264092, 29331824, 264508, 264682, 264369, 264686, 264630, 264563
1598	87862939 (3195, 3196)				264259, 264634
1599	87649829 (3197, 3198)	Novel Protein sim. GBank gi 4506797 ref NP_000324.1 pSCA7 - spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	Contains protein domain (PF01581) - FMRFamide related peptide family	UNCLASSIFIED	52645080, 29331824, 29331828, 264511, 265009, 265011, 264805, 264448, 264764, 265020, 264692, 264693, 18108370, 264635, 18108385
1600	80056002 (3199, 3200)				29331826, 264603, 264691, 264563
1601	15023246 (3201, 3202)			UNCLASSIFIED	264635
1602	86926987 (3203, 3204)	Novel Protein sim. GBank gi 5305704 gb AAD41780.1 AF12853 - (AF128535) cytoplasmic phosphoprotein PACSIN2 [Mus musculus]	Contains protein domain (PF00018) - SH3 domain	struct	29146499, 264112, 264762, 18108351, 29148627, 263974
1603	80502072 (3205, 3206)	Novel Protein sim. GBank gi 283920 pir S27939 - tensin - chicken		collagen	264490, 29331824, 264907, 264909, 264511, 265008, 264592, 265010, 265011, 264782, 264784, 264389, 264288, 264687, 264769, 264693, 264628, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 18108385
1604	80221813 (3207, 3208)	Novel Protein sim. GBank gi 4788831 gb AAD29633.1 AF11682 - (AF116827) unknown [Homo sapiens]		ATPase-associated	263977



1605	91221129 (3209, 3210)				struct	264905, 264509, 264906, 264907, 264908, 264909, 264604, 264768, 264768, 264692, 264693, 33657109, 264629, 35695855, 264635, 264636, 264637
1606	94312703 (3211, 3212)	Novel Protein sim. GBank gij4505313[ref]NP_003794.1[pm]OM - UNKNOWN	Contains protein domain (PF00047) - Immunoglobulin domain	struct		22278996, 22278999, 264259, 33657402, 265017, 18108351, 264448, 21806767, 21906769, 52844150, 264691, 87168518, 264689
1607	10671605 (3213, 3214)	Novel Protein sim. GBank gij5174473[ref]NP_005888.1[pm]PI - Intracisternal A particle; promoted polypeptide		transcriptfactor		
1608	80428900 (3215, 3216)	Novel Protein sim. GBank gij2224629[dbj]BAA20802 - (AB002342) KIAA0344 [Homo sapiens]		UNCLASSIFIED		264094, 264906, 264907, 264909, 264910, 264591, 264603, 264768, 264693, 264634, 264635, 264637, 264639
1609	94311572 (3217, 3218)	Novel Protein sim. GBank gij4884073[emb]CAB43213.1 - (AL049934) hypothetical protein [Homo sapiens]				52844507, 52845156, 52846365, 52846842, 56182575, 22278994, 56994075, 35696288, 22278997, 22278998, 22278999, 264259, 52645080, 29147620, 29331828, 35696052, 33656970, 264508, 264509, 264907, 52644045, 56182435, 264510, 264511, 264512, 33657402, 21906754, 52646317, 33109954, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264769, 52844229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 52645129, 27486261, 27486262, 35695763, 264628, 18108370, 18108376, 35698423, 264638, 52644332, 18108387, 87168518, 22279000, 264563, 264486
1610	85468200 (3219, 3220)	Novel Protein sim. GBank gij283920[pm]IS27939 - tensin - chicken		UNCLASSIFIED		264593, 264757, 55812038, 265018, 265020, 264691, 264692, 264693, 264631, 264634, 264635, 264555, 22279000, 264564
1611	94122843 (3221, 3222)	Novel Protein sim. GBank gij107284[pm]JA35415 - peroxidase (EC 1.11.1.7), thyroid (Grave's disease) - human (fragment)	Contains protein domain (PF00008) - EGF-like domain	peroxidase		35698286, 21906765, 264691, 35698423
1612	85746031 (3223, 3224)	Novel Protein sim. GBank gij3874946[emb]CAA94337 - (Z70307) Similarity to B. subtilis tetracycline resistance protein (SW:TCR2_BACSU); cDNA EST EMBL: C09951 comes from this gene; cDNA EST EMBL: C08265 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED		264488, 264509, 18108370, 18108387, 264486
1613	82247354 (3225, 3226)			UNCLASSIFIED		264759

1614	81228634 (3227, 3228)	Novel Protein sim. GBank gi4680673 gb AAD27726.1 AF13295 - (AF13295) CGI-17 protein [Homo sapiens]	Contains protein domain (PF01605) - eRF1-like proteins	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 264908, 264512, 265008, 265011, 265017, 265018, 265019, 18108351, 264683, 264288, 264766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 35698423, 35695855, 60170394, 56182323, 83373044, 264566
1615	86121808 (3228, 3230)	Novel Protein sim. GBank gi5689485 dbj BAA83026.1  - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265018, 264766, 264767, 264768, 265020, 264691, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22278902
1616	94311819 (3231, 3232)	Novel Protein sim. GBank gi3876260 emb CAB01696  - (Z78418) cDNA EST EMBL:D71020 comes from this gene; cDNA EST EMBL:D73593 comes from this gene; cDNA EST EMBL:C07649 comes from this gene; cDNA EST EMBL:C08081 comes from this gene; cDNA EST yk39912.3 comes from this gene; cDNA ...	UNCLASSIFIED	UNCLASSIFIED	264488, 52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35696286, 22278996, 22278997, 22278999, 52645080, 29331822, 29331824, 29331825, 29331827, 29331828, 35696052, 33656970, 264905, 264909, 264584, 52646317, 21906754, 33657094, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264681, 264448, 264684, 52644229, 21906784, 264689, 21906765, 21906766, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695783, 18108378, 35696423, 35695855, 264557, 52644332, 264558, 18108385, 87168518
1617	88080742 (3233, 3234)	Novel Protein sim. GBank gi466053 sp P34879 YO41_CAEEL - HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III	Contains protein domain (PF01529) - DHHC zinc finger domain	peptidase	35696052, 264905, 264509, 264907, 264908, 264510, 264511, 264764, 264766, 264768, 264689, 264693, 18108374, 264635, 264638, 264638
1618	86272860 (3235, 3236)	Novel Protein sim. GBank gi424023 dbj BAA74894.1  - (AB020678) KIAA0871 protein [Homo sapiens]		struct	35696286, 22278999, 264092, 29331824, 29331825, 35696052, 33657084, 21906765, 27486284
1619	95354580 (3237, 3238)	Novel Protein sim. GBank gi5031763 ref NP_005515.1 pHRY  - hairy (Drosophila)- homolog	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcription factor	52646842, 65274572, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 56182435, 265007, 265008, 264910, 60170831, 60432229, 60433356, 60433438, 265019, 264448, 264288, 264686, 21906768, 265021, 60170615, 33657023, 65274620, 33657109, 18108374, 18108376, 35698423, 35695855, 56182323, 56526486
1620	87344655 (3239, 3240)	Novel Protein sim. GBank gi1351047 sp P45843 SCRT_DROME - SCARLET PROTEIN	UNCLASSIFIED	UNCLASSIFIED	264684

1621	87076708 (3241, 3242)	Novel Protein sim. GBank gi 3822553 (AF098788) - nuclear calmodulin-binding protein [Gallus gallus]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	264910 18108392, 65274572, 18108398, 22278996, 22278997, 22278999, 29146498, 29148499, 264905, 264908, 264909, 264928, 52644045, 264592, 60433356, 21906754, 264602, 265017, 264369, 21908768, 55811957, 265021, 60170615, 264635, 264557, 60170394, 83373044, 18108385, 22279000, 22279002, 264566
1622	84741739 (3243, 3244)	Novel Protein sim. GBank gi 731086 sp P40389 UV22_SCHPO - UV-INDUCED PROTEIN UV22		UNCLASSIFIED	18108398, 264259, 264909, 56182435, 87168474, 264448, 21906768, 35685917, 264691, 87188518, 264563
1623	87779106 (3245, 3246)	Novel Protein sim. GBank gi 731086 sp P40389 UV22_SCHPO - UV-INDUCED PROTEIN UV22		ribosomalprot	66714117, 29331825, 284909, 265008, 264758
1624	87338178 (3247, 3248)	Novel Protein sim. GBank gi 3875666 emb CAB05478  (Z83104) cDNA EST EMBL: T00015 comes from this gene; cDNA EST EMBL: D33665 comes from this gene; cDNA EST EMBL: D36540 comes from this gene; cDNA EST yk24018.3 comes from this gene; cDNA EST yk387c8.3 comes from this gene; cDNA ES...		UNCLASSIFIED	
1625	95354748 (3249, 3250)	Novel Protein sim. GBank gi 4589622 dbj BAA76833.1  (AB023206) KIAA0989 protein [Homo sapiens]		kinase	264488, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331824, 29331825, 29331827, 29331828, 264102, 264106, 264508, 33657084, 265017, 265018, 18108351, 264683, 264369, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 264691, 65274620, 18108368, 263972, 18108376, 35696423, 264631, 264634, 22279000, 22279002
1626	94734369 (3251, 3252)	Novel Protein sim. GBank gi 5679070 gb AAD4844.1 AF16090 - (AF160904) BcDNA HL05936 [Drosophila melanogaster]			52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 60432289, 29331827, 29331828, 35696052, 264906, 88712502, 264909, 265008, 265009, 60432229, 60433356, 60433438, 21906754, 52646317, 52644296, 265011, 87168559, 264604, 265018, 264448, 264369, 264288, 264766, 52644229, 264689, 21906765, 21906768, 35695917, 265021, 265022, 52644150, 33657023, 65274620, 27486261, 27486262, 27486265, 35695763, 263972, 52644332, 60170394, 87168518, 60432113, 264567
1627	83368773 (3253, 3254)	Novel Protein sim. GBank gi 3668087 (AC004667) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264288
1628	85708459 (3255, 3256)			eph	264288, 264686, 264767, 22279002

1629	84983841 (3257, 3258)	Novel Protein sim. GBank gl 4240175 dbj BAA74866.1  - (AB020650) KIAA0843 protein [Homo sapiens]		struct	264555
1630	87779027 (3259, 3260)			UNCLASSIFIED	28331822, 29331827, 265010, 264693, 264634, 22278002
1631	87758454 (3261, 3262)	Novel Protein sim. GBank gl 1915892 emb CAA69995  - (Y08740) tom-1A protein [Gallus gallus]		UNCLASSIFIED	55811857, 264259, 33657023, 284683, 29331822, 29331824, 29331827, 29331828, 264906, 264908, 55811576, 264910, 264634, 264636, 264637, 56182323, 264559, 264758, 18108385, 264593, 264764, 264768
1632	87871682 (3263, 3264)	Novel Protein sim. GBank gl 2559507 dbj BAA22896  - (D83850) hepatoma-derived growth factor [Mus musculus]		UNCLASSIFIED	264687, 264769, 264691, 284692, 29148499, 284509, 264905, 264907, 284511, 284512, 264482, 264681, 264763, 284682, 284683, 264488, 264259, 264907, 284908, 264909, 264628, 264629, 264631
1633	87773683 (3265, 3266)				265007, 284637, 22278002
1634	85992817 (3267, 3268)	Novel Protein sim. GBank gl 4887228 gb AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - spectrin repeat	struct	
1635	94232600 (3269, 3270)			UNCLASSIFIED	65274572, 22278998, 35696052, 52644045, 264511, 265008, 265009, 285010, 265011, 265018, 265019, 264448, 284369, 21908765, 21908768, 265021, 284690, 284482
1636	80413227 (3271, 3272)	Novel Protein sim. GBank gl 4557511 ref NP_001339.1 pDAPK - death-associated protein kinase 3	Contains protein domain (PF00069) - kinase	UNCLASSIFIED	22278995, 264594, 264763, 265020
1637	80070435 (3273, 3274)	Novel Protein sim. GBank gl 3420051 AC004680  - unknown protein [Arabidopsis thaliana]	Eukaryotic protein kinase domain	kinase	264558
1638	87101854 (3275, 3276)				21908765, 21908767, 22278998, 35696286, 22278999, 264259, 264692, 264693, 29331824, 33857109, 264508, 264906, 18108370, 264629, 265007, 33657402, 21908754, 264602, 264604, 284764, 264683, 264566, 264288
1639	94322184 (3277, 3278)	Novel Protein sim. GBank gl 5420389 emb CAB46680.1  - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	284488, 18108394, 65274572, 56182575, 35696286, 28331824, 29331826, 29331827, 35696052, 264908, 56182435, 264112, 265006, 265008, 264757, 284758, 55811386, 264603, 264760, 18108351, 264764, 264288, 264766, 264768, 21906767, 55811957, 264691, 33657023, 65274620, 18108370, 55810784, 55811576, 284558, 284639, 83373044, 18108365, 87168518

1640	94143185 (3278, 3280)	Novel Protein sim. GBank gij284249[emb]CAA16847.1] - (AL021747) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	56182575, 56994075, 35696286, 60432049, 60432289, 29331827, 35696052, 52644045, 58182435, 264510, 265006, 265007, 265008, 264910, 265009, 33657402, 55812038, 265010, 265011, 265017, 265018, 264288, 52644229, 21906785, 21906786, 21906788, 35695917, 265021, 60170615, 52644150, 33657023, 33657108, 33657349, 18108374, 35696423, 65274791, 35685855, 264632, 264555, 56182323, 2279000
1641	87625160 (3281, 3282)			UNCLASSIFIED	29146498, 265006, 265007, 265008, 265009, 55812038, 265010, 265011, 264555, 264556, 264558, 18108383
1642	94312557 (3283, 3284)	Novel Protein sim. GBank gij1575333 (U60416) - myr 6 myosin heavy chain [Rattus norvegicus]	Contains protein domain (PF01843) - struct DIL domain		22278999, 29147820, 29331826, 29331828, 33656970, 55812038, 265010, 265018, 265019, 18108351, 264689, 265020, 265022, 264690, 33657023, 65274620, 35695763, 52644332, 18108381, 60170394, 58182323, 18108388, 87168518, 22279002, 264564
1643	94131766 (3285, 3286)				29331825, 29331827, 29331828, 21906754, 265019, 264288, 264693, 33657349, 18108370, 18108376, 264555, 83373044, 22278002, 264482
1644	88095125 (3287, 3288)			UNCLASSIFIED	264905, 264907, 264908, 264910, 265009, 264757, 264758, 264761, 264762, 264763, 264766, 264768, 264769, 264628, 264629, 264630, 264631, 264632, 264563, 264564, 264565, 264566, 264567
1645	95013858 (3289, 3290)			UNCLASSIFIED	264685, 264693
1646	95362691 (3291, 3292)	Novel Protein sim. GBank gij1076802[pil]S49915 - extensin like protein - maize		UNCLASSIFIED	22278994, 56994075, 35696286, 264259, 29331824, 29331825, 29331826, 60432289, 284508, 60433356, 60433438, 87168559, 265018, 264687, 35695917, 264692, 33657023, 33657182, 27486261, 27486265, 33657349, 60432113, 264563, 264564
1647	94278428 (3293, 3294)	Novel Protein sim. GBank gij5002573[emb]CAB44338.1] - (Y17466) alpha-N-acetylgalactosamine alpha-2,6-sialyltransferase [Fugu rubripes]		UNCLASSIFIED	29331822, 264906, 264908, 264369, 21906768, 60170615, 284639, 22279000
1648	87642098 (3295, 3296)		Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	265009, 264686, 55811957, 35695917, 55810784, 264558, 56182323, 264558, 18108385

1649	95347628 (3297, 3298)	Novel Protein sim. GBank gji854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]		cadherin	264488, 22278995, 35696286, 22278998, 22278997, 22278999, 80432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 66712502, 264908, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264591, 264593, 60433438, 264596, 55812038, 21906754, 265011, 264601, 264602, 265017, 265018, 265019, 264682, 264448, 264764, 264683, 264288, 264766, 264685, 264687, 264768, 264688, 264769, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 55811957, 35895917, 265021, 265022, 52644150, 264692, 33657023, 33657109, 20281149, 18108370, 264628, 18108374, 18108376, 35696423, 35695955, 264632, 264634, 264635, 264636, 18108380, 264639, 264558, 18108382, 18108384, 18108385, 18108387, 264080, 264404, 60432113, 22279000, 22279002, 264482, 264565, 264566, 264487
1650	87418539 (3299, 3300)	Novel Protein sim. GBank gji3647335[emb]CAA21058] - (AL031644) possible zinc-finger protein [Schizosaccharomyces pombe]			285011, 264802, 21908767, 18108374, 18108377, 18108385
1651	91639773 (3301, 3302)	Novel Protein sim. GBank gji4884278[emb]CAB43247.1] - (AL050037) hypothetical protein [Homo sapiens]		synthase	264488, 52645156, 18108397, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264508, 264908, 29331830, 264910, 60432229, 21906754, 265010, 265011, 265017, 265019, 264448, 18108354, 264288, 264688, 21906765, 21906766, 21906768, 21906769, 265022, 264692, 264693, 264629, 35695955, 264556, 264637, 264557, 264559, 83373044, 56528486, 22279000, 22278998, 264564
1652	86598622 (3303, 3304)	Novel Protein sim. GBank gji1657837 (U73200) - p118Rip [Mus musculus]	Contains protein domain (PF00169) - struct PH domain		22278997, 29146498, 56182435, 21906754, 264389, 21906765, 21906768, 21906769, 265020, 52644150, 33657109, 22279000, 22279002
1653	94255993 (3305, 3306)	Novel Protein sim. GBank gji3776054[emb]CAA06273] - (AJ004899) Tapasin [Gallus gallus]	Contains protein domain (PF00047) - glycoprotein Immunoglobulin domain		18108398, 22278995, 22278998, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331830, 264909, 265006, 265009, 60432229, 60433356, 60433438, 21906754, 265017, 265019, 264448, 264683, 264288, 265021, 265022, 264692, 18108384, 65274781, 18108384, 60432113, 264567
1654	79756471 (3307, 3308)		UNCLASSIFIED		33657109, 264565

1655	86689346 (3309, 3310)	Novel Protein sim. GBank gij3355171embjCAA73496j - (Y13053) seryl-tRNA synthetase [Zea mays]		synthase	52844507, 35696286, 22278998, 22278999, 29331824, 29331825, 29331828, 33656970, 264908, 52844045, 264511, 264910, 52846317, 264288, 52644229, 33657023, 33657109, 52644332, 264557, 58182323, 56526486, 60432113
1656	78962287 (3311, 3312)	Novel Protein sim. GBank gij1890141dbjBAA18947j - (D83206) P24 protein [Mus musculus]		UNCLASSIFIED	29331822, 29331824, 29331825, 264563
1657	87771994 (3313, 3314)	Novel Protein sim. GBank gij4557645relnp_001524.1pHNRP - heterogeneous nuclear ribonucleoprotein L	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331827, 265009, 21906766, 21906767, 265020, 265022, 33657109, 264638, 56526486, 264482
1658	87773778 (3315, 3316)	Novel Protein sim. GBank gij3877072embjCAA87060j - (Z48937) similarity with ribosomal protein L21 [Caenorhabditis elegans]	Contains protein domain (PF00829) - Ribosomal prokaryotic L21 protein	UNCLASSIFIED	52846365, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 264905, 264908, 52844045, 265006, 60433356, 264757, 60433438, 21906754, 265011, 18108351, 284448, 264369, 264288, 264766, 264768, 21908785, 21908787, 21908788, 21908769, 29146629, 265021, 285022, 18108362, 263969, 263971, 18108374, 35696423, 18108383, 22279000, 264482
1659	88230101 (3317, 3318)	Novel Protein sim. GBank gij539218iprijS38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	52846317, 21908766, 21908767, 21908768, 87168518, 22278996, 265020, 22278999, 87168559, 264603, 265017, 264631, 265018, 265019, 22278002, 264482, 264635, 264565
1660	94315313 (3319, 3320)	Novel Protein sim. GBank gij2487012spjQ10010Y5V4_CAEEL - HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III		UNCLASSIFIED	264488, 35696286, 264259, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265009, 264910, 264592, 264596, 265010, 264600, 264602, 265017, 265018, 264605, 264760, 264764, 264288, 264766, 264666, 264788, 264769, 264689, 21906766, 35695917, 264690, 33657023, 264693, 33657109, 264629, 35696423, 35695855, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264639, 264559, 18108385, 18108388, 264563, 264483, 264564, 264565, 264566, 264486, 264567

1661	94234071 (3321, 3322)	Novel Protein sim. GBank gi 4759100 ref NP_004759.1 pSFRS - splicing factor, arginine/serine-rich 11	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264468, 2227898, 264259, 29331824, 29331826, 28331827, 28331828, 264509, 66712502, 29331830, 264908, 52644045, 265007, 264512, 60433356, 60433438, 55812038, 21908754, 265019, 284448, 264766, 264788, 264789, 21908788, 21908769, 265020, 33657023, 33657109, 65274791, 87168518, 264482, 264563, 264564, 264565, 264567
1662	94135172 (3323, 3324)	Novel Protein sim. GBank gi 1730502 sp P52875 PF27_MOUSE - TRANSMEMBRANE PROTEIN PF27			18108392, 29331822, 29331828, 20281100, 264106, 265006, 265007, 265008, 18108348, 21908766, 18108365, 18108366, 18108374, 83373044, 18108385
1663	94217146 (3325, 3326)	Novel Protein sim. GBank gi 4884136 emb CAB43275.1  - (AL050107) hypothetical protein [Homo sapiens]	Contains protein domain (PF00397) - kinase VW domain		52645156, 56182575, 22278994, 22278995, 35696286, 22278996, 58894075, 22278997, 22278998, 22278999, 264259, 29331822, 29331826, 29331827, 29331828, 33856970, 29331830, 264908, 56182435, 264511, 60433356, 33657402, 33109954, 87168474, 87168559, 265017, 265018, 264605, 18108351, 264764, 264288, 264766, 264768, 21908765, 21908766, 21908767, 21908768, 21908769, 265021, 265022, 264691, 33657023, 264693, 263967, 33657109, 264630, 52644332, 83373044, 87168518, 60432113, 22278000
1664	94234076 (3327, 3328)	Novel Protein sim. GBank gi 3043692 dbj BAA25510  - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	264488, 263894, 35696286, 29331824, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 255009, 264910, 60170831, 264581, 264592, 264595, 87168474, 265011, 264600, 264601, 264604, 264605, 264760, 264762, 18108351, 264681, 264682, 264763, 264683, 264784, 264288, 264684, 264766, 264687, 264768, 264769, 21908764, 21908765, 21908767, 35695917, 265021, 264534, 60170815, 264690, 264691, 264892, 33657109, 33657182, 264628, 18108370, 264629, 35696423, 35695855, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264566, 264486



1665	91226952 (3328, 3330)	Novel Protein sim. GBank gij1083506 pij1 S50085 - sialoadhesin - mouse	Contains protein domain (PF00047) - Immunoglobulin domain	immunoglob	264488, 28331826, 28331828, 284509, 284906, 284907, 284909, 284510, 284511, 284910, 284592, 284593, 284595, 284758, 284596, 284600, 284760, 284762, 284764, 284766, 284768, 284629, 284630, 284634, 284636, 83373044, 284564, 284568, 284567, 284488
1666	85358160 (3331, 3332)	Novel Protein sim. GBank gij3913431 sp Ox2843 DDX8 SCHPO - PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C	Contains protein domain (PF00575) - S1 RNA binding domain	helicase	58994075, 22278999, 284259, 29331824, 29331826, 29331827, 29148498, 285009, 33109854, 87168559, 285018, 284288, 284688, 21906767, 21906769, 284691, 33657182, 18108370, 18108374, 18108385, 22279002
1667	91226655 (3333, 3334)	Novel Protein sim. GBank gij5689535 bj BAA83051.1  - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	transport	284259, 29331822, 29331826, 284905, 284906, 284908, 284510, 285009, 284595, 284758, 285011, 87168559, 285017, 285018, 285019, 284448, 284766, 284686, 21906765, 21906767, 21906769, 285020, 285021, 60170615, 284690, 284692, 284693, 18108368, 18108370, 283972, 58810764, 284555, 83373044, 60432113, 22278000, 22279002
1668	88095135 (3335, 3336)	Novel Protein sim. GBank gij2076894 gb AA853983.1  - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE_bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]		kinase	66714117, 284508, 284509, 284906, 284907, 284908, 284511, 284910, 284764, 284687, 284689, 33657109, 35696423, 35695855, 284632
1669	91227846 (3337, 3338)	Novel Protein sim. GBank gij3875371 emb CAA85414.1  - (Z36948) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes fr...		UNCLASSIFIED	29331825, 33109954, 284369, 284767, 284689, 33657109, 83373044
1670	87628009 (3339, 3340)			UNCLASSIFIED	284259, 29331824, 29331827, 60433438, 285022, 284636
1671	87346372 (3341, 3342)	Novel Protein sim. GBank gij462451 sp P34244 KKK1_YEAST - PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W	Contains protein domain (PF00089) - Eukaryotic protein kinase domain	kinase	35696286, 22278997, 29331825, 284909, 21906754, 285017, 285018, 285019, 284682, 284683, 284768, 284688, 21906768, 21906767, 21906769, 284691, 284555, 284556, 22279000, 284566
1672	86291834 (3343, 3344)	Novel Protein sim. GBank gij1814270 (U74566) - double-stranded RNA specific adenosine deaminase [Rattus norvegicus]		deaminase	284906, 284909, 284632, 18108381

1673	88095137 (3345, 3346)	Novel Protein sim. GBank gjl2076894[gb AA853983.1] - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG-PE-binding), Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	264488, 264569, 18108394, 56994075, 22278996, 264259, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60170831, 264592, 264594, 264595, 264758, 264601, 264760, 264762, 264683, 264764, 264288, 264766, 264686, 264768, 264687, 264769, 264689, 264690, 33657023, 264692, 264693, 33657109, 264628, 264629, 18108374, 35696423, 35695855, 264631, 264632, 264634, 264635, 264637, 264556, 264638, 264639, 264563, 264482, 264564, 264565, 264566, 264567, 264488
1674	88258028 (3347, 3348)	Novel Protein sim. GBank gjl5262467[emb CAB45693.1] - (AL080062) hypothetical protein [Homo sapiens]		kinase	29331822, 29331824, 264906, 52644045, 60433356, 87168559, 264448, 264288, 264686, 264691
1675	87606466 (3349, 3350)	Novel Protein sim. GBank gjl3128366 (AF010496) - 50S ribosomal protein 19 [Rhodospirillum rubrum]		UNCLASSIFIED	56181686, 35686286, 22278997, 22278998, 264259, 29331824, 29331827, 35696052, 66712502, 264764, 264288, 264686, 264687, 35695917, 285020, 264690, 264693, 35695763, 18108370, 35696423, 35695855, 264637, 264639, 18108385, 264584
1676	95358086 (3351, 3352)	Novel Protein sim. GBank gjl4164065[gb AAD05327] - (AF111091) latrophilin 3 splice variant bbaf [Bos taurus]		UNCLASSIFIED	264259, 29331827, 29331828, 264108, 264907, 265009, 264600, 265019, 264288, 21906765, 265020, 265022, 35685855, 83373044, 18108385
1677	87408587 (3353, 3354)	Novel Protein sim. GBank gjl3327046[dbj BAA31591] - (AB014516) KIAA0616 protein [Homo sapiens]		UNCLASSIFIED	264908
1678	88668829 (3355, 3356)			UNCLASSIFIED	29331824, 264102
1679	91214106 (3357, 3358)	Novel Protein sim. GBank gjl550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	carboxylase	264488, 18108392, 18108394, 52646842, 18108397, 18108398, 35696286, 29331824, 265006, 265007, 265008, 265009, 18108348, 285011, 18108351, 284683, 18108354, 18108358, 18108359, 21906765, 29148627, 29148629, 264690, 18108361, 18108362, 18108364, 18108365, 18108368, 264628, 18108379, 35696423, 35695855, 264635, 18108381, 18108382, 18108383, 18108384, 18108385, 18108388
1680	91005372 (3359, 3360)	Novel Protein sim. GBank gjl2394478 (AF024500) - No definition line found [Caenorhabditis elegans]		transport	65274572, 22278994, 22278999, 66714117, 29331827, 56182435, 21906754, 265018, 264288, 21906769
1681	94324150 (3361, 3362)	Novel Protein sim. GBank gjl5689537[dbj BAA83052.1] - (AB029023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	22278996, 29331822, 264908, 264593, 264604, 265019, 264683, 55811957, 264690, 33657023, 35696423, 83373044, 264563
1682	86042710 (3363, 3364)			UNCLASSIFIED	264909, 265017, 264605

1683	94316213 (3365, 3366)	Novel Protein sim. GBank gii5031717[fe]NP_005704.1 pGPBP - goodpasture antigen- binding protein	Contains protein domain (PF01852) - START domain	UNCLASSIFIED	263994, 35698286, 35698052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 265007, 265009, 264810, 264593, 264758, 265010, 265011, 264760, 264761, 264762, 264763, 264764, 264388, 264766, 264768, 35695917, 264892, 33657109, 35698423, 35695855, 264634, 264635, 264636, 264638, 264639, 83373044, 264486
1684	80063409 (3367, 3368)			UNCLASSIFIED	264563, 264566
1685	94323182 (3368, 3370)	Novel Protein sim. GBank gii1255371 (U53147) - coded for by C. elegans cDNA yk34a9.5; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase. [Caenorhabditis elegans]	Contains protein domain (PF00625) - Guanylate kinase		60424179, 52646842, 22278994, 35698286, 22278998, 264259, 52645080, 29331824, 29331826, 265007, 33657084, 265018, 264681, 264448, 264683, 264369, 264689, 21908765, 21908767, 21908768, 21908769, 265021, 264692, 65274620, 33657109, 27486262, 264635, 52644332, 56182323, 22278000
1686	87820710 (3371, 3372)	Novel Protein sim. GBank gii2244707[db]BAA21115.1  - (AB005287) thrombospondin 1 [Bos taurus]		UNCLASSIFIED	56182575, 264259, 264508, 264905, 264509, 264907, 264908, 264510, 264511, 265006, 264512, 265009, 264910, 264758, 265010, 265011, 264605, 18108351, 264764, 264766, 18108357, 264768, 18108362, 264628, 264630, 264631, 264634, 264635, 264637, 264638, 264639, 264585, 264486, 264587
1687	94719400 (3373, 3374)	Novel Protein sim. GBank gii4680679[gb]AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264906, 264907, 264908, 264510, 265008, 265007, 264910, 264556, 18108381, 18108383, 265011
1688	82158442 (3375, 3376)			UNCLASSIFIED	264905, 264910, 264760, 264629, 264555
1689	94325049 (3377, 3378)	Novel Protein sim. GBank gii4240193[db]BAA74875.1  - (AB020659) KIAA0852 protein [Homo sapiens]		UNCLASSIFIED	264569, 35696286, 22278999, 264508, 264908, 264909, 56182435, 33657402, 60433438, 55812038, 265017, 265018, 264448, 264764, 264288, 264686, 29148629, 35695917, 265020, 265021, 263972, 18108374, 65274791, 83373044, 264089
1690	83255346 (3378, 3380)	Novel Protein sim. GBank gii3800736 (AF031572) - seven- pass transmembrane receptor precursor [Mus musculus]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264369, 21906766, 264692, 264639, 87168518
1691	88095223 (3381, 3382)	Novel Protein sim. GBank gii2773208 (AF039713) - No definition line found [Caenorhabditis elegans]			264768, 33657109, 29331827, 29148629, 264510, 264106, 264910, 264109, 264508, 60170831, 264563, 264905, 264564, 264691, 264637, 264628, 264907, 264908, 33657023, 264587, 264766, 263974
1692	86106709 (3383, 3384)				264106
1693	87012775 (3385, 3386)	Novel Protein sim. GBank gii121271[sp]P02207[GLB_LAMFL - GLOBIN	Contains protein domain (PF00042) - Globin	UNCLASSIFIED	29331826, 264508, 264905, 264907, 264595, 265010, 265011, 21908768, 33657023, 264629, 263978, 264558

1694	94208168 (3387, 3388)	Novel Protein sim. GBank gi 5453932 ref NP_006225.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Contains protein domain (PF01193) - RNA polymerases L / 13 to 18 kDa subunit	mapolymerase	35698286, 22278996, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331828, 35698052, 29146499, 284905, 284908, 52844045, 264511, 265008, 265007, 265009, 264592, 60433356, 21906754, 265010, 265011, 18108351, 264763, 264682, 284448, 264683, 264288, 264768, 264689, 21906768, 60170815, 264691, 264692, 264693, 18108370, 18108374, 263978, 35698423, 35698585, 264556, 18108381, 18108385, 87168518, 264482, 264488 264634
1695	94719325 (3389, 3390)	Novel Protein sim. GBank gi 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	
1696	87824038 (3391, 3392)	Novel Protein sim. GBank gi 4220517 emb CAA22990 - (AL035356) hypothetical protein [Arabidopsis thaliana]			22278997, 264259, 265010, 18108351, 264764, 21908766, 18108370 264682
1697	85740963 (3393, 3394)	Novel Protein sim. GBank gi 505652 (U10362) - GP36b glycoprotein [Homo sapiens]		glycoprotein	
1698	87445285 (3395, 3396)	Novel Protein sim. GBank gi 5052031 gb AAD38411.1 AF15573 - (AF155739) axotrophin [Mus musculus]			56994075, 22278998, 22278999, 264509, 33657402, 264758, 87168474, 87168559, 265017, 265018, 264448, 264687, 29148627, 21908769, 29148629, 265020, 265022, 33657023, 264558, 87168518, 22278902 35698286, 264635
1699	87424793 (3397, 3398)	Novel Protein sim. GBank gi 543344 pir jS41647 - zinc finger 5 protein - mouse	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED nucl_recpt	29331824, 52844045, 265008, 265009, 263968, 263971 264092, 264110, 263977
1700	87659161 (3399, 3400)	Novel Protein sim. GBank gi 3877439 emb CAA98652  - (Z72510) similarity to yeast UTR3 protein (Swiss Prot accession number P21374); cDNA EST EMBL:D72822 comes from this gene; cDNA EST EMBL:D75763 comes from this gene; cDNA EST yk274e3.3 comes from this gene; cDNA EST yk274e3.5 c...		MHC	22278995, 22278997, 264092, 29146498, 29146499, 264107, 264508, 264907, 264110, 284112, 265009, 60170831, 21906754, 265011, 265017, 264762, 18108351, 264288, 21908765, 35695917, 265021, 60170615, 263967, 33657109, 18108370, 263972, 263974, 18108374, 263976, 35695855, 264555, 263981, 60170394, 18108385, 56528486, 87168518, 60432113 264908, 265017, 264628, 264628, 264638
1701	86570488 (3401, 3402)	Novel Protein sim. GBank gi 451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	
1702	87795092 (3403, 3404)	Novel Protein sim. GBank gi 1263289 (U47656) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	264369
1703	79568651 (3405, 3406)	Novel Protein sim. GBank gi 4519621 dbj BAA75670.1  - (AB017614) OASIS protein [Mus musculus]			264569, 35696286, 264907, 265010, 264687, 264768, 264692, 264693, 264636, 264586 22278996, 22278998, 264259, 264509, 265018, 264764, 264685, 264686, 21906768, 21908769, 265022, 264691, 264558, 22279000
1704	86622979 (3407, 3408)	Novel Protein sim. GBank gi 1263289 (U47656) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	
1705	87795175 (3409, 3410)	Novel Protein sim. GBank gi 4519621 dbj BAA75670.1  - (AB017614) OASIS protein [Mus musculus]			
1706	87790987 (3411, 3412)	Novel Protein sim. GBank gi 3123034 sp Q15011 Y025_HUMAN - HYPOTHETICAL PROTEIN KIA00025			

1707	88041230 (3413, 3414)	Novel Protein sim. GBank glij4321684[gb AAD15797] - (AF055470) ZNF258 [Homo sapiens]		UNCLASSIFIED	18108396, 22278997, 264259, 29147620, 29331826, 29146498, 264905, 264906, 265008, 264593, 264595, 264758, 264596, 265018, 264760, 18108351, 264764, 264766, 264689, 264693, 18108370, 35698423, 55811576, 264558, 87168518, 60432113, 264567
1708	91220519 (3415, 3416)	Novel Protein sim. GBank glij5174591[ref NP_005947.1 pMTHF - 5,10-methylene tetrahydrofolate dehydrogenase, 5,10-methylene tetrahydrofolate cyclohydrolase, 10-formyl tetrahydrofolate synthetase	Contains protein domain (PF01268) - Formate-tetrahydrofolate ligase	- synthase	56182575, 22278996, 56994075, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 29146498, 29146489, 29331830, 265009, 60170831, 33657402, 33109854, 87168559, 265019, 18108351, 264448, 21806765, 21906767, 21906768, 29148627, 29148629, 29148784, 60170615, 52644150, 33657023, 33657109, 18108374, 55811576, 264559, 18108385, 22279000, 264563
1709	80222583 (3417, 3418)			UNCLASSIFIED	264107, 55811957, 263974, 263976, 263977, 263981
1710	20754572 (3419, 3420)			UNCLASSIFIED	264556
1711	91013728 (3421, 3422)	Novel Protein sim. GBank glij5031735[ref NP_005780.1 pHEC - N-acetylglucosamine 6-O-sulfotransferase		sulfotransferase	65274572, 29331824, 29331826, 264768, 60431528, 35696423, 60432113, 264563
1712	95330184 (3423, 3424)	Novel Protein sim. GBank glij5454168[ref NP_006453.1 pXAP4 - HBV associated factor	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	- Kinase	56994075, 264093, 264259, 29331822, 264099, 29331824, 29331827, 264107, 264110, 264511, 264592, 265011, 265018, 264683, 264686, 264689, 265020, 33657023, 263987, 33657109, 263974, 35698423, 35695855, 264630, 264636, 264558, 264566
1713	94143453 (3425, 3426)	Novel Protein sim. GBank glij160409 (M69183) - mature parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	Contains protein domain (PF00843) - B-box zinc finger.	UNCLASSIFIED	22278995, 264508, 264758, 18108351, 18108370, 263974, 18108374, 264634, 56182323, 83373044, 60432113
1714	87420048 (3427, 3428)				22278997, 264757, 21806765, 265020, 265021, 264692, 56526486
1715	94260257 (3429, 3430)	Novel Protein sim. GBank glij5689537[dbj BAA83052.1 ] - (AB029023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	264509, 264905, 264906, 264907, 264908, 264909, 264910, 264591, 265011, 264766, 264768, 264769, 264691, 264692, 264632, 264634, 264635, 264636, 264637, 264558, 264639, 264564
1716	87400449 (3431, 3432)	Novel Protein sim. GBank glij4589468[dbj BAA76761.1 ] - (AB012808) mBOCT [Mus musculus]		transport	56182575, 29331824, 60432289, 264109, 264909, 265007, 264600, 265019, 264686, 265020, 264693, 55811576, 264558, 60432113, 22279002

1717	87563223 (3433, 3434)	Novel Protein sim. GBank gi 2765411 emb CAA74749  - (Y14391) GTP-binding protein [Homo sapiens]		UNCLASSIFIED	264588, 264259, 29331825, 29331826, 29331828, 35696052, 264509, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264592, 264595, 264758, 264759, 265017, 264681, 264764, 264768, 264888, 18108357, 35695917, 264690, 264692, 264693, 264628, 264629, 35696423, 264630, 264631, 264635, 264636, 18108380, 264638, 264639, 18108388, 18108391
1718	87032828 (3435, 3436)	Novel Protein sim. GBank gi 2833282 sp Q14999 Y076_HUMAN - HYPOTHETICAL PROTEIN KIAA0076 (HA0936)		UNCLASSIFIED	265011, 264681, 264682, 264684, 264688, 264689, 21906765, 265021, 264691, 33657023, 264693, 18108370, 35695855, 264632, 264634, 264636, 18108388, 22279002
1719	94315259 (3437, 3438)	Novel Protein sim. GBank gi 4505197 ref NP_003473.1 pMLL2 - myeloid/lymphoid or mixed-lineage leukemia 2		UNCLASSIFIED	18108396, 65274572, 35698286, 22278997, 60432049, 58182181, 66714117, 60432289, 29331826, 35696052, 29331828, 264908, 29331830, 58182435, 264592, 60431735, 60433438, 5812038, 264759, 265010, 264600, 264601, 265017, 264448, 264764, 264288, 264769, 21908766, 21908769, 55811957, 265020, 265021, 52644150, 33657023, 33657108, 33657182, 27486262, 33657348, 35695763, 18108370, 60431528, 18108374, 35696423, 55811576, 35695855, 264631, 58182323, 264559, 264584, 264486
1720	94853063 (3439, 3440)	Novel Protein sim. GBank gi 2129478 pir S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	56182575, 22278999, 264259, 29331824, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 264758, 21908754, 265011, 264601, 264760, 264762, 264288, 264768, 264688, 18108357, 264689, 21908765, 55811957, 264693, 20281149, 264629, 18108374, 55811576, 65274791, 264630, 20281071, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 56182323, 87168518
1721	91722288 (3441, 3442)	Novel Protein sim. GBank gi 4886461 emb CAB43381.1  - (AL050280) hypothetical protein [Homo sapiens]		UNCLASSIFIED	22278994, 22278999, 29331822, 265006, 265007, 265008, 5812038, 21906754, 60174639, 265011, 87168559, 18108351, 18108354, 21908765, 21908766, 21908768, 21908769, 265020, 33657109, 18108370, 18108374, 264556, 80170394, 83373044, 18108385, 264486
1722	94134549 (3443, 3444)	Novel Protein sim. GBank gi 5689375 dbj BAA82968.1  - (AB030644) tudor repeat associator with PCTAIRE 2 [Rattus norvegicus]	Contains protein domain (PF00567) - Tudor domain	UNCLASSIFIED	56894075, 29331824, 29331828, 265009, 18108351, 21906768, 265020, 33657023, 18108374, 83373044

1723	95359181 (3445, 3446)	Novel Protein sim. GBank gi 4428962 gb AAD20633  - (AF126082) Arf-like 2 binding protein BART1 [Homo sapiens]	UNCLASSIFIED	264488, 264887, 264769, 21906767, 21906768, 58182575, 55811957, 22278997, 22278998, 265020, 264259, 264692, 33657023, 29331822, 29331824, 29331825, 60432289, 33657182, 33656970, 33657349, 29146498, 264508, 264907, 18108370, 264629, 264908, 264909, 18108374, 55811576, 264510, 265008, 264511, 265007, 264910, 264632, 264591, 60432229, 264592, 60433356, 264594, 60433438, 264595, 83373044, 55812038, 33108954, 33657084, 87168518, 87168474, 265010, 265011, 87168559, 264600, 60432113, 264604, 265019, 264563, 264448, 264682, 264566, 264764, 264288, 264587, 264486, 264369, 264766
1724	87713806 (3447, 3448)	Novel Protein sim. GBank gi 2340162 (AF005083) - dsRBP-ZFa [Xenopus laevis]	UNCLASSIFIED	264905, 18108359, 264693, 264628, 264631, 264636, 264555, 264556, 264558, 264559
1725	85655191 (3449, 3450)	Novel Protein sim. GBank gi 3152862 (AF064604) - KE03 protein [Homo sapiens]	homeobox	35696286, 264259, 29331822, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264910, 265008, 264591, 264801, 264760, 18108351, 264881, 264764, 264288, 264766, 264768, 21906769, 35695917, 264628, 35696423, 264630, 264831, 264632, 264635, 264636, 264638, 87168518, 264586
1726	85754255 (3451, 3452)	Novel Protein sim. GBank	UNCLASSIFIED	29146498, 264683, 264689
1727	85298362 (3453, 3454)	Novel Protein sim. GBank gi 4889348 gb AAD27861.1 AF13256 - (AF132562) BcDNA LD14270 [Drosophila melanogaster]	UNCLASSIFIED	264905, 265011, 264689, 21906768

1728	85348515 (3455, 3456)	Novel Protein sim. GBank gi 4406549 gb AAD2027  - (AF131738) Unknown [Homo sapiens]	UNCLASSIFIED	60424179, 18108397, 56182575, 22278995, 56994075, 3568286, 22278997, 22278998, 22278999, 264094, 60432048, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331826, 29331827, 35696052, 264905, 264906, 264907, 29331830, 66712502, 264908, 56182435, 264511, 265008, 265009, 60432229, 60433356, 33657402, 60433438, 264759, 21908754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 55811150, 264681, 264448, 264682, 264763, 264683, 264288, 264684, 264389, 264685, 264766, 264687, 264769, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 264535, 264691, 264692, 33657023, 264693, 33657109, 18108370, 264628, 263972, 264629, 18108374, 18108376, 55810784, 65274791, 35695855, 264631, 264634, 264635, 60431850, 264636, 264638, 60170394, 264639, 83373044, 58528486, 87168518, 60432113, 22279000, 22279002, 264564, 264566
1729	91227948 (3457, 3458)	Novel Protein sim. GBank gi 854065 emb CAA5837  - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	264906, 264907, 264908, 264511, 264555, 83373044, 264596, 264566
1730	85483474 (3459, 3460)		UNCLASSIFIED	29331822, 29331825, 29331828, 264907, 264908, 264909, 265011, 264784, 264629
1731	88266088 (3461, 3462)	Novel Protein sim. GBank gi 631600 pir S47084 - hypothetical protein - rabbit	UNCLASSIFIED	52646842, 264907, 264909, 56182435, 55811386, 87168559, 265018, 265019, 264760, 52644229, 55811576
1732	91218878 (3463, 3464)	Novel Protein sim. GBank gi 424023 dbj BAA74894.1  - (AB020678) KIAA0871 protein [Homo sapiens]	struct	56182575, 29331822, 29331824, 29331827, 66712502, 264591, 33657402, 60433356, 265018, 21906768, 21906769, 35695917, 265020, 265021, 264638, 56182323
1733	87617178 (3465, 3466)	Novel Protein sim. GBank gi 1575756 (U70674) - m-Numb [Mus musculus]	synthase	264907, 264910, 33657402, 265010, 264681, 264683, 264684, 264688, 264769, 264691, 264692, 264693, 264628, 264636, 264558
1734	87795261 (3467, 3468)			264693



1735	88318638 (3469, 3470)	Novel Protein sim. GBank gi4836807 gb AAD30566.1 AF14679 - (AF146793) PFT27 [Mus musculus]	Contains protein domain (PF01169) - Uncharacterized protein family UPF0016		264488, 18108394, 18108398, 22278998, 60432049, 264259, 29331822, 264908, 265006, 265007, 265008, 265009, 264591, 33657402, 265010, 265011, 87168559, 265017, 18108351, 264682, 18108354, 264769, 264689, 21906765, 21906768, 21906769, 29148629, 29148784, 265021, 265022, 52644150, 18108384, 18108365, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564 264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1736	85362884 (3471, 3472)	Novel Protein sim. GBank gi4883647 ref NP_005472.1 pTRAP - thyroid hormone receptor-associated protein complex component	UNCLASSIFIED		264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1737	88165549 (3473, 3474)	Novel Protein sim. GBank gi2143607 pir S66895 - B/K protein - rat	Contains protein domain (PF00168) - C2 domain	Kinase	264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1738	85788811 (3475, 3476)	Novel Protein sim. GBank gi2225941 emb CAA69714 - (Y08460) Mdes protein [Mus musculus]	UNCLASSIFIED		264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1739	87328576 (3477, 3478)		UNCLASSIFIED		264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1740	83592839 (3479, 3480)	Novel Protein sim. GBank gi4809 emb CAA44309 - (X82482) YCR601 [Saccharomyces cerevisiae]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	Traffic	264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1741	95010100 (3481, 3482)	Novel Protein sim. GBank gi4883898 gb AAD31695.1 AF13042 - (AF130420) serine protease-like protein isoform [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1742	85788814 (3483, 3484)	Novel Protein sim. GBank gi4505193 ref NP_003667.1 pMLD - membrane fatty acid (lipid) desaturase	UNCLASSIFIED		264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1743	86966475 (3485, 3486)	Novel Protein sim. GBank	UNCLASSIFIED		264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1744	91224003 (3487, 3488)	Novel Protein sim. GBank gi728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	UNCLASSIFIED		264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1745	20290075 (3489, 3490)	Novel Protein sim. GBank	UNCLASSIFIED		264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1746	94326110 (3491, 3492)	Novel Protein sim. GBank gi731758 sp P38873 YHY6_YEAST - HYPOTHETICAL 175.8 KD PROTEIN IN GND1-IK1 INTERGENIC REGION	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564
1747	94324333 (3493, 3494)	Novel Protein sim. GBank gi1658503 (U75467) - Alu [Drosophila melanogaster]	transcript factor		264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264564

1748	88003580 (3495, 3496)	Novel Protein sim. GBank gi 4504511 ref NP_001530.1 pHSJ2 - heat shock protein, DNAJ-like 2	Contains protein domain (PF00684) - DnaJ central domain (4 repeats)	eph	264489, 56182575, 29331824, 56182435, 264112, 265007, 265019, 284784, 21906788, 265020, 264891, 55811576, 264835, 264555, 264556, 264557, 264559 264106
1749	83383091 (3497, 3498)	Novel Protein sim. GBank gi 5650780 gb AAD45948.1 AF15196 - (AF151968) RGS protein RGS-17 [Gallus gallus]	Contains protein domain (PF00615) - Regulator of G protein signaling domain	oncogene	
1750	94321664 (3499, 3500)	Novel Protein sim. GBank gi 4986894 gb AAC28444.2  - (AF065164) hyperpolarization-activated, cyclic nucleotide- gated channel 2 [Homo sapiens]			33657402, 264288, 52644150, 263974, 83373044
1751	83373058 (3501, 3502)	Novel Protein sim. GBank gi 2760161 dbj BA024184  - (AB010054) outer arm dynein light chain 2 [Anthracidaris crassispina]	Contains protein domain (PF00560) - Leucine Rich Repeat	ATPase-associated	265010, 264369
1752	88456530 (3503, 3504)	Novel Protein sim. GBank gi 3915482 sp P74346 YG29_SYN13 - HYPOTHETICAL 36.0 KD PROTEIN SLR1629	Contains protein domain (PF00849) - RNA pseudouridylation synthase	deaminase	264510, 264593, 264682, 21908765, 18108370
1753	94235159 (3505, 3506)	Novel Protein sim. GBank gi 2852636 (AF007155) - unknown [Homo sapiens]	Contains protein domain (PF01553) - Acyltransferase	phosphatase	56994075, 22278986, 264908, 60170831, 264682, 264784, 264369, 264288, 264685, 264687, 21906766, 264692, 264693, 65274620, 65274791, 35695855, 264637, 264564
1754	88095323 (3507, 3508)	Novel Protein sim. GBank gi 731421 sp P39881 YEH4_YEAST - HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION		transport	264488, 35696286, 264509, 264906, 264807, 264908, 264909, 264511, 264910, 264591, 33657402, 264594, 264757, 264758, 264600, 264604, 264762, 264763, 264685, 264766, 264691, 264628, 35696423, 264632, 264634, 264637, 264638, 263981, 264558, 264639, 264563, 264584, 264565, 264566, 264567, 264686
1755	78470282 (3509, 3510)	Novel Protein sim. GBank gi 1176422 (U43194) - rhophilin [Mus musculus]		UNCLASSIFIED	
1756	92862614 (3511, 3512)	Novel Protein sim. GBank gi 4432860 gb AAD20708  - (ACO06300) putative glucose-induced repressor protein [Arabidopsis thaliana]			52646842, 22278984, 22278985, 56994075, 22278986, 22278987, 264259, 29331822, 60432289, 29331827, 33656970, 265006, 285009, 60432229, 60433356, 60433436, 33109954, 21906754, 265017, 265018, 265019, 264448, 264369, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 27486262, 27486264, 18108376, 20281152, 264558, 18108388, 87168518, 60432113, 22279000, 22279002, 264482
1757	95357380 (3513, 3514)	Novel Protein sim. GBank gi 5441615 emb CA046856.1  - (A388557) zinc finger protein [Canis familiaris]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	22278987, 264259, 60432289, 29331827, 264908, 52644045, 265008, 264593, 265019, 264766, 21906768, 65274620, 18108385, 60432113, 264566, 264487

1758	87612971 (3515, 3516)	Novel Protein sim. GBank gjl38810401embj[CAA18403] - (AL021497) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	22278994, 22278999, 29331822, 29331824, 29331825, 33656970, 264508, 265006, 265007, 265009, 264591, 33657402, 33108954, 87168474, 264600, 265017, 265018, 21906769, 265020, 265021, 33657023, 33657109, 264629, 18108374, 35695855, 264632, 52644332, 22279002, 264563
1759	36894372 (3517, 3518)			UNCLASSIFIED	264759
1760	87329716 (3519, 3520)	Novel Protein sim. GBank gjl5282748[embj[CAB45688.1] - (A1133120) Proline rich synapse associated protein 2 [Rattus norvegicus]		UNCLASSIFIED	56182575, 60432049, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265009, 264910, 60432228, 264592, 264595, 55812038, 264758, 264762, 18108351, 264764, 264766, 264768, 264769, 21906765, 55811857, 35695817, 264690, 264692, 264628, 264629, 55811576, 35698423, 264632, 264634, 264636, 264557, 264639, 60432113, 264565, 264486
1761	87409586 (3521, 3522)	Novel Protein sim. GBank gjl127749[spP10569]MYSC_ACACA - MYOSIN IC HEAVY CHAIN	Contains protein domain (PF00618) - Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif	UNCLASSIFIED	29331822, 264910, 264685, 264686
1762	95319887 (3523, 3524)	Novel Protein sim. GBank gjl3169159 (AC004770) - BC269730_2 [Homo sapiens]	Contains protein domain (PF00173) - desaturase Heme-binding domain in cytochrome b5 and oxidoreductases		22278999, 264259, 264905, 264907, 60170831, 265010, 265011, 265017, 264448, 21906765, 21906766, 21906767, 21906768, 265021, 264690, 33657109, 18108374, 264558, 60170394
1763	91224013 (3525, 3526)	Novel Protein sim. GBank gjl4809028[gbjAAD30062.1] - (AF132855) suppressor of G2 allele of skp1 homolog [Homo sapiens]			56181686, 29331825, 35696052, 264905, 264906, 264909, 264763, 264682, 264769, 35695917, 265022, 33657023, 18108374, 35698423, 264634
1764	87757697 (3527, 3528)	Novel Protein sim. GBank gjl1360669[pirj]CGHUV - collagen alpha 1(V) chain precursor - human	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	22278999, 264259, 35696052, 29331828, 56182435, 265008, 265017, 265018, 264448, 264286, 21906766, 21906767, 29148627, 35695917, 264691, 33657023, 60432113, 22279002
1765	91230091 (3529, 3530)	Novel Protein sim. GBank gjl486806[pirj]S55503 - finger protein neutralized - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	264488, 18108394, 22278995, 22278997, 22278999, 264259, 264104, 264508, 264905, 264907, 264511, 265007, 265008, 264910, 265009, 21906754, 265010, 265017, 264603, 265018, 265019, 18108351, 264682, 264448, 264369, 264288, 264766, 18108359, 21906766, 21906767, 29148627, 29148629, 35695917, 265020, 265021, 264692, 264628, 264629, 18108374, 263976, 264636, 83373044, 22279000, 22279002

1766	95081201 (3531, 3532)	Novel Protein sim. GBank gi 2499087 sp Q09332 UGGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)			glycoprotein	52645156, 87168559, 80170615, 33657023, 264683, 33657109, 27486261, 264555, 83373044
1767	87755988 (3533, 3534)	Novel Protein sim. GBank gi 4176443 emb CAA18263.1  - (AL022238) dJ1042K10.4 (novel protein) [Homo sapiens]			UNCLASSIFIED	265017, 265019, 264688, 264768, 265020, 264892
1768	80253216 (3535, 3536)				UNCLASSIFIED	29331824, 29331825, 264591, 56182323
1769	87388988 (3537, 3538)				UNCLASSIFIED	264563
1770	95413144 (3539, 3540)	Novel Protein sim. GBank gi 115204 sp P00736 C1R_HUMAN - COMPLEMENT C1R COMPONENT PRECURSOR	Contains protein domain (PF00089) - Trypsin		complement	264488, 264768, 264769, 56182575, 55811957, 264690, 264691, 35696052, 284905, 264509, 264906, 264907, 264628, 264908, 264909, 264910, 264634, 264635, 264636, 264558, 264757, 264758, 55812038, 65274444, 264760, 264563, 264762, 264764, 264684, 264766
1771	94233542 (3541, 3542)	Novel Protein sim. GBank gi 3914181 sp P56558 OGT1_RAT - UDP-N- ACETYLGLUCOSAMINE--PEPTIDE N- ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT)	Contains protein domain (PF00515) - TPR Domain		transferase	264758, 264600, 264369, 55811957, 265020, 83373044, 22279000
1772	87643510 (3543, 3544)	Novel Protein sim. GBank gi 4959442 gb AA034351.1 AF12136 - (AF121360) DNZDHC/NEW1 zinc finger protein 11 [Drosophila melanogaster]	Contains protein domain (PF01529) - DHC zinc finger domain			22278998, 28331828, 33109854, 265018, 265019, 264764, 21906765, 265020, 265021, 264556
1773	94116824 (3545, 3546)	Novel Protein sim. GBank gi 3978464 (AF085693) - G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf		potassium_channel	65274572, 56182575, 22278996, 35696286, 22278999, 264259, 29331824, 60424269, 29331825, 60432289, 35696052, 264106, 264509, 264906, 264907, 29331830, 264908, 52644045, 264511, 265008, 265007, 265008, 60170831, 60433438, 264758, 55811388, 87168559, 265017, 264604, 265019, 55811150, 264288, 56181562, 264689, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265022, 52644150, 264691, 33657023, 264692, 264693, 60431528, 35696423, 35695855, 264636, 56182323, 18108387, 56526488, 22279000, 22279002, 264563, 264564, 264585, 264566, 264567
1774	94232573 (3547, 3548)	Novel Protein sim. GBank gi 24956899 sp Q15034 Y032_HUMAN - HYPOTHETICAL PROTEIN KIAA0032	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)		UNCLASSIFIED	65274572, 56182575, 35696052, 55812038, 33109854, 21906754, 265017, 21906767, 21906768, 21906769, 265020, 264691, 264636, 56182323, 22279002

1775	95359330 (3549, 3550)	Novel Protein sim. GBank gij1469199[dbj BAA09487] - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]		UNCLASSIFIED	85274572, 56182575, 56994075, 35696286, 22278997, 29331822, 29331826, 60432289, 29331828, 35996052, 29331830, 86712502, 264828, 56182435, 264511, 265007, 265009, 60170831, 60432229, 60433438, 55812038, 21906754, 85658542, 87168559, 264601, 265017, 265018, 265019, 264762, 284448, 264288, 264689, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 265022, 264691, 33657023, 264692, 33657109, 27486261, 33657349, 18108370, 18108377, 35696423, 55811576, 35695855, 264632, 264634, 264636, 264639, 56182323, 83373044, 56526486, 87168518, 60432113, 22279000, 22279002, 264482, 264486, 264490
1776	94133758 (3551, 3552)	Novel Protein sim. GBank gij4589676[dbj BAA76857.1] - (AB023230) KIAA1013 protein [Homo sapiens]			
1777	87447171 (3553, 3554)	Novel Protein sim. GBank gij3219939[sp P87115 YDK9_SCHPO - HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME 1	nucl_recl		56994075, 29331826, 265008, 87168474, 265017, 265018, 264761, 55811150, 264764, 56181562, 264689, 21906765, 21906768, 21906769, 35695917, 264690, 33657023, 35695783, 60431528, 35696423, 55811576, 35695855, 22279000, 22279002, 264564
1778	94851624 (3555, 3556)	Novel Protein sim. GBank gij367564[emb CAA91454.1] - (Z66561) Similarity to Human rab13 protein (PIR Acc. No. A49647). Contains the ATP/GTP-binding site motif (PROSITE PS00017); cDNA EST EMBL:M89412 comes from this gene; cDNA EST yk212g9.3 comes from this gene; cDNA EST yk212g9...		UNCLASSIFIED	29331826, 29331827, 35696052, 264512, 265007, 265009, 265017, 265019, 264762, 18108351, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264691, 264693, 18108370, 264556, 83373044
1779	94133758 (3557, 3558)	Novel Protein sim. GBank gij4589676[dbj BAA76857.1] - (AB023230) KIAA1013 protein [Homo sapiens]		UNCLASSIFIED	29148627, 35696286, 29147620, 265006, 265007, 265008, 18108385, 85274727, 264482, 264369, 264768
1780	87023497 (3559, 3560)		Contains protein domain (PF00807) - Apidaecin	UNCLASSIFIED	264107, 33657109, 56526486
1781	84047477 (3561, 3562)			UNCLASSIFIED	264508, 264906, 264639
1782	88094607 (3563, 3564)	Novel Protein sim. GBank gij729225[sp P41237 CTNX_RAT - CORTEXIN			264259, 29331822, 264508, 264905, 264908, 264907, 264908, 265007, 265009, 264910, 264591, 264758, 264764, 264286, 264768, 264769, 264635, 264636, 264637, 264639, 264583
1783	85717805 (3565, 3566)	Novel Protein sim. GBank gij2257543[dbj BAA21436] - (AB004538) protein arginine N-methyltransferase [Schizosaccharomyces pombe]	interferon		264768

1784	95197093 (3567, 3568)	Novel Protein sim. GBank gj1755049 (U55042) - myosin X [Bos taurus]	Contains protein domain (PF00169) - struct PH domain	UNCLASSIFIED	35698286, 284259, 35696032, 284508, 284905, 284906, 284907, 66712502, 284908, 284909, 285007, 285008, 285009, 284910, 284591, 284594, 284757, 284758, 284759, 285010, 285011, 284601, 284602, 284604, 284605, 18108351, 284762, 284763, 284764, 284368, 284766, 284887, 284768, 284688, 21908768, 35695917, 284690, 284691, 284692, 284693, 284628, 18108374, 35696423, 284631, 284632, 284635, 284637, 284638, 284639, 18108385, 22279000, 22279002, 284555, 284556, 284488
1785	95357475 (3569, 3570)	Novel Protein sim. GBank gj4589552[jdb]BAA76798.1] - (AB023171) KIAA0954 protein (Homo sapiens)	UNCLASSIFIED	29331825, 29331827, 29331828, 284905, 284906, 284908, 66712502, 56182435, 284511, 265007, 60433356, 55811150, 284683, 284369, 284687, 52644229, 21908767, 52644150, 33657023, 65274620, 33657182, 65274791, 35695855, 284555, 65274727, 22279002	
1786	85298465 (3571, 3572)	Novel Protein sim. GBank gj117788[sp]P26770[CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)]	UNCLASSIFIED	284908, 35696423, 284636	
1787	87434784 (3573, 3574)	Novel Protein sim. GBank gj3877175[emb]CAA80338.1] - (Z50028) cDNA EST yk321h8.5 comes from this gene; cDNA EST EMBL:D68896 comes from this gene; cDNA EST yk395f9.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	284488, 284905, 284908, 284909, 284595, 284764, 284766, 284692, 60431528, 284629, 284636, 284564, 284566	
1788	91228779 (3575, 3576)		UNCLASSIFIED	284488, 83373044	
1789	88094529 (3577, 3578)	Novel Protein sim. GBank gj2088669 (AF003130) - F55A12.9 gene product [Caenorhabditis elegans]	UNCLASSIFIED	284488, 29331828, 284909, 18108351, 284288, 285021, 284555, 284636	
1790	82489734 (3579, 3580)			35696052, 284905, 284906, 284907, 284908, 284909, 285008, 284910, 284758, 265011, 265019, 284784, 284766, 284769, 284628, 284635	

1791	95197259 (3581, 3582)	Novel Protein sim. GBank gjl2114321[dbj BAA20037] - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	264488, 264686, 264687, 264768, 18108394, 264769, 18108397, 264259, 264691, 264692, 33657023, 264693, 264509, 264905, 264906, 264628, 264907, 264629, 264908, 264909, 264510, 265006, 264511, 265008, 264630, 265009, 264631, 264910, 264632, 264634, 264635, 264555, 264636, 264592, 264637, 264638, 18108381, 264639, 264758, 265010, 265011, 264602, 22279000, 264604, 264760, 264564, 264681, 264762, 264565, 264763, 264683, 264566, 264764, 264288, 264684, 264567, 18108354, 18108391, 264685, 264766
1792	87792690 (3583, 3584)	Novel Protein sim. GBank gjl4337106[gbl AAD18082] - (AF129756) BAT4 [Homo sapiens]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED	22278997, 264259, 264508, 265007, 33657402, 87168559, 264369, 33657023, 35695855, 20261071, 264559, 18108387, 87168518
1793	95337877 (3585, 3586)	Novel Protein sim. GBank gjl5579331[gbl AAD45504.1 AF145732] endoplasmic reticulum alpha-mannosidase 1 [Homo sapiens]	Contains protein domain (PF01532) - Glycosyl hydrolase family 47	ATPase-associated	65274572, 22278995, 22278996, 22278997, 22278998, 264093, 264259, 29331824, 68714117, 60432289, 29331827, 29331828, 264103, 264105, 29331830, 265007, 264910, 265009, 60170831, 60433356, 21906754, 265010, 265017, 265019, 264681, 264682, 264288, 5264229, 21906785, 21906786, 21908767, 21908768, 21906769, 265020, 265021, 265022, 60170615, 52644150, 33657023, 33657109, 18108370, 18108374, 65274791, 20281071, 60432113, 22279000, 264482, 264564
1794	87759806 (3587, 3588)	Novel Protein sim. GBank gjl4914604[emb CAB43677.1] - (AL050389) hypothetical protein [Homo sapiens]	Contains protein domain (PF01798) - Putative snRNA binding domain	UNCLASSIFIED	18108394, 22278995, 22278999, 264259, 29331822, 29331824, 29331825, 29146498, 29146499, 264508, 264905, 52644045, 264112, 265006, 265008, 264910, 60433356, 264757, 55812038, 87168474, 265011, 265017, 18108351, 264763, 264448, 264683, 264369, 21908765, 21908766, 21906767, 21906769, 29148784, 35695917, 60170815, 33657023, 264629, 18108374, 18108376, 35696423, 35695855, 264556, 264557, 264638, 264558, 18108385, 264564, 264632, 264635, 264636, 264595, 264596, 264907, 264568, 264909
1795	79747656 (3589, 3590)			UNCLASSIFIED	264907, 264568, 264909
1796	86599486 (3591, 3592)	Novel Protein sim. GBank gjl585084[sp Q07803 EFGM_RAT]- ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)		glycoprotein	264488, 264907, 264908, 264594, 264595, 264768, 264687, 21906765, 21906767, 264628, 264630, 264559

1797	91223219 (3593, 3594)	Novel Protein sim. GBank gl 1842111 (U87586) - decoy (Arabidopsis thaliana)		ribosomalprot	22278896, 22278897, 22278898, 22278899, 29331822, 264910, 60170831, 21906754, 52644229, 21906765, 21906768, 21906769, 35695917, 265022, 52644150, 264691, 35657023, 263967, 33637109, 22279000
1798	91221276 (3595, 3596)	Novel Protein sim. GBank gl 2832906(dbj BAA24608.1) - (D89340) dipeptidyl peptidase III [Rattus norvegicus]		peptidase	22278994, 56994075, 22278997, 22278998, 22278999, 264259, 29331826, 60432289, 29331828, 33656970, 265008, 60432229, 264757, 60433438, 21906754, 33657084, 87168559, 265017, 18108351, 264882, 264448, 264288, 21906765, 21906768, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 33657182, 27486261, 27486265, 33657349, 263973, 18108374, 55811576, 35695855, 18108385, 87168518, 22279000, 264488
1799	86321713 (3597, 3598)	Novel Protein sim. GBank gl 5689541(dbj BAA83054.1) - (AB029025) KIAA1102 protein [Homo sapiens]		eph	264908, 21906754, 21906767, 21906768, 265020, 33657023, 264692, 264693, 264404, 22279000
1800	87080118 (3599, 3600)	Novel Protein sim. GBank		UNCLASSIFIED	264691, 264556, 264568
1801	95060723 (3601, 3602)	gl 4680678 gb AAD27729.1 AF13295 - (AF132954) CGI:20 protein [Homo sapiens]			52644045, 265007, 264632
1802	87771012 (3603, 3604)	Novel Protein sim. GBank gl 134920 sp P21897 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			35686286, 66714117, 264508, 264509, 56182435, 264512, 18108351, 264888, 55811957, 264692, 55811576, 35695855, 264486
1803	95060725 (3605, 3606)	Novel Protein sim. GBank gl 4680678 gb AAD27729.1 AF13295 - (AF132954) CGI:20 protein [Homo sapiens]			264686, 264488, 264687, 264489, 264768, 264768, 264689, 21906769, 35686286, 35695917, 264259, 264691, 264692, 264693, 20281099, 18108364, 35686052, 264508, 264509, 264905, 264906, 18108370, 264628, 264907, 66712502, 264908, 264909, 18108374, 18108376, 35686423, 35695855, 264610, 264511, 265008, 265007, 264512, 265008, 264910, 264631, 264632, 264634, 264635, 264591, 264636, 264637, 264592, 264638, 264593, 264639, 264594, 83373044, 264758, 264598, 18108385, 18108387, 265011, 264760, 264563, 18108351, 264762, 264564, 264448, 264565, 264763, 264683, 264764, 264568, 264288, 264486, 264567, 264765, 264766



1804	87770203 (3607, 3608)	Novel Protein sim. GBank gij3879914[emb]CAA8538.1]- (Z74043) predicted using GeneFinder; cDNA EST EMBL:C13850 comes from this gene; cDNA EST EMBL:C11575 comes from this gene; cDNA EST yk34314.5 comes from this gene [Caenorhabditis elegans]			52646365, 22278997, 22278999, 264905, 264908, 264909, 264910, 21906754, 264766, 21906765, 21906768, 35695917, 285020, 265022, 264691, 264637, 264639, 22279000, 264564, 264566
1805	95330375 (3609, 3610)	Novel Protein sim. GBank gij5453644[ref]NP_006461.1 pEBBP - estrogen-responsive B box protein			29331824, 29331825, 29331826, 29331827, 29331828, 87168559, 264288, 264687, 52644229, 35696423, 264636, 60432113
1806	94133762 (3611, 3612)	Novel Protein sim. GBank gij4589678[dbj]BAA76857.1]- (AB023230) KIAA1013 protein [Homo sapiens]	struct		264094, 264105, 264908, 35698423, 265008, 265007, 265008, 264555, 264592, 265011, 265018, 264369
1807	86943032 (3613, 3614)				29331824, 264908, 264910, 33657023, 263978
1808	87642711 (3615, 3616)	Novel Protein sim. GBank gij4884079[emb]CAB43235.1]- (AL050008) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264486, 35696286, 66714117, 35696052, 66712502, 264592, 80433438, 52644296, 265010, 264683, 264369, 264689, 55811957, 35695917, 33657109, 35695763, 55810764, 18108379, 35696423, 35695955, 56182323, 264563, 264564, 264487
1809	95321468 (3617, 3618)	Novel Protein sim. GBank gij1916927 (U87965) - putative G protein [Mus musculus]	UNCLASSIFIED		264594, 55811150, 264686, 29148629, 29148784, 264690, 264629, 18108374, 264558, 264557, 264558
1810	88086316 (3619, 3620)	Novel Protein sim. GBank gij1352944[sp]P47179 JRP_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR	UNCLASSIFIED		264486, 35696052, 264905, 264906, 264907, 264908, 264909, 264511, 265009, 264910, 264592, 264593, 264594, 33657402, 264757, 264595, 264758, 264596, 264759, 264600, 264601, 264762, 264683, 264764, 264288, 264684, 264766, 264767, 264686, 264768, 264687, 264769, 264689, 265021, 264690, 264691, 264693, 264628, 264629, 18108374, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264566, 264486, 264567
1811	88086272 (3621, 3622)	Novel Protein sim. GBank gij2134984[pir]J37275 - death-associated protein kinase (EC 2.7.1.-) - human	kinase	Contains protein domain (PF00023) - Ank repeat	264486, 264259, 264508, 264509, 264905, 264906, 264907, 56182435, 264511, 264512, 264910, 264758, 265011, 264600, 264604, 18108354, 264766, 264686, 264769, 264534, 60170615, 33657023, 264629, 264631, 264639, 264563, 264482, 264483
1812	78245772 (3623, 3624)				29331822, 29331824, 265019, 18108351, 21906769

1813	88090972 (3625, 3626)	Novel Protein sim. GBank gl 5051636 gb AAD38326.1 AF07372 - (AF073727) EH domain-binding mitotic phosphoprotein [Homo sapiens]	Contains protein domain (PF01417) - ENTH domain	glucoamylase	56182575, 264259, 29331824, 86714117, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 265007, 264910, 264591, 264593, 55812038, 265011, 265018, 264760, 264682, 264764, 264683, 264369, 264766, 264768, 264769, 21906768, 21906768, 264691, 264693, 18108374, 35695855, 264634, 264635, 264637, 264638, 264559, 22279000, 22279002, 264568
1814	88178047 (3827, 3628)	Novel Protein sim. GBank gl 3643608 (AC005395) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 35696286, 22278998, 264082, 264094, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264107, 52644045, 56182435, 265009, 60432229, 60433356, 87168474, 87168559, 264368, 264288, 21906765, 35695917, 265021, 265022, 33657023, 33657109, 18108374, 35696423, 264638, 56526486, 264482
1815	85298473 (3629, 3630)	Novel Protein sim. GBank gl 117788 sp P26770 CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)		strucd	22278999, 264508, 264509, 264907, 264908, 264910, 265011, 264760, 264766, 264634, 264636
1816	83738845 (3631, 3632)	Novel Protein sim. GBank gl 1176823 sp P41846 YO86 CAEL - HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III		UNCLASSIFIED	18108394, 18108397, 264509, 264907, 264908, 264909, 265009, 264591, 265011, 265017, 264687, 264689, 265022, 264691, 18108362, 18108368, 18108370, 18108374, 18108379, 264635, 264557, 264564, 264587
1817	88095268 (3633, 3634)	Novel Protein sim. GBank gl 3766377 emb CAA21428  - (AL031907) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	histone	264488, 22278997, 22278999, 60432049, 29331822, 29331824, 60432289, 52644045, 60170831, 265017, 265018, 265019, 18108351, 264682, 52644229, 21906765, 21906767, 21906768, 52644150, 33657023, 33657109, 27466262, 18108370, 18108374, 60170394, 56182323, 22279002
1818	85806775 (3635, 3636)	Novel Protein sim. GBank gl 3879121 emb CAA94370  - (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S3771); cDNA EST EMBL: T01923 comes from this gene; cDNA EST EMBL: D32335 comes from this gene; cDNA EST EMBL: D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	35696286, 60433356, 264758, 264369, 264686, 21906769, 264693, 264632
1819	87759572 (3637, 3638)	Novel Protein sim. GBank gl 5031865 ref NP_005771.1 pLHFP - lipoma HMGIC fusion partner		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331826, 264908, 265007, 265008, 265009, 60432229, 265017, 265018, 265019, 264448, 264288, 21906768, 21906769, 265020, 18108381, 18108384, 22279000, 22279002, 264587

1820	87769455 (3639, 3640)				264905, 264907, 264594
1821	80431510 (3641, 3642)				264907, 264768, 263978
1822	91221523 (3643, 3644)	Novel Protein sim. GBank gll4884130[emb]CAB43272.1] - (AL050101) hypothetical protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 35698052, 29331828, 264908, 29331830, 60170831, 264591, 264593, 60433356, 264596, 265017, 265018, 18108351, 264763, 264683, 21906765, 21908767, 21908768, 21906769, 35695917, 265020, 265021, 33657023, 18108364, 18108370, 35695855, 22279000, 22279002
1823	85522330 (3645, 3646)			UNCLASSIFIED	264488, 264259, 264511, 264288, 264768, 264693, 35698423, 264634, 18108385, 264486
1824	86612025 (3647, 3648)	Novel Protein sim. GBank gll477072[pri]A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00047) - immunoglobulin domain	UNCLASSIFIED	264907, 264908, 264909, 264511, 264631, 264634, 264635, 264637, 264638, 264639, 264758, 264568
1825	87430125 (3649, 3650)	Novel Protein sim. GBank gll3036803[emb]CAA18493] - (AL022373) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60432049, 264910, 264487
1826	91723612 (3651, 3652)	Novel Protein sim. GBank gll4880685[gb]AAD27732.1[AF13295] CGI-23 protein [Homo sapiens]		ATPase-associated	52644507, 52645156, 52646842, 22278994, 22278996, 56994075, 264259, 60432049, 52645080, 35698052, 66712502, 52644045, 265008, 265009, 60432228, 60433356, 60433438, 52646317, 52644296, 265011, 87168559, 264448, 264288, 264369, 264688, 52644229, 264689, 21906765, 21906768, 265020, 60170815, 52644150, 33657023, 27486262, 27486264, 27486265, 35695763, 35698423, 35695855, 83373044, 87168518, 264404, 22279002
1827	81647212 (3653, 3654)				264758

1828	95074017 (3655, 3656)	Novel Protein sim. GBank gi14503571 ref NP_001419.1 pENO1 - enolase 1, (alpha)	Contains protein domain (PF00113) - Enolase	oncogene	264488, 52646842, 56182575, 22278986, 35986286, 22278997, 22278999, 264091, 264093, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264508, 264907, 66712502, 52644045, 56182435, 265008, 264511, 264512, 265007, 265008, 265009, 60170831, 60432228, 264593, 60433356, 60433438, 264758, 33109954, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265019, 264761, 264762, 264448, 264764, 264683, 264288, 264389, 18108355, 264768, 18108357, 18108358, 264688, 264769, 264688, 21906769, 21906769, 35695917, 265021, 60170615, 33657023, 33657349, 263972, 55611576, 35695855, 264635, 264555, 264556, 264638, 264557, 87168518, 22279000, 22279002, 264563, 264482, 264565, 264484, 264567
1829	80197720 (3657, 3658)				264508, 264634, 264509, 264482, 29331827, 264908, 265009, 264810
1830	94312942 (3659, 3660)	Novel Protein sim. GBank gi12246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		nuclease	52645156, 22278994, 22278995, 35695286, 22278996, 22278997, 22278998, 22278999, 29331822, 29331825, 35696052, 52646317, 52644296, 87168559, 265018, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 35695763, 263974, 35696423, 35695855, 52644332
1831	94138063 (3661, 3662)			UNCLASSIFIED	29331824, 35696052, 29331830, 264595, 264758, 265010, 265019, 265022, 264693, 65274791
1832	84521663 (3663, 3664)	Novel Protein sim. GBank gi1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46ds.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....			264602

1833	195314184 (3665, 3666)	Novel Protein sim. GBank gi 5174413 ref NP_006026.1 pCDC4 - CDC42-binding protein kinase beta (DNPK-like)	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	22278994, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 35696052, 29146499, 264508, 264509, 264905, 264907, 66712502, 264908, 5284045, 264909, 264512, 265008, 264591, 264593, 60433358, 21906754, 33857084, 265011, 265017, 264604, 265018, 265019, 264681, 18108351, 264683, 264288, 264685, 264766, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 29146629, 285020, 285021, 264690, 264692, 33657023, 65274620, 33657182, 27466264, 33657349, 65274791, 264634, 264635, 264556, 264557, 264558, 264559, 18108385, 56526488, 87188518, 60432113, 22278000, 22279002, 264553
1834	80562790 (3667, 3668)			264259, 264907, 264689, 22279000, 22278002
1835	94135718 (3669, 3670)		UNCLASSIFIED	22278998, 29331822, 29331826, 87168474, 264603, 21906768, 263976, 35695855, 83373044
1836	87348450 (3671, 3672)	Novel Protein sim. GBank gi 4759286 ref NP_004288.1 pUCP4 - uncoupling protein 4	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	29331825, 264808, 265019, 264764, 264688, 21906765, 264635
1837	94234297 (3673, 3674)	Novel Protein sim. GBank gi 3334400 sp Q24574 UBPE, DROME - UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)	Contains protein domain (PF00443) - ubiquitin Ubiquitin carboxyl-terminal hydrolase family 2	22278995, 29146499, 265006, 265008, 265009, 265010, 264683, 21906765, 29148827, 29148629, 285020, 265021, 285022, 65274620, 18108370, 18108374, 264556, 18108385
1838	94324369 (3675, 3676)	Novel Protein sim. GBank gi 1362599 pir JAS6154 - Abl substrate ena (enabled) - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00568) - WH1 domain	29331822, 265017, 264760, 265020, 83373044
1839	87456508 (3677, 3678)	Novel Protein sim. GBank gi 2117310 emb CAB09116.1  - (Z95620) hypothetical protein [Schizosaccharomyces pombe]	UNCLASSIFIED	60433438, 264601, 21906765, 21806766, 265021, 33657109, 264556
1840	87391708 (3679, 3680)	Novel Protein sim. GBank gi 127560 sp P23249 MV10_MOUSE - PROTEIN MOV-10	UNCLASSIFIED	264683
1841	85818445 (3681, 3682)	Novel Protein sim. GBank gi 4572484 gb AAD23834.1 AF123653 (AF123653) FEZ1 [Homo sapiens]		56182575, 29331824, 29331826, 60433356, 264764, 264288, 33657023, 263967, 18108370, 18108374, 264631, 264555, 264556, 264639

1842	80982645 (3683, 3684)	Novel Protein sim. GBank gi 1326268 (U58728) - C54H2.1 gene product [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 28331822, 28331824, 28331825, 66714117, 29331826, 29331827, 284907, 284909, 52844045, 56182435, 284510, 285006, 285007, 285009, 284910, 60433356, 284757, 60433436, 55812038, 265017, 18108354, 264688, 284769, 33657023, 284693, 18108384, 33657109, 18108386, 284628, 55810764, 56182323, 18108384, 284563, 284584
1843	95292692 (3685, 3686)			UNCLASSIFIED	264488, 56182435, 284769, 29331826, 29331828, 284511, 285006, 285007, 284910, 284631, 284509, 284690, 284836, 284584, 284891, 60432229, 60432049, 284259, 284629, 33657023, 284486, 284908, 284587, 284595, 284766
1844	87444764 (3687, 3688)	Novel Protein sim. GBank gi 2496887 (sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III)		UNCLASSIFIED	264908, 285022, 33657023, 87168518, 22279002
1845	95096673 (3689, 3690)	Novel Protein sim. GBank gi 1175484 (sp Q08819 YAC5_SCHPO - HYPOTHETICAL 45.0 KD PROTEIN C16C9.05 IN CHROMOSOME I)	Contains protein domain (PF00628) - PHD-finger	transcriptfactor	264259, 29331824, 284807, 284908, 66712502, 284510, 285007, 285008, 55812038, 285018, 21908765, 52644150, 33657109, 284555, 284556, 284557, 56182323, 18108382, 83373044, 18108385, 284564
1846	84287872 (3691, 3692)	Novel Protein sim. GBank gi 3881080 (emb CAA21739  - (AL032857) similar to EGF-like domain; cDNA EST yk298a12.3 comes from this gene; cDNA EST EMBL:D35398 comes from this gene; cDNA EST yk331h6.5 comes from this gene; cDNA EST yk298a12.5 comes from this gene; cDNA EST yk467g8.5 c...	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	284905, 284908
1847	87821487 (3693, 3694)	Novel Protein sim. GBank gi 5059323 (gb AAD38967.1 AF151522) hairy and enhancer of split related-1 [Homo sapiens] (AJ245417) G5b protein [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	22278997, 284259, 29331824, 284909, 18108351, 263974, 22278002
1848	86789360 (3695, 3696)	Novel Protein sim. GBank gi 5701854 (emb CAB52191.1  - (AJ245417) G5b protein [Homo sapiens])	Im7		29331825, 29331826, 29331827, 265017, 284683, 284288, 284766, 284768, 21906767, 21906768, 284692, 22279002
1849	84287874 (3697, 3698)	Novel Protein sim. GBank gi 4503665 (ref NP_001989.1 pFBLN - fibulin 2 precursor	Contains protein domain (PF00008) - ATPase-associated EGF-like domain	ATPase-associated	56182575, 265018
1850	86689650 (3699, 3700)	Novel Protein sim. GBank gi 4589582 (dbj BAA76813.1  - (AB023186) KIAA0969 protein [Homo sapiens]	Contains protein domain (PF00169) - struct PH domain	struct	60432049, 284908
1851	95419789 (3701, 3702)	Novel Protein sim. GBank gi 220637 (dbj BAA01477  - (D10627) zinc finger protein [Mus musculus])	Contains protein domain (PF00096) - dna_ma_bind Zinc finger, C2H2 type	dna_ma_bind	29331824, 35696052, 284910, 60433438, 284688, 35695917, 265020, 52644150, 65274620, 52644332

1852	95413170 (3703, 3704)	Novel Protein sim. GBank gil5174629[re]NP_000890.1pPIAS - protein inhibitor of activated STAT3		UNCLASSIFIED	56182575, 35696286, 22278996, 22278997, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 35696052, 52644045, 265007, 264910, 60432228, 60433356, 60433438, 55812038, 65274444, 265018, 265019, 18108351, 264448, 264686, 264687, 21906765, 21906767, 21906769, 265021, 265022, 52644150, 264683, 33657109, 18108370, 18108374, 55811576, 35695855, 58182323, 60432113, 22279002, 264563
1853	91222287 (3705, 3706)	Novel Protein sim. GBank gil854065[emb]CAA583371 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	21906765, 21906767, 21906768, 22278995, 56994075, 22278999, 52644150, 264259, 264692, 29331822, 29331824, 52645129, 29331827, 33656970, 33657349, 35695763, 264508, 264908, 264628, 264907, 264629, 284909, 35698423, 35695855, 264510, 285008, 264511, 264512, 264630, 265009, 264631, 264910, 264634, 264635, 264637, 264593, 264638, 264639, 33657402, 18108385, 52646317, 52644296, 87168518, 87168559, 264602, 265017, 22279000, 265018, 264760, 264762, 264682, 264448, 264764, 264684, 264567, 264288, 264369, 264766
1854	86038152 (3707, 3708)	Novel Protein sim. GBank gil2072964 (U93569) - putative p150 [Homo sapiens]	nuclease		264592
1855	91221459 (3709, 3710)	Novel Protein sim. GBank gil4539520[emb]CAB39994.1 - (AL035424) dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogeneous set of other types of proteins) [Homo sapiens]	Contains protein domain (PF01344) - nucl_recpt Kelch motif		18108392, 52646365, 65274572, 56182575, 22278994, 56994075, 22278996, 35696286, 22278999, 264259, 60432049, 264908, 264510, 265007, 265008, 265009, 264595, 21906754, 87168474, 265011, 87168559, 264681, 264288, 264768, 18108359, 21906764, 21906768, 29148627, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108372, 18108374, 18108376, 35696423, 264631, 264636, 18108381, 264482
1856	94231871 (3711, 3712)	Novel Protein sim. GBank gil3954978[emb]CAA06945 - (AJ008278) acetylglucosaminyltransferase-like protein [Mus musculus]		UNCLASSIFIED	56994075, 264259, 29331828, 264511, 264910, 264758, 264693, 264637, 18108381, 83373044
1857	94324455 (3713, 3714)	Novel Protein sim. GBank gil4322670[gb]AAD16120 - (AF094508) dentin phosphoryn [Homo sapiens]	ATPase-associated		22278999, 264259, 264906, 60170831, 264448, 264686, 265020, 265022, 33657109, 60170394, 83373044

1858	87628311 (3715, 3716)	Novel Protein sim. GBank gi4981903 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomal prot	264757
1859	84407484 (3717, 3718)	Novel Protein sim. GBank gi424037 dbj BAA74937.1  - (AB020721) KIAA0914 protein [Homo sapiens]			22278996, 29331824, 265007, 33109954, 265019, 264368, 21908768, 29148784, 27486261, 52644332, 22279002 265019
1860	17829308 (3719, 3720)	Novel Protein sim. GBank gi4009522 (AF099731) - connexin 31.1 [Homo sapiens]			
1861	88086370 (3721, 3722)	Novel Protein sim. GBank gi2143637 pir j184505 - calcium- dependent actin-binding protein - rat	Contains protein domain (PF00285) - Citrate synthase		264887, 284259, 29331822, 29331824, 29331825, 265007, 285009, 264591, 33109954, 265010, 265019, 264389, 264288, 264886, 264691, 264693, 27486264, 18108370, 18108374, 263977, 55811576, 56182323, 264639, 22279000, 22279002, 264482
1862	87372923 (3723, 3724)	Novel Protein sim. GBank gi125493 sp P07313 KMLC_RABIT - MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35696286, 264259, 87188474, 264389, 21905766, 264558, 264563
1863	85775037 (3725, 3726)	Novel Protein sim. GBank gi3820909 emb CAA09299  - (AJ010842) Dof protein [Drosophila melanogaster]		UNCLASSIFIED	264801, 264766, 29148627, 29148629, 264692, 284628, 284635
1864	85547832 (3727, 3728)	Novel Protein sim. GBank gi4322263 gb AAD15985  - (AF077738) metalloproteinase CPX-1 [Mus musculus]	Contains protein domain (PF00754) - F5/8 type C domain	synthase	22278999, 284259, 284807, 265018, 18108370, 264634, 284635, 264555, 264556, 264638, 18108387
1865	87740827 (3729, 3730)	Novel Protein sim. GBank gi2495727 sp Q83073 Y256_HUMAN - HYPOTHETICAL PROTEIN KIAA0256			22278999, 284490, 29331822, 66714117, 66712502, 265006, 265007, 265008, 265009, 264591, 60433438, 265010, 265019, 284760, 264448, 264768, 29148627, 29148629, 265020, 265022, 18108385, 60432113
1866	87266816 (3731, 3732)	Novel Protein sim. GBank gi5282617 emb CAB45748.1  - (AL080157) hypothetical protein [Homo sapiens]		kinase	18108374, 264769, 18108377, 21908765, 21906766, 35698423, 56182575, 21908769, 29148629, 35698286, 35695917, 265021, 264510, 264511, 264512, 264534, 264535, 60170831, 52844150, 264555, 264691, 264259, 264556, 264692, 264557, 33657023, 60433356, 29331822, 264559, 264595, 29331824, 18108385, 21906754, 33657182, 29331827, 35698052, 33658970, 87188518, 265017, 60431602, 22279000, 284508, 284509, 18108351, 264907, 264682, 264567, 18108372, 264765, 264486
1867	84579159 (3733, 3734)	Novel Protein sim. GBank gi3859930 (AF078096) - forkhead/winged helix-like transcription factor 7 [Homo sapiens]		UNCLASSIFIED	264094



1868	87357459 (3735, 3736)	Novel Protein sim. GBank gij388152[emb]CA93884] - (Z70038) cDNA EST EMBL:D32579 comes from this gene; cDNA EST EMBL:D35254 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk357110.5 comes from this gene [Caenorhabditis elegans]		nuclease	264489, 22278997, 22278999, 29331825, 29331828, 265008, 265009, 33857402, 87168474, 18108351, 21908765, 21908768, 21908769, 265020, 265021, 60170615, 27486284, 264628, 18108374, 264631, 18108385, 87168518, 22278000, 22278002, 264569, 264587
1869	86977282 (3737, 3738)	Novel Protein sim. GBank gij4828772[ref]NP_004961.1[pl]GFA - Insulin-like growth factor binding protein, acid labile subunit	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264508, 264509, 264906, 264908, 264909, 264910, 264591, 264600, 18108351, 264683, 264766, 264769, 35695855, 264634, 264558, 264639, 18108385, 264583, 264486
1870	95349488 (3739, 3740)	Novel Protein sim. GBank gij1689859[emb]CAB06722] - (Z86099) very large tegument protein [human herpesvirus 2]		UNCLASSIFIED	29331824, 60424269, 265007, 265008, 21908754, 265017, 265018, 265019, 264288, 264766, 264886, 264888, 21908768, 21908769, 35695917, 60170615, 264692, 18108388, 35695763, 35698423, 65274791, 264638, 264639, 56526486
1871	80234464 (3741, 3742)			UNCLASSIFIED	264509, 264905, 264585, 264768, 264635, 264636, 264563, 264486
1872	80235355 (3743, 3744)	Novel Protein sim. GBank gij2460316 (AF022147) - uterus-ovary specific putative transmembrane protein [Rattus norvegicus]		protease	264510, 264594, 264565
1873	80213890 (3745, 3746)				
1874	95351136 (3747, 3748)		Contains protein domain (PF00293) - Bacterial mutT protein	UNCLASSIFIED	264509, 264512, 265009, 265011, 18108351, 264687, 264691, 18108370, 18108374, 264635
1875	87330516 (3749, 3750)	Novel Protein sim. GBank gij4589520[dbj]BAA76782.1] - (AB023155) KIAA0938 protein [Homo sapiens]		UNCLASSIFIED	264488, 35695917, 264259, 284905, 264907, 264908, 264909, 263978, 264511, 264635, 264636, 264637, 264638, 33657402, 264558, 18108385, 264600, 264604, 264764, 264587, 264766
1876	87112950 (3751, 3752)	Novel Protein sim. GBank gij263810[bbst]122920 - collagen alpha chain [Riftia pachyptila=tube worms, Peptide, 1027 aa]		UNCLASSIFIED	35698286, 264828, 264582, 264557, 264558
1877	87315208 (3753, 3754)	Novel Protein sim. GBank gij3983358[gb]AAC83924.1] - (AF102545) riboflavin binding protein precursor [Scaphiopus couchii]		UNCLASSIFIED	264259, 29331822, 60432289, 264908, 264909, 264604, 264764, 264288, 264769, 18108376, 264558, 264558, 264559, 18108385
				UNCLASSIFIED	264767, 264686, 264768, 263978, 264693, 264639, 265010, 264563, 264805, 264906, 264907

1878	95351056 (3755, 3756)	Novel Protein sim. GBank gij4510345[gbjAAD21434.1] - (AC006921) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF01428) - ubiquitin AN1-like Zinc finger	264569, 264488, 35696286, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 29146498, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 264512, 285008, 264910, 33657402, 264594, 264758, 55812038, 265011, 264602, 264760, 18108351, 264762, 264681, 264682, 264784, 264369, 264288, 264786, 264887, 264788, 264769, 21906766, 35695917, 265021, 60170815, 33857023, 264692, 264693, 33657109, 27486265, 264628, 18108370, 264629, 18108374, 35696423, 264634, 264635, 264555, 264638, 264639, 83373044, 18108385, 58526486, 87168518, 264563, 264584, 264566, 264486, 264567
1879	95310883 (3757, 3758)	Novel Protein sim. GBank gij4929843[gbjAAD34082.1]AF15184 - (AF151845) CGI-87 protein [Homo sapiens]	UNCLASSIFIED	264905, 264907, 264908, 265007, 264565, 264566
1880	91012978 (3759, 3760)	Novel Protein sim. GBank gij1550765[embjCAA69283] - (Y08026) Immune associated protein 38 [Mus musculus]	UNCLASSIFIED	264766, 264691, 264692, 83373044
1881	80214949 (3761, 3762)	Novel Protein sim. GBank gij83144[piljIB40505] - hypothetical protein - suis herpesvirus 1 (strain Indiana-Funkhouser or Becker)	UNCLASSIFIED	264508, 264905, 264908, 264909, 264910, 264762, 264687, 33657023, 264632
1882	86582450 (3763, 3764)	Novel Protein sim. GBank gij2384956 (AF022985) - No definition line found [Caenorhabditis elegans]		264908, 21906766, 18108370, 263974, 87168518
1883	94216817 (3765, 3766)	Novel Protein sim. GBank gij1351218[spjP47228]TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - homeobox LIM domain containing proteins	264908, 264910, 87168559, 21908766, 264636

1884	95310885 (3767, 3768)	Novel Protein sim. GBank gi 4829643 gb AACD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108394, 56181886, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264512, 265009, 264910, 264592, 264593, 33657402, 55812038, 264758, 55811388, 265010, 265011, 87168559, 264600, 265017, 264604, 265019, 264605, 264760, 55811150, 264761, 264682, 264763, 264683, 264764, 264288, 264369, 264768, 264886, 264768, 264769, 29148784, 35695917, 264890, 264881, 33657023, 264692, 264693, 33857109, 18108370, 264628, 60431528, 264629, 263973, 18108374, 55810764, 55811576, 35696423, 35695855, 264631, 264634, 60431850, 264637, 264638, 56182323, 264639, 18108382, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264565, 264566, 264488, 264567
1885	87644280 (3769, 3770)	Novel Protein sim. GBank gi 2507155 sp P37370 VRP1_YEAST - VERPROLIN		UNCLASSIFIED	56182575, 264259, 264905, 264909, 265008, 264598, 264766, 265020, 264628, 60431528, 264634, 55829486, 264080, 264563
1886	86674062 (3771, 3772)	Novel Protein sim. GBank gi 2854158 gb AAC02577.1  - (AF045641) No definition line found [Caenorhabditis elegans]			22278988, 22278999, 60432049, 264910, 265018, 264766, 21906768, 29148629, 264690, 264693, 264628, 264555, 264486
1887	94139139 (3773, 3774)	Novel Protein sim. GBank gi 5174421 ref NP_006023.1 pCPNE - copine VI (neuronal)	Contains protein domain (PF00168) - C2 domain	ATPase_associated	29331822, 29331824, 29331825, 29331826, 29331827, 264908, 265007, 264681, 264768, 29148627, 264693, 18108364, 35696423, 65274791, 35695855, 264632, 56182323, 264639, 264563
1888	87622804 (3775, 3776)	Novel Protein sim. GBank gi 3319931 emb CAC10841  - (Z98046) dJ1409.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens]	Contains protein domain (PF01454) - MAGE family		263978
1889	91255783 (3777, 3778)	Novel Protein sim. GBank gi 1083308 pr JA56559 - enhancer-trap-locus-1 protein - mouse (fragment)	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	264906, 55812038, 264758, 265010, 265018, 265019, 18108351, 264288, 21906765, 21908788, 21908769, 265021, 33657023, 33657109, 56182323, 83373044, 18108385, 22279000, 22279002
1890	87626705 (3779, 3780)	Novel Protein sim. GBank gi 4240185 db BAA74876.1  - (AB020860) KIAA0853 protein [Homo sapiens]		UNCLASSIFIED	18108398, 29147620, 264907, 265009, 264600, 265018, 18108351, 264288, 264688, 21908785, 21906768, 21906769, 264691, 264692, 264693, 264628, 18108370, 264636, 264556, 264404

1891	87013895 (3781, 3782)			UNCLASSIFIED	264686, 264768, 264687, 264692, 264693, 29331822, 29331824, 264508, 264905, 264806, 18108370, 264628, 264907, 264908, 264809, 18108378, 265007, 265008, 264910, 264632, 264591, 264639, 264596, 18108384, 265010, 265011, 264601, 264605, 264563, 264369
1892	87642825 (3783, 3784)	Novel Protein sim. GBank gl 5688535 gb BAA83051.1  - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	struct	22278985, 264509, 87168559, 18108351, 264448, 264682, 265020, 264693, 18108374, 22279000
1893	88533828 (3785, 3786)			tannin	264589, 65274572, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331826, 264906, 265006, 265008, 265009, 284592, 265018, 264681, 264448, 264683, 18108354, 264369, 264684, 264685, 264768, 264687, 264689, 21906788, 265020, 265022, 60170615, 52844150, 264690, 264691, 264692, 33857023, 264693, 33857109, 264628, 18108374, 35695855, 264630, 264632, 264634, 264557, 264558, 60170394, 18108381, 18108385, 22279000
1894	86989120 (3787, 3788)				264508, 264905, 264908, 264907, 264584, 264694, 264690, 264692, 264630, 264635, 264636, 264639, 264583
1895	87631891 (3789, 3790)	Novel Protein sim. GBank gl 5262574 emb CAB45729.1  - (AL080133) hypothetical protein [Homo sapiens]	Contains protein domain (PF00435) - Spectrin repeat		56182575, 264259, 60432289, 29331826, 264107, 264905, 264908, 264910, 60170831, 264736, 265010, 265018, 264448, 264288, 264768, 33857109, 264628, 55810784, 18108379, 264634, 58182323, 56526486
1896	85873555 (3791, 3792)		Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	264807, 265008, 264682, 264686, 21906768, 264629, 264631, 264634, 264555
1897	80585569 (3793, 3794)	Novel Protein sim. GBank gl 728836 sp P38193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		cadherin	264259
1898	87617637 (3795, 3796)	Novel Protein sim. GBank gl 127560 sp P23249 MV10_MOUSE - PROTEIN MOV-10		helicase	22278996, 22278998, 22278999, 29331824, 29331825, 60432289, 29331827, 35698052, 29331828, 265008, 265019, 264681, 264682, 264448, 264369, 52644229, 21906765, 21906766, 21906768, 21906769, 60170615, 55810764, 22279000
1899	86873087 (3797, 3798)	Novel Protein sim. GBank gl 2909819 (AF031548) - erythrocyte membrane glycoprotein Rh50 [Homo sapiens]	Contains protein domain (PF00909) - Ammonium Transporter Family	glycoprotein	264259, 264508, 264909, 60432229, 264769, 21906765, 21906769
1900	87641858 (3799, 3800)	Novel Protein sim. GBank gl 4102881 (AF017250) - vitellogenin precursor [Oreochromis aureus]		UNCLASSIFIED	264683

1901	95196647 (3801, 3802)	Novel Protein sim. GBank gij565859[sp]P38378[S61A_RAT PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	Contains protein domain (PF00242) - DNA polymerase (viral) N-terminal domain	transport	264488, 52644507, 52645156, 18108396, 52646365, 52646842, 18108397, 56182575, 22278994, 22278995, 56994075, 35696286, 22278997, 22278998, 264490, 60432049, 264259, 29331822, 52645080, 29331824, 29331825, 66714117, 29331826, 604322289, 29331827, 29331828, 35696052, 33656970, 29146498, 284906, 264907, 29331830, 264908, 52644045, 264909, 284112, 285006, 264512, 265008, 284910, 265009, 60170831, 60432229, 60433356, 33657402, 60433438, 55812038, 264758, 33108954, 21908754, 33657084, 52644296, 87168474, 265010, 285011, 87168558, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 52644229, 21908785, 21906786, 21908767, 21906769, 55811857, 35695917, 265020, 265021, 52644150, 18108362, 33657023, 264693, 263987, 33657109, 33657182, 27488264, 33657349, 35695763, 18108370, 18108376, 55811576, 35696423, 35695855, 60431850, 264636, 263981, 52644332, 60170394, 83373044, 18108385, 87168518, 60432113, 264584, 264107, 263976
1902	80202013 (3803, 3804)	Novel Protein sim. GBank gij426613[gb]/AAD20451] - (AF098796) SLM-1 [Mus musculus]		dna_ma_bind	
1903	87778554 (3805, 3806)	Novel Protein sim. GBank gij3747107 (AF095741) - unknown [Rattus norvegicus]		UNCLASSIFIED	264259, 29331825, 29331827, 264508, 264907, 265008, 60170831, 60433356, 60433438, 264759, 21906754, 264448, 264288, 265021, 265022, 33657023, 264693, 55811576, 264555, 264558, 22279000
1904	80434213 (3807, 3808)	Novel Protein sim. GBank gij1352911[sp]P47147[YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-NNF1 INTERGENIC REGION		struct	264509, 264905, 264906, 264907, 264908, 264909, 265007, 264910, 264688, 264768, 264687, 264769, 264693, 264628, 18108374, 264634, 264636, 264637, 264585
1905	95351140 (3809, 3810)	Novel Protein sim. GBank gij3043714[dbj]/BAA25521] - (AB011167) KIAA0595 protein [Homo sapiens]	Contains protein domain (PF00293) - Bacterial mutT protein		264488, 264768, 264789, 264689, 29148629, 35695917, 35696286, 264259, 264692, 18108362, 33657023, 29331824, 33657109, 29146499, 264508, 264509, 264905, 264906, 264907, 66712502, 264908, 264909, 35696423, 35695855, 264510, 264511, 264512, 264910, 264634, 264635, 264637, 264638, 33657402, 264758, 85658542, 264602, 264760, 264761, 264482, 264563, 264762, 264483, 264764, 264566, 264288, 264766
1906	12763822 (3811, 3812)			UNCLASSIFIED	264637

1907	95351144 (3813, 3814)	Novel Protein sim. GBank gi 4929585 gb AAD34053.1 AF15181 - (AF151816) CGI-58 protein [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	hydrolase	65274572, 22278996, 35696286, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 60424269, 29331828, 35696052, 264593, 60433356, 21906754, 55811386, 85658542, 87168559, 265018, 264681, 264682, 264684, 264288, 21906765, 21906766, 21906768, 265020, 265022, 264690, 52644150, 264692, 33657023, 264693, 33657109, 35695855, 264636, 264638, 60432113
1908	95313641 (3815, 3816)	Novel Protein sim. GBank gi 3986770 (AF109806) - NG22 [Mus musculus]		UNCLASSIFIED	264488, 65274572, 56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 60432289, 29331826, 29331827, 29331828, 29146499, 264905, 264906, 264907, 264908, 86712502, 264909, 56182435, 264510, 264511, 265008, 264910, 60170831, 264592, 60433356, 33657402, 264594, 60433438, 264596, 55812038, 33109954, 52646317, 265011, 265017, 264604, 265018, 265019, 264905, 55811150, 264681, 264448, 264288, 264686, 264688, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 55811857, 29148629, 35695917, 265020, 265022, 264691, 264692, 18108364, 65274820, 33657109, 33657349, 35695763, 18108374, 263978, 55810784, 55811576, 35696423, 65274791, 264631, 264632, 264556, 264557, 60170394, 56182323, 83373044, 18108385, 60432113, 22278000, 22278002, 264566, 264488
1909	85514505 (3817, 3818)	Novel Protein sim. GBank gi 2224653 dbj BAA20813  - (AB002354) KIAA0356 [Homo sapiens]		UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 264511, 264910, 264593, 264758, 264764, 264766, 18108370, 264634, 264637, 264486
1910	94216821 (3819, 3820)	Novel Protein sim. GBank gi 1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	35696286, 22278998, 22278999, 35696052, 264509, 264905, 264908, 264907, 264908, 264909, 264511, 265007, 264512, 264910, 264758, 265011, 264601, 264602, 264604, 264605, 264761, 264764, 264288, 264766, 264768, 264687, 264769, 35695917, 265021, 52644150, 264692, 264628, 18108370, 264629, 18108372, 18108374, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 18108385, 264565, 264566, 264486

1911	91725345 (3821, 3822)	Novel Protein sim. GBank gi 4809339 gb AAD30184.1 ACO06530 - (ACO06530) hypothetical protein [Homo sapiens]	Contains protein domain (PF01119) - DNA mismatch repair protein	nuclease	18108394, 56182575, 56182181, 29331828, 29331827, 33656970, 264906, 265007, 264591, 55812038, 87168559, 264448, 264369, 21806765, 21906768, 265022, 264691, 264693, 18108385, 55811576, 264556, 18108385, 18108388
1912	95413518 (3823, 3824)	Novel Protein sim. GBank gi 5689439 dbj BAA83003.1  - (AB028974) KIAA1051 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	18108397, 56182575, 56181686, 22278984, 22278985, 56984075, 22278996, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 66714117, 35696052, 264905, 264906, 264907, 264908, 52844045, 56182435, 265007, 265008, 264910, 265009, 264591, 264596, 65274444, 55811386, 87168474, 265011, 87168559, 265018, 265019, 264760, 18108351, 264681, 264369, 264684, 264288, 264686, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264692, 33657023, 264693, 18108376, 55811576, 35698423, 65274791, 264637, 56182323, 83373044, 56526486, 22278002, 264583, 264568
1913	95305546 (3825, 3826)	Novel Protein sim. GBank gi 5032245 ref NP_005665.1 pZNF2 - zinc finger protein (C2H2) homologous to mouse MOK-2			56182575, 22278984, 22278995, 56994075, 22278996, 22278998, 22278999, 29331828, 29331827, 265006, 55812038, 265010, 265017, 265018, 265019, 264681, 18108351, 264683, 264764, 264369, 264288, 264685, 264686, 264769, 21906765, 21906768, 21906768, 21906769, 55811957, 265020, 265022, 264891, 55811576, 264634, 264635, 264638, 56182323, 83373044, 18108385
1914	83423982 (3827, 3828)	Novel Protein sim. GBank gi 4589604 dbj BAA76824.1  - (AB023187) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	56182575, 29331824, 35696052, 264906, 264908, 264628, 264909, 264592, 264758, 87168559, 18108351, 18108354, 264684, 264686, 33657023, 264693, 264628, 264631, 264632, 264634, 264635, 264639
1915	95340459 (3829, 3830)	Novel Protein sim. GBank gi 5689415 dbj BAA82991.1  - (AB028962) KIAA1039 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331824, 29331826, 29331827, 264508, 264909, 265009, 265017, 265019, 264768, 264769, 264689, 264628, 264635, 264637, 264639, 83373044, 264565
1916	79640761 (3831, 3832)				264693, 264639

1917	87621680 (3833, 3834)	Novel Protein sim. GBank gij5689391[jdbj BAA82979:1] - (AB028850) KIAA1027 protein [Homo sapiens]		struct	264769, 264689, 21906765, 21906769, 22278996, 264259, 264691, 264693, 29331824, 29331825, 29331826, 29331828, 264905, 264906, 264628, 264907, 264908, 264909, 264510, 264630, 264910, 264634, 264635, 264636, 264637, 264638, 263981, 264639, 264758, 18108385, 21906754, 265011, 264604, 264563, 18108351, 264762, 264763, 264566, 264764, 264766
1918	95302785 (3835, 3836)	Novel Protein sim. GBank gij6281517[jgb AAD41524.1 AF15483] PV.1 [Rattus norvegicus]		struct	264488, 18108392, 18108357, 21906765, 21906767, 21906768, 56182575, 21906769, 22278994, 35696286, 35695917, 22278996, 22278997, 265021, 265022, 264534, 264680, 264691, 264692, 33657023, 264693, 29331824, 29331825, 33657109, 29331826, 52845129, 35698052, 29331828, 27486262, 27486264, 35695763, 284508, 264905, 264508, 264906, 264628, 264907, 18108370, 18108374, 263978, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264631, 265009, 264910, 264634, 264635, 264555, 264636, 264556, 264637, 264557, 264593, 264638, 264594, 60170394, 264595, 264558, 264596, 83373044, 264758, 52646317, 18108385, 52644286, 56526486, 87168518, 265010, 265011, 87168559, 264600, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 264760, 264761, 264482, 264564, 18108351, 264762, 264682, 264585, 264448, 264764, 264586, 264486, 264567, 264369, 264288, 264766, 264487, 264685
1919	94143847 (3837, 3838)	Novel Protein sim. GBank gij3878584[jemb CA501237] - (Z77667) cDNA EST EMBL:CO8125 comes from this gene; cDNA EST EMBL:CO9753 comes from this gene [Caenorhabditis elegans]		oxidase	22278997, 29331822, 265007, 60170831, 60432229, 80433438, 264448, 264682, 264286, 55811957, 33657023, 33657109, 65274781, 56182323, 22279002
1920	91229953 (3839, 3840)	Novel Protein sim. GBank gij1809231 (AC000115) - coded for by human cDNAs R76043 (NID:g850725), R65857 (NID:g838495) and H12668 (NID:g877688) [Homo sapiens]		UNCLASSIFIED	264510, 264511, 264512, 264566
1921	79555226 (3841, 3842)	Novel Protein sim. GBank gij4580987[jgb AAD24571.1 AF12108] cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	264693



1922	87641863 (3843, 3844)	Novel Protein sim. GBank gi 138595 sp P02845 VIT2_CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP40]		UNCLASSIFIED	264686, 264688, 264490, 18108370, 264909, 18108374, 265008, 264557, 264564, 18108351
1923	84323589 (3845, 3846)	Novel Protein sim. GBank gi 119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	264488, 264489, 22278995, 264094, 264259, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264908, 264511, 264512, 265007, 264910, 265008, 264591, 264592, 264593, 264594, 264595, 264758, 264596, 264759, 265011, 265017, 265018, 265019, 55811150, 264681, 264762, 264448, 264764, 264288, 264369, 264766, 264767, 264686, 264687, 264768, 264769, 56181562, 264689, 21908766, 264691, 33657023, 264693, 65274620, 33657109, 18108370, 264628, 264629, 35696423, 264630, 264631, 264632, 264634, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264564, 264585, 264568, 264567, 29331826, 264806, 264908, 264595, 265017, 265018, 265019, 265021, 264691, 264693, 264637, 18108385, 264565
1924	87338925 (3847, 3848)	Novel Protein sim. GBank gi 3877655 emb CAA96657  - (Z72511) possible zinc finger protein; cDNA EST EMBL:M89115 comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST EMBL:D75164 comes from this gene; cDNA EST EMBL:G1...	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		
1925	87628338 (3849, 3850)	Novel Protein sim. GBank gi 4981803 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomalprot	22278995, 22278996, 22278997, 264259, 29331824, 68714117, 29148499, 264909, 52644045, 265008, 265009, 264758, 265011, 265017, 264605, 264448, 264288, 264892, 35657109, 18108374, 60170394
1926	88094739 (3851, 3852)	Novel Protein sim. GBank gi 2246532 U93872  - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		struct	264905, 264906, 264907, 264910, 264593, 265018, 264760, 264764, 264288, 264692, 264893, 263978, 264631, 264634, 264637, 264563
1927	85654857 (3853, 3854)	Novel Protein sim. GBank gi 3043632 dbj BAA25480  - (AB011126) KIAA0554 protein [Homo sapiens]			264689, 264631
1928	87798054 (3855, 3856)	Novel Protein sim. GBank gi 1665761 dbj BAA13371  - (D87433) KIAA0246 [Homo sapiens]	Contains protein domain (PF00193) - Inf	Inf	264489, 264259, 265017, 265021, 264692
1929	86997238 (3857, 3858)	Novel Protein sim. GBank gi 5001993 gb AAD37247.1 AF13432 - (AF134321) chimeric AFGP/hypsinogen-like serine protease precursor [Dissostichus mawsoni]	Extracellular link domain	UNCLASSIFIED	264508, 264591, 33657402, 265017, 264768, 264632, 264556, 264639

1830	87889128 (3859, 3860)	Novel Protein sim. GBank gi 1709230 sp P52963 NBL4_MOUSE - NBL4 PROTEIN		phosphatase	35686286, 29331828, 264905, 264907, 264908, 264909, 264511, 264910, 264758, 264601, 265017, 265019, 264805, 264760, 264764, 264766, 264686, 264769, 265022, 35698423, 284638, 60432113
1831	87797279 (3861, 3862)	Novel Protein sim. GBank gi 404634 (U01840) - serine/threonine kinase [Mus musculus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264906, 60432229, 264758, 264784, 264288, 265020, 264692, 264634, 264637, 264684, 264691, 264635
1832	15030972 (3863, 3864)			UNCLASSIFIED	264595
1833	11613668 (3865, 3866)	Novel Protein sim. GBank gi 4115748 db BAA36494  - (AB022023) nonmuscle myosin heavy chain B [Bos taurus]		struct	56182575, 56182435, 284510, 264757, 264758, 55812038, 55811388, 265018, 55811150, 21908765, 264691, 284631, 264635, 264637
1834	84426360 (3867, 3868)			UNCLASSIFIED	264686, 265011, 264511, 264805, 18108351, 264564, 264681, 264259, 18108370, 284566, 264764, 264359, 264595
1835	87752511 (3869, 3870)			UNCLASSIFIED	60432288, 265007, 265010, 265011, 285019, 33657109, 18108374
1836	85414338 (3871, 3872)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit		kinase	85658542, 21906767, 35685917, 60170615, 264693, 33657109
1837	94847141 (3873, 3874)	Novel Protein sim. GBank gi 543187 pir S37771 - ankyrin, erythrocyte - mouse	Contains protein domain (PF00023) - Ank repeat	kinase	264488, 29146498, 264905, 264559
1838	87403277 (3875, 3876)	Novel Protein sim. GBank gi 4544431 gb AAD22340.1 AC00695 - (AC006955) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00888) - Cullin family	collagen	
1839	91004978 (3877, 3878)	Novel Protein sim. GBank gi 500858 db BAA03210  - (D14168) 50kDa lectin [Bombyx mori]		UNCLASSIFIED	65274572, 22278999, 60432289, 56182435, 60433356, 265017, 21908765, 21908768, 21908768, 55811957, 27486264, 35696423, 60432113, 264564
1840	87348810 (3879, 3880)	Novel Protein sim. GBank gi 1946300 emb CAA73132  - (Y12529) hypothetical protein [Silene latifolia]	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	264488, 29331822, 264448, 264683, 264288, 265020, 33657023, 264631
1841	9417177 (3881, 3882)	Novel Protein sim. GBank gi 4206386 (AF060570) - rig-1 protein [Mus musculus]		UNCLASSIFIED	56994075, 22278998, 264259, 29331824, 29331827, 264905, 265008, 33657084, 265017, 265018, 264288, 264687, 21908765, 21908766, 21906767, 265020, 52644150, 27486284, 83373044, 18108387, 60432113, 22279002, 264565
1842	87641870 (3883, 3884)	Novel Protein sim. GBank gi 4927204 gb AAD33049.1 AF13391 - (AF13391) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	264488, 18108398, 29331825, 27486261, 264509, 18108370, 18108374, 264482
1843	94325298 (3885, 3886)	Novel Protein sim. GBank gi 3122952 sp O15736 TIPD_DICD1 - TIPD PROTEIN	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	22278988, 29331822, 29331827, 35696052, 264511, 265009, 264592, 60432229, 265017, 265018, 285019, 264684, 264692, 33657108, 65274791, 264638

1944	84232858 (3887, 3888)	Novel Protein sim. GBank gi 1799570 dbj BAA13432  - (D8787.1) TIP120 [Rattus norvegicus]		UNCLASSIFIED	65274572, 22278994, 22278995, 22278996, 22278998, 22278999, 264259, 52645080, 29331824, 29331826, 29331827, 66712502, 56182435, 264512, 264910, 60170831, 60432229, 60433356, 33657402, 60433438, 264596, 33109954, 21906754, 87168474, 87168559, 285017, 285018, 265019, 18108351, 264369, 264688, 264768, 21906765, 21908766, 21908767, 21906769, 35695917, 265020, 265021, 60170615, 264692, 33657023, 18108370, 18108374, 35696423, 35695855, 264634, 60170394, 264639, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264563
1945	87641872 (3888, 3889)	Novel Protein sim. GBank gi 4927204 gb AAD33049.1 AF13391 - (AF13391) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	264488, 22278996, 264510, 264511, 18108351, 264683, 264486, 264567
1946	87443880 (3891, 3892)	Novel Protein sim. GBank gi 2498104 sp Q27969 AD50_BOVIN - ADRENAL MEDULLA 50 KD PROTEIN		UNCLASSIFIED	60432289, 29331827, 35696052, 265007, 265008, 60433356, 60433438, 264369, 56181562, 21908767, 52644150, 264693, 27486264, 264637, 87168518, 264563
1947	86438862 (3893, 3894)	Novel Protein sim. GBank gi 3914801 sp Q54888 PPA2_RAT - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)		mapolymerase	22278998, 264905, 264906, 264908, 264809, 264512, 264758, 264762, 264682, 264683, 264764, 264288, 264768, 264688, 21908768, 264683, 18108374, 35695855, 264635, 264637, 264638, 18108385, 22279002
1948	95169174 (3895, 3896)	Novel Protein sim. GBank gi 5420387 emb CAB46678.1  - (AJ243459) proteophosphoglycan [Leishmania major]		struct	264909, 60170831, 264591, 264594, 235010, 265011, 264764, 264369, 264689, 264631, 264638
1949	7640129 (3897, 3898)	Novel Protein sim. GBank gi 3876766 emb CAA83466.1  - (Z69837) predicted using GeneFinder; Similarity to E. coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]	Contains protein domain (PF00857) - Isochorismatase family	UNCLASSIFIED	264369
1950	87786531 (3898, 3899)	Novel Protein sim. GBank gi 2626753 dbj BAA23424  - (AB008782) sulfate transporter [Arabidopsis thaliana]	Contains protein domain (PF00816) - Sulfate transporter family	transport	264488, 264768, 264688, 264689, 264259, 29331822, 33657109, 29331828, 264103, 264509, 18108370, 35695855, 264510, 265008, 265009, 33657402, 18108385, 265018, 264563, 55811150, 18108351, 264369, 264288, 18108354
1951	86988253 (3901, 3902)	Novel Protein sim. GBank gi 4928633 gb AAD34077.1 AF15184 - (AF15184) CGI-82 protein [Homo sapiens]	Contains protein domain (PF00106) - short chain dehydrogenase	reductase	56182575, 22278997, 52645080, 29331824, 29331825, 29331827, 55812038, 52646317, 265018, 265019, 264369, 21906765, 21906767, 55811857, 265020, 265021, 33657023, 264693, 35695763, 56182323, 22279002
1952	87069775 (3903, 3904)	Novel Protein sim. GBank gi 4928633 gb AAD34077.1 AF15184 - (AF15184) CGI-82 protein [Homo sapiens]	Contains protein domain (PF00106) - short chain dehydrogenase	reductase	264591, 264593, 264594, 264595, 264555, 264556, 264557, 264558, 264565

1953	20470371 (3905, 3906)	Novel Protein sim. GBank gjl1168715[sp]P31721[C1QB_RAT - COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR (AB020698)] KIAA0891 protein [Homo sapiens]	Contains protein domain (PF00386) - C1q domain	complement	264259, 264558 264488, 263994, 18108394, 35698288, 22278998, 29331822, 66714117, 29331828, 29331827, 264508, 264509, 264905, 264806, 264907, 264908, 264909, 264510, 265008, 265007, 265008, 264810, 265009, 60170831, 60432228, 265011, 265017, 264603, 264604, 265019, 18108351, 264885, 264786, 264789, 35695817, 265020, 265021, 264691, 33857023, 264692, 33857109, 264628, 18108374, 35698423, 55811576, 35695855, 264630, 264635, 264636, 264555, 264556, 264638, 264557, 264639, 264558, 264559, 83373044, 18108385, 264563, 264564, 264566, 264488, 264567
1954	91226025 (3907, 3908)	Novel Protein sim. GBank gjl4240271[dbj]BAA74914.1] - (AB020698)] KIAA0891 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	264259, 29331822, 56182181, 29331824, 29331825, 29331828, 29331827, 35696052, 264508, 29331830, 265008, 265009, 264591, 55812038, 87168474, 265017, 265018, 265019, 264448, 264766, 21906765, 21906768, 21906767, 55811957, 265020, 265021, 52645129, 33657109, 27486264, 33657349, 35695763, 60431528, 18108374, 55811576, 35695855, 264635, 60431850, 264639, 83373044
1955	95308310 (3909, 3910)			UNCLASSIFIED	56182575, 56181686, 22278994, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331828, 29331827, 35696052, 264508, 29331830, 265008, 265009, 264591, 55812038, 87168474, 265017, 265018, 265019, 264448, 264766, 21906765, 21906768, 21906767, 55811957, 265020, 265021, 52645129, 33657109, 27486264, 33657349, 35695763, 60431528, 18108374, 55811576, 35695855, 264635, 60431850, 264639, 83373044
1956	95092121 (3911, 3912)	Novel Protein sim. GBank gjl1665821[dbj]BAA134071 - (D87469) Similar to D.melanogaster cadherin-related tumor suppressor [Homo sapiens]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264488, 56182575, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264508, 264906, 264908, 264909, 264511, 265007, 264910, 264591, 55812038, 265010, 265018, 18108351, 264768, 56181562, 264689, 21906768, 21906769, 265022, 264691, 264628, 18108374, 55810764, 55811576, 35695855, 264631, 264632, 264635, 264637, 264639, 60170394, 56182323, 83373044, 18108385, 22278999, 22279002, 264563, 264564

1857	94326510 (3913, 3914)	Novel Protein sim. GBank gi 4589674 dbj BAA76856.1  - (AB023229) KIAA1012 protein [Homo sapiens]		UNCLASSIFIED	52646842, 56182575, 22278997, 22278998, 22278999, 29331824, 66714117, 29331827, 29146498, 264593, 33657402, 33109954, 87168474, 265018, 264448, 264369, 264288, 264766, 21908766, 21908767, 21906768, 21906769, 265020, 265021, 264692, 65274620, 27486264, 33857349, 27486265, 35695855, 22279002, 264482
1858	95313902 (3915, 3916)	Novel Protein sim. GBank gi 4240227 dbj BAA74892.1  - (AB020676) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	22278998, 264092, 264094, 264259, 60432049, 29331824, 56182181, 66714117, 264107, 264109, 264909, 264511, 60170831, 60432229, 21906754, 265010, 21908769, 35695917, 265022, 65274620, 263987, 263976, 35698423, 264631, 264632, 264634, 264635, 18108385, 22279000, 22279002, 264593, 265019
1859	85701470 (3917, 3918)	Novel Protein sim. GBank gi 2281983 emb CAB10860  - (Z98056) hyppothetical protein [Schizosaccharomyces pombe]		ubiquitin	
1860	80308608 (3919, 3920)	Novel Protein sim. GBank gi 2274851 dbj BAA21515  - (D64159) 3-7 gene product [Homo sapiens]		struct	264905, 264806, 264907, 264908, 264909, 265006, 265007, 264910, 264595, 265017, 264604, 265018, 18108351, 264764, 264369, 264766, 264768, 21908765, 18108368, 264628, 18108379, 264635, 264636, 264637, 264638, 264486
1861	16292607 (3921, 3922)				264635
1862	91008385 (3923, 3924)			UNCLASSIFIED	65274572, 264592, 264593, 265019, 264691
1863	80936017 (3925, 3926)	Novel Protein sim. GBank gi 3721653 dbj BAA33581  - (AB012933) acyl-CoA synthetase 5 [Rattus norvegicus]		eph	65274572, 18108398, 35696286, 29331825, 60432289, 29331827, 264828, 265006, 265008, 60433356, 60433438, 21908754, 265020, 265021, 33657023, 33657109, 27486285, 35695855, 264555
1864	94317605 (3927, 3928)	Novel Protein sim. GBank gi 5262638 emb CAB45757.1  - (AL080169) hypothetical protein [Homo sapiens]		cadherin	264488, 264092, 264259, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 265007, 265009, 264910, 264592, 264593, 264594, 264595, 264758, 264600, 264603, 264604, 264605, 264760, 264762, 264448, 264764, 264288, 264885, 264766, 264768, 264769, 21906766, 264691, 264692, 264693, 18108370, 264628, 264629, 18108374, 264630, 264631, 264634, 264636, 264637, 264638, 18108382, 83373044, 18108385, 264483, 264564, 264565, 264566, 264486, 264567
1865	94317445 (3929, 3930)	Novel Protein sim. GBank gi 4107017 dbj BAA36294  - (AB001773) PEM-6 [Ciona savignyi]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264488, 264510, 264760, 264768, 264486

1866	94192058 (3931, 3932)	Novel Protein sim. GBank gij4929707[gb AAD34114.1 AF15187 - (AF151877) CGI-119 protein [Homo sapiens]	Contains protein domain (PF01027) - glycoprotein Uncharacterized protein family	22278999, 264092, 264259, 29331826, 29331828, 28146498, 264595, 265011, 264448, 18108354, 264288, 264684, 264766, 264685, 264688, 265022, 264691, 264692, 18108370, 18108377, 264555, 18108381, 18108385, 264486, 264587
1867	87398123 (3933, 3934)	Novel Protein sim. GBank gij2957270 (AF044576) - phospholipase C PLC210 [Caenorhabditis elegans]	Contains protein domain (PF00388) - Phosphatidylinositol-specific phospholipase C, X domain	29331824, 265010, 265017, 264288, 21906764, 263981, 56526486
1868	88095641 (3935, 3936)	Novel Protein sim. GBank gij2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	35688286, 264805, 264509, 264908, 264907, 284908, 264909, 264511, 264512, 265008, 284910, 265009, 264594, 264757, 264758, 264604, 264605, 264760, 264762, 264682, 264764, 264685, 264766, 264767, 264689, 264691, 264693, 264628, 264629, 35688423, 35695855, 264631, 284632, 264634, 264635, 264636, 264637, 18108380, 264584, 264585, 264586, 264587
1869	84328529 (3937, 3938)	Novel Protein sim. GBank gij2911274 (U20329) - spidroin 1 [Nephila clavipes]	UNCLASSIFIED	22278995, 22278996, 35696052, 264906, 264908, 18108351, 264482
1870	80596049 (3939, 3940)	Novel Protein sim. GBank gij4050087 (AF109907) - S164 [Homo sapiens]	UNCLASSIFIED	264808, 264288, 264766, 264636
1871	94843914 (3941, 3942)	Novel Protein sim. GBank gij134208[sp P09583 SANT_PLAFV - S-ANTIGEN PROTEIN PRECURSOR	collagen	264488, 264489, 22278998, 264259, 60432049, 66714117, 29331826, 60432289, 29331827, 35698052, 264508, 264905, 264509, 264806, 264807, 264908, 264909, 264510, 264511, 264512, 264910, 264591, 264592, 60432229, 60433356, 264595, 264596, 264600, 264604, 264605, 264760, 18108351, 264448, 264764, 264288, 264766, 264768, 264769, 21908765, 33657023, 264692, 18108370, 264629, 35696423, 65274791, 35695855, 264632, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 60432113, 22278000, 264583, 264584, 264565, 264586, 264486
1872	87645444 (3943, 3944)	Novel Protein sim. GBank gij4519623[dj BAA75671.1 ] - (AB017616) homologous to the yeast YGR163 gene [Mus musculus]	Contains protein domain (PF01462) - Leucine rich repeat N-terminal domain	22278999, 264259, 29331822, 56182181, 60432289, 29331827, 52844045, 264909, 265006, 264511, 265008, 52844296, 265018, 265019, 264761, 264688, 21908768, 21908769, 264691, 264693, 33657109, 33657182, 264556, 52644332, 264558, 60432113
1873	86395533 (3945, 3946)		UNCLASSIFIED	29331828, 264692, 35696423, 264631, 264555, 264556, 264557, 264558, 264559
1874	80396629 (3947, 3948)	Novel Protein sim. GBank gij3308543 (AF036382) - MLL [Fugu rubripes]	UNCLASSIFIED	264682, 264764, 264583

1984	85760889 (3967, 3968)	Novel Protein sim. GBank gij2896695[embjCAA17174.1] - (AL021897) fadD14 [Mycobacterium tuberculosis]		synthase	264688, 21906766, 55811857, 56994075, 265020, 265021, 22278999, 265022, 264259, 29331822, 33657182, 29146499, 264628, 18108370, 264908, 264628, 55811576, 35695855, 265006, 285007, 264591, 21908754, 33657084, 265010, 265017, 265019, 264288
1985	85636897 (3969, 3970)	Novel Protein sim. GBank gij5712131[gbjAAD47379.1]AF12049 - (AF120499) DEM1 protein [Homo sapiens]		glycoprotein	264760, 264288, 263978, 55811576, 264637, 56182323, 18108385, 264584
1986	80200507 (3971, 3972)	Novel Protein sim. GBank gij4868443[gbjAAD31319.1]AF14457 - (AF144573) Mx-Interacting protein kinase PKM [Mesocricetus auratus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	UNCLASSIFIED	264488, 264629
1987	87011117 (3973, 3974)	Novel Protein sim. GBank gij4868443[gbjAAD31319.1]AF14457 - (AF144573) Mx-Interacting protein kinase PKM [Mesocricetus auratus]			22278999, 29331830, 265007, 265018, 21908768, 33657023, 264692, 264693, 18108377, 264635, 60170394, 22279002
1988	94122108 (3975, 3976)			UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264910, 264591, 264593, 264758, 264764, 264686, 264768, 265021, 264692, 264628, 264628, 35695855, 264630, 264635, 264636, 264637, 264638, 264639, 264483
1989	91225225 (3977, 3978)	Novel Protein sim. GBank gij2801701 (AF042379) - spindle pole body protein spc87 homolog GCP2 [Homo sapiens]		tubulin	60432049, 60432289, 52644045, 56182435, 264112, 265007, 33657402, 52644229, 21908765, 21908768, 21908769, 55811957, 33657023, 263967, 33657109, 18108370, 22279000, 22279002
1990	85698888 (3979, 3980)	Novel Protein sim. GBank gij5707127[dbjBAA83074.1] - (AB024729) alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homologue [Homo sapiens]			264508, 264757, 264764, 18108381
1991	95353114 (3981, 3982)	Novel Protein sim. GBank gij4240287[dbjBAA74922.1] - (AB020708) KIAA0899 protein [Homo sapiens]	Contains protein domain (PF01602) - Adaptin N terminal region	glycoprotein	18108394, 56182575, 22278994, 35696286, 56994075, 22278997, 22278999, 29331822, 29331824, 29331825, 60432289, 29331828, 264508, 264906, 264907, 264908, 56182435, 264510, 265007, 21908754, 33109954, 87168474, 265017, 265018, 265019, 264762, 18108351, 264763, 264683, 264369, 264288, 264685, 264766, 264687, 264769, 21908765, 21908768, 21908769, 55811857, 265020, 60431528, 263974, 18108379, 35695855, 264555, 264557, 264638, 83373044, 18108384, 87168518, 60432113, 22279000, 22279002, 264584, 264486
1992	95317232 (3983, 3984)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	struc	29331827, 264906, 264907, 264909, 265007, 264603, 264766, 264686, 264768, 21908768, 264628, 264635, 264638, 18108385, 56526486, 264566, 264567
1993	80054763 (3985, 3986)	Novel Protein sim. GBank gij2565091 (U80761) - CTG26 alternate open reading frame [Homo sapiens]		UNCLASSIFIED	264592, 35696423

1975	84316479 (3949, 3950)			UNCLASSIFIED	264488, 66714117, 29331826, 29331828, 58182435, 265006, 264757, 55812038, 265010, 265017, 264369, 55811957, 65274781, 35895855, 58182323, 60432113
1976	95358914 (3951, 3952)			UNCLASSIFIED	264259, 35696052, 265018, 265020, 265021, 35657109, 56526486
1977	94852664 (3953, 3954)	Novel Protein sim. GBank gi 249528 sp Q07782 NASU_RAT - SODIUM/SULFATE COTRANSPORTER (NA(+)/SULFATE COTRANSPORTER)		homeobox	264908, 264596, 265021, 264566
1978	87447645 (3955, 3956)	Novel Protein sim. GBank gi 103421 pri A33471 - transcription factor NTF1 - fruit fly (Drosophila melanogaster) (fragment)		transcription factor	60170831, 264566
1979	87627708 (3957, 3958)	Novel Protein sim. GBank gi 2244815 emb CAB10238.1  - (Z97336) hypothetical protein (Arabidopsis thaliana)		UNCLASSIFIED	29331826, 29146498, 264905, 264907, 265007, 265009, 265010, 265018, 264886, 18108359, 21906768, 35695917, 265020, 60170615, 264693, 18108368, 18108370, 264631, 264635, 264556, 264558, 18108384, 22279000, 264565
1980	86577059 (3959, 3960)	Novel Protein sim. GBank gi 4759280 ref NP_004642.1 pUSP1 - Ubiquitin carboxyl- terminal hydrolase, X-linked		ubiquitin	264489
1981	87606974 (3961, 3962)	Novel Protein sim. GBank gi 4406693 gb AAD20060  - (AF131848) Unknown [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331825, 29331826, 29146498, 29146499, 264107, 264906, 264910, 264595, 21906754, 265010, 265017, 265018, 265019, 264448, 264288, 21906767, 33657023, 27486284, 18108370, 18108374, 18108376, 264630, 264631, 264635, 18108385, 87168518, 22279000, 264482, 264564
1982	90995387 (3963, 3964)	Novel Protein sim. GBank gi 5689523 dbj BAA83045.1  - (AB029016) KIAA1093 protein [Homo sapiens]			65274572, 29331825, 35696052, 33656970, 264909, 265008, 55811386, 284780, 264686, 264691, 27486264
1983	95098688 (3965, 3966)	Novel Protein sim. GBank gi 3417297 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcription factor	22278996, 35696286, 264259, 29331822, 20281099, 29331824, 60432289, 29331827, 264508, 264905, 264906, 264907, 66712502, 264908, 52844045, 264909, 264510, 264512, 264910, 265009, 264591, 264592, 60433356, 60433438, 264758, 265010, 264600, 264603, 264604, 264760, 264762, 264763, 264764, 264766, 264687, 264768, 264769, 21906765, 55811957, 35695917, 264690, 264692, 264693, 264628, 264629, 263978, 18108379, 35696423, 35695855, 20281071, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 83373044, 18108385, 22279000, 22279002



1984	94329114 (3987, 3988)	Novel Protein sim. GBank gi 5630077 gb AAD45822.1 AC00601 - (AC006017) similar to ALR; similar to AAC51735 (PID:g2358287) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	inapolymerase	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 264908, 265006, 60432229, 33657402, 60433356, 264757, 60433438, 264758, 33109954, 265011, 265017, 265018, 265019, 264684, 264368, 264685, 264686, 264768, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 18108362, 264693, 65274620, 18108370, 264635, 264555, 264556, 264557, 56182323, 83373044, 56528488, 22279000, 22279002, 264564
1995	95414353 (3989, 3990)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit		UNCLASSIFIED	264488, 18108396, 22278994, 56994075, 22278996, 35696286, 22278997, 22278999, 264258, 29147620, 56182181, 29331824, 60432289, 29331828, 29331827, 35696052, 29146499, 264905, 264907, 66712502, 56182435, 265006, 265007, 265008, 265009, 60431735, 60433356, 33657402, 264595, 55812038, 33657084, 55811386, 55858542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 56181562, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 21906769, 29148629, 29148784, 265020, 265021, 264690, 18108361, 264693, 27486262, 27486264, 27486265, 18108370, 60431528, 18108374, 18108377, 35696423, 55811576, 65274791, 35695855, 264631, 264634, 264635, 264555, 264636, 60431850, 264557, 264558, 264559, 83373044, 20798451, 87188518, 264404, 60432113, 264567 264564
1996	80254186 (3991, 3992)	Novel Protein sim. GBank gi 791146 emb CAA60020  - (X86028) extensin-like protein [Vigna unguiculata]		UNCLASSIFIED	
1997	87028423 (3993, 3994)	Novel Protein sim. GBank gi 2642034 (AF034547) - protein phosphatase M130 myosin binding subunit [Ovis aries]	Contains protein domain (PF00023) - Ank repeat	phosphatase	264908, 264908, 264592, 264593
1998	85262704 (3995, 3996)	Novel Protein sim. GBank gi 459834 dbj BAA76839.1  - (AB023212) KIAA0995 protein [Homo sapiens]		UNCLASSIFIED	264113, 264685, 264555, 264567

1999	94324803 (3987, 3988)	Novel Protein sim. GBank gij5225312[gb]AAD40846.1[AF072441] calicheurin binding protein cabin 1 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	UNCLASSIFIED	18108394, 18108397, 35696286, 60424269, 29331827, 29331828, 35696052, 265006, 264512, 55811386, 265010, 265018, 265019, 55811150, 18108351, 264763, 264682, 264369, 264685, 264686, 56181592, 265020, 264691, 33657023, 264693, 33657109, 27466264, 18108370, 18108379, 35695855, 264634, 264635, 264636, 264555, 264557, 56182323, 18108382, 264559, 83373044, 60432113, 22278000, 264563, 264564, 264566
2000	95413705 (3999, 4000)	Novel Protein sim. GBank gij1723232[sp]Q10155[YATA_SCHPO - HYPOTHETICAL 90.6 KD PROTEIN C1D4.10 IN CHROMOSOME I		UNCLASSIFIED	52646365, 52646842, 22278994, 22278995, 22278998, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 28331822, 28331826, 29331827, 29331828, 35696052, 264106, 29331830, 52644045, 265007, 265008, 60170831, 264592, 264593, 33657402, 60433438, 21906754, 52644266, 265017, 265018, 265019, 264761, 264369, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 33657023, 65274620, 52645129, 27466261, 27466262, 27466264, 35695763, 35696423, 35695855, 264631, 52644332, 56182323, 60170394, 83373044, 56528486, 22278002, 264586, 264587
2001	95072534 (4001, 4002)	Novel Protein sim. GBank gij107560[pri]B38637 - Ras inhibitor (clone JC285) - human (fragment)		UNCLASSIFIED	264769, 52644229, 65274572, 21906768, 22278996, 35696286, 35695917, 265020, 22278999, 264534, 264490, 264259, 264692, 60432289, 33657109, 35696052, 264508, 264509, 18108370, 60431528, 18108374, 35696423, 65274791, 35695855, 264510, 264511, 264512, 265009, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 60433438, 83373044, 264759, 18108385, 265011, 264600, 264601, 60432113, 264603, 264604, 264605, 264448, 264288, 264765
2002	80236368 (4003, 4004)	Novel Protein sim. GBank gij729433[sp]P38657[ER60_BOVIN - PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (ERP60) (58 KD MICROSOMAL PROTEIN) (P58)	Contains protein domain (PF00085) - Thioredoxin	isomerase	264907, 265006, 264910, 264603, 264692, 264629, 18108374, 264556, 264557
2003	80074449 (4005, 4006)	Novel Protein sim. GBank gij86388[pri]A27040 - neurofilament triplet M protein - chicken (fragment)		UNCLASSIFIED	264905, 264906, 264908, 264910, 264596, 265017, 18108351, 264692, 264629, 264634, 264565

2004	95317318 (4007, 4008)	Novel Protein sim. GBank gi 4884249 emb CAB43230.1  - (AL048988) hypothetical protein [Homo sapiens]	Contains protein domain (PF000076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	52645158, 52646842, 52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 35698286, 22278997, 22278998, 22278999, 60432049, 284259, 52845080, 29331824, 29331826, 29331827, 35698052, 29331828, 33656970, 29331830, 264908, 264592, 60433356, 33657402, 52846317, 21906754, 33657084, 52844298, 87188474, 87168559, 265017, 265018, 265019, 264763, 264683, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 18108374, 18108376, 18108377, 35696423, 35695855, 264631, 52644332, 264558, 18108385, 56526486, 87168518, 60432113, 264483, 264488, 264908
2005	87400664 (4009, 4010)	Novel Protein sim. GBank gi 3878950 emb CAA87795  - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33985 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...		ubiquitin	
2006	95351177 (4011, 4012)	Novel Protein sim. GBank gi 4106873 emb CAA22613  - (AL035064) queuine trna-ribosyltransferase [Schizosaccharomyces pombe]	Contains protein domain (PF01702) - Queuine tRNA-ribosyltransferase	UNCLASSIFIED	56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 56182181, 60424269, 86714117, 35698052, 264906, 66712502, 264909, 264510, 60433356, 85658542, 265010, 265018, 265019, 264682, 264448, 264288, 264768, 29148627, 21906769, 29148784, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 55810764, 55811576, 35695855, 87168518, 60432113, 264563, 264482, 264488, 263994, 35698052, 264508, 264905, 264906, 264907, 264908, 264909, 265007, 264910, 264592, 264595, 264758, 265011, 264760, 264762, 264764, 264766, 264685, 264767, 264768, 264769, 55811957, 35695917, 265020, 264691, 264693, 264628, 264629, 65274791, 35695855, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 264566
2007	94325558 (4013, 4014)	Novel Protein sim. GBank gi 2662161 db BAA23712  - (AB007900) HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]		UNCLASSIFIED	
2008	85084428 (4015, 4016)	Novel Protein sim. GBank gi 150783 emb CAA69257  - (Y07960) homeodomain protein [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264909, 264768, 35695855

2009	85749240 (4017, 4018)	Novel Protein sim. GBank gji3882305[dbj BAA34512.1] - (AB018335) KIAA0792 protein [Homo sapiens]		UNCLASSIFIED	22278998, 264259, 264910, 264591, 265017, 264681, 264683, 21906768, 264691, 33657182, 33657349, 264631, 87168518, 264404, 22279002, 264563
2010	95422458 (4019, 4020)	Novel Protein sim. GBank gji5262829[emb CAB45753.1] - (AL080184) hypothetical protein [Homo sapiens]	Contains protein domain (PF00057) - eph Low-density lipoprotein receptor domain class A		52644507, 52645156, 52646365, 52646842, 18108397, 65274572, 22278994, 56994075, 35695286, 22278996, 22278997, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264511, 265007, 264512, 265008, 265009, 60432229, 60433356, 21906754, 52646317, 33109954, 52644298, 87168474, 87168559, 265017, 265018, 265019, 264681, 264685, 264687, 52644229, 264689, 21908785, 21908768, 21908767, 21908788, 35695917, 265020, 52644150, 264691, 264692, 33657023, 263967, 52645129, 35695763, 18108376, 35698423, 65274791, 35695855, 264631, 264634, 60431850, 264637, 264638, 52644332, 60170394, 18108385, 87168518, 22279002, 264584, 264585, 264586, 264567
2011	94328149 (4021, 4022)	Novel Protein sim. GBank gji3347953 (AF076183) - cytosolic sorting protein PACS-1a [Rattus norvegicus]		UNCLASSIFIED	56182575, 56994075, 22278999, 264259, 29331824, 29331826, 29331827, 29331828, 35696052, 264906, 66712502, 265006, 265007, 265008, 265010, 265011, 265017, 265019, 264681, 264448, 264683, 264369, 284288, 264685, 264766, 264687, 21908765, 21906767, 21906768, 21908789, 265020, 265022, 264691, 33657023, 65274620, 33657109, 264629, 264557, 264559, 83373044, 87168518, 60432113, 22279002, 264259, 29331822, 29331824, 29331825, 29146498, 87168559, 265019, 264682, 264288, 264686, 21906764, 265020, 265022, 33657023, 264693, 33657109, 55811576, 264632, 264558, 56182323, 264639, 18108383, 18108384, 18108388, 22279000, 22279002, 264567
2012	87772137 (4023, 4024)	Novel Protein sim. GBank gji1086678 (U41020) - coded for by C. elegans cDNA yk100g4.5; coded for by C. elegans cDNA yk100g4.3; weakly similar to human SREBP-2 basic-helix-loop-helix-leucine zipper transcription factor [Caenorhabditis elegans]	Contains protein domain (PF00409) - Kinesin light chain repeat	UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29146498, 87168559, 265019, 264682, 264288, 264686, 21906764, 265020, 265022, 33657023, 264693, 33657109, 55811576, 264632, 264558, 56182323, 264639, 18108383, 18108384, 18108388, 22279000, 22279002, 264567
2013	94843842 (4025, 4026)	Novel Protein sim. GBank gji4507985[ref NP_003427.1 pZNF1 - zinc finger protein 135 (clone pHZ-17)]	Contains protein domain (PF00098) - dna_ma_bind Zinc finger, C2H2 type		18108398, 264808, 265007, 265010, 265018, 265019, 264689, 21908767, 265020, 264692
2014	87347840 (4027, 4028)	Novel Protein sim. GBank gji12720[sp P20938 MYPO_HETFR - MYELIN P0 PROTEIN PRECURSOR]		UNCLASSIFIED	264488, 29331826, 264907, 264636, 264555, 264639, 264558

2015	88094922 (4029, 4030)	Novel Protein sim. GBank gll1286lpir  S22697 - extensin - Volvox carteri (fragment)		UNCLASSIFIED	56182576, 35696286, 264259, 35696052, 264508, 264906, 264907, 264510, 264512, 87168474, 265010, 264681, 264288, 264689, 264628, 35696423, 35695855, 264639, 264563, 264564
2016	85298641 (4031, 4032)	Novel Protein sim. GBank gll285046lpir  S26413 - t-complex protein Tcp-10 - mouse		struct	264102, 264508, 264110, 265009, 33109954, 21906768, 265021, 33657109, 27486282, 263972, 18108374, 263976, 264555, 264564
2017	79464293 (4033, 4034)			UNCLASSIFIED	264685, 264636
2018	79637067 (4035, 4036)	Novel Protein sim. GBank gll124735lsp P18175 INVO_PIG - INVOLUCRIN			264693
2019	87787900 (4037, 4038)	Novel Protein sim. GBank gll2143910lpir  S68216 - phosphatase-1 glycogen-binding (GL)-chain - rat		phosphatase	264107, 264110, 264112, 265017, 263976
2020	94674476 (4039, 4040)	Novel Protein sim. GBank gll2078483 (U43200) - antifreeze glycopeptide AFGP polypeptide precursor [Boreogadus salda]		UNCLASSIFIED	264259, 264508, 264591, 265018, 264682, 264288, 264688, 22279002
2021	86718818 (4041, 4042)	Novel Protein sim. GBank gll585084lsp Q07803 EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)			56994075, 264593, 33109954, 21906754, 21906768, 33657023, 33657109, 27486261, 87168518
2022	95295665 (4043, 4044)	Novel Protein sim. GBank gll4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]			264757, 264767, 60170615, 18108385
2023	87722976 (4045, 4046)	Novel Protein sim. GBank gll5410230lgb AAD2992.1 AF07334 - (AF073344) ubiquitin specific protease 3 [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	18108394, 22278999, 264259, 264905, 264906, 264908, 264595, 264762, 264769, 264634, 264636, 87168518, 60432113, 22279000, 264482, 264565
2024	87896443 (4047, 4048)				60433438, 265017, 264686, 264692, 264693, 264636
2025	87858863 (4049, 4050)	Novel Protein sim. GBank gll4755188lgb AAD29055.1 AC00701 - (AC007018) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF00637) - 7-fold repeat in Clathrin and VPS	UNCLASSIFIED	22278997, 264509, 264906, 264909, 55812038, 265017, 265021, 265022, 60170815, 264556
2026	94122114 (4051, 4052)	Novel Protein sim. GBank gll1655699lmb CAA69032  - (Y07752) pterophorin-S [Volvox carteri]		UNCLASSIFIED	56994075, 60432049, 264508, 66712502, 264112, 60170831, 87168559, 264288, 264686, 264689, 21906766, 33657109, 18108370, 264638, 18108385, 60432113, 22279000, 22279002, 264564, 264566, 264567
2027	80249001 (4053, 4054)			UNCLASSIFIED	263978, 264634, 264486

2028	94699884 (4055, 4056)	Novel Protein sim. GBank gll1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	Contains protein domain (PF00632) - ubiquitin-HECT-domain (ubiquitin-transferase).	5264507, 52645156, 52646842, 56182575, 56994075, 35696286, 22278997, 22278998, 22278998, 60432049, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 35696052, 264906, 264907, 264908, 29331830, 52644045, 56182435, 265006, 265009, 60432229, 33637402, 264595, 264757, 55612038, 21906754, 52646317, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 18108354, 264288, 264369, 264766, 52644229, 21908765, 21906768, 21908767, 21908768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 65274820, 33657109, 52645129, 18108368, 27486261, 27486282, 27486264, 27486265, 35695763, 264629, 55811576, 35696423, 35695855, 264635, 264636, 52644332, 264558, 83373044, 56528486, 22279000, 22279002, 264563, 285009, 264595, 85658542, 264555, 264556, 284557, 264558, 264559, 83373044
2029	95362032 (4057, 4058)	Novel Protein sim. GBank gll3599940 (AF017368) - facioligental dysplasia protein 2 [Mus musculus]	UNCLASSIFIED	18108394, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 264108, 66712502, 264828, 265009, 265018, 265019, 264681, 264682, 264684, 264685, 56181562, 264689, 21908769, 265022, 264692, 264693, 264628, 18108370, 18108374, 264634, 264636, 264556, 18108385, 87168518, 22279002, 264565
2030	91213734 (4059, 4060)	Novel Protein sim. GBank gll5630080 (gb)AAD45825.1 (AC004890) similar to HUB1; similar to BAA24380 (PID:g2789430) [Homo sapiens]	Contains protein domain (PF00086) - transcrip factor Zinc finger, C2H2 type	264591, 55811957, 18108365, 264557, 264558, 18108382, 18108384
2031	80245281 (4081, 4082)			63274572, 35696286, 29331824, 264908, 265009, 264593, 265018, 264288, 264686, 264769, 21906766, 21906767, 28148627, 264628, 35696423, 264634, 264556, 18108381, 50170394, 264559, 83373044, 18108385, 264482, 264484
2032	91232607 (4083, 4084)	Novel Protein sim. GBank gll5689491 (dbj)BAA83029.1 - (AB029000) KIAA1077 protein [Homo sapiens]	Contains protein domain (PF00884) - hydrolase Sulfatase	56181562, 264628, 264632, 264555, 264556
2033	95000809 (4085, 4086)	Novel Protein sim. GBank gll2494828 (sp)Q64686 (CAG7_RAT - ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (ST6GALNACIII) (STY)		22278996, 22278999, 264907, 29331830, 265008, 265018, 264681, 264682, 264684, 21906767, 21906768, 21906769, 33657109, 83373044, 56528486
2034	91232529 (4087, 4088)	Novel Protein sim. GBank gll4826984 (ref)NP_005147.1 (pROD1 - UNKNOWN	Contains protein domain (PF00076) - dna_rna_bind RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	

2035	83553451 (4069, 4070)				264369, 264686, 265022, 26526486, 264567
2036	87115833 (4071, 4072)				29331827, 29331828, 264682, 264369, 29148627, 60432113
2037	94324833 (4073, 4074)	Novel Protein sim. GBank gij2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331824, 60432289, 29331826, 29331828, 35696052, 264907, 29331830, 66712502, 56182435, 265008, 265009, 60170831, 284594, 55812038, 33109954, 21906754, 87168559, 265017, 265018, 265019, 264762, 284368, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 35695763, 35695855, 264632, 264634, 264636, 56182323, 83373044, 60432113, 22279000, 22279002, 264563
2038	95422384 (4075, 4076)	Novel Protein sim. GBank gij3880625[emb]CAB07858] - (Z93785) predicted using GeneRinder; similar to RNA recognition motif, (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL:D27559 comes from this gene	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Art	UNCLASSIFIED	22278995, 22278996, 56994075, 264259, 29331824, 35696052, 264905, 264906, 52644045, 265007, 265009, 87168559, 265017, 18108351, 264448, 264369, 264766, 264767, 264686, 18108358, 21908765, 21906769, 52644150, 33657023, 264692, 18108362, 33657109, 27486262, 18108370, 18108374, 18108379, 35696423, 65274791, 264632, 264636, 18108383, 83373044, 18108385, 87168518, 22279000, 22279002, 264563, 264564, 264566
2039	95514626 (4077, 4078)	Novel Protein sim. GBank gij2224653[dbj]BAA20813] - (AB002354) KIAA0356 [Homo sapiens]	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278997, 264259, 29331822, 264905, 264906, 264907, 264908, 264909, 264510, 265009, 264910, 264593, 264758, 265011, 265018, 264762, 264288, 264766, 264768, 264769, 21906766, 33657023, 264692, 264693, 33657109, 35696423, 264631, 264632, 264634, 264635, 264636, 264637, 264639, 87168518, 264486
2040	95308417 (4079, 4080)			UNCLASSIFIED	264592
2041	95071736 (4081, 4082)	Novel Protein sim. GBank gij2500825[sp]P70700[RPA2 MOUSE - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135)]	mapolymerase	UNCLASSIFIED	264488, 22278998, 35696052, 264905, 264907, 264908, 264910, 265018, 264605, 265019, 18108351, 264766, 264769, 21906766, 265021, 265022, 264692, 33657109, 264628, 264629, 35696423, 35695855, 264637, 264638, 264563, 264564, 264565, 264567

2042	95307447 (4083, 4084)	Novel Protein sim. GBank gij4406590[gbjAAD20040] - (AF131786) Similar to Ena-VASP like protein [Homo sapiens]	Contains protein domain (PF00566) - WH1 domain	UNCLASSIFIED	60424179, 35696286, 264259, 29331828, 35696052, 29331828, 264508, 264509, 264907, 264909, 264510, 264511, 265009, 264910, 264591, 60433356, 264595, 265017, 265019, 264681, 264764, 264369, 264765, 264684, 264288, 264766, 264686, 52644229, 264769, 21906765, 35695917, 264535, 52644150, 264691, 264692, 18108365, 27486261, 27486262, 27486265, 18108374, 35696423, 65274791, 35695855, 264555, 264556, 60170394, 18108385, 264404, 22279000, 22279002, 264482, 264563, 264564, 264566
2043	94328076 (4085, 4086)	Novel Protein sim. GBank gij505254[gbjAAD38607.1]AF14563 - (AF145632) BcDNA, GH06032 [Drosophila melanogaster]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	264488, 52644507, 52646365, 56994075, 22278997, 22278998, 20281171, 264259, 29331822, 29331824, 66714117, 29331826, 29331828, 33656970, 29146498, 264509, 264908, 52644045, 56182435, 265006, 33657402, 21906754, 52644296, 87168559, 265017, 265018, 265019, 264681, 264288, 264766, 264685, 264686, 21908766, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 33657349, 35695763, 18108374, 55811576, 35695855, 18108380, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264567
2044	87106927 (4087, 4088)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	264083, 29331827, 264905, 66712502, 264592, 264689, 21906765, 21908769, 265020, 264692, 264482, 264588
2045	78635532 (4089, 4090)	Novel Protein sim. GBank gij4406698[gbjAAD20062] - (AF131852) Unknown [Homo sapiens]			264692
2046	87320849 (4091, 4092)	Novel Protein sim. GBank gij4406698[gbjAAD20062] - (AF131852) Unknown [Homo sapiens]			264259, 264806, 264683, 22279002
2047	84578601 (4093, 4094)	Novel Protein sim. GBank gij4101720 (AF006466) - lymphocyte specific formin related protein [Mus musculus]			22278999, 29147620, 29331824, 29146498, 264508, 265007, 265008, 265019, 264605, 264681, 29148627, 29148629, 265021, 33657023, 18108365, 33657109, 33657182, 18108377, 264556, 264638, 264559, 18108386
2048	84606378 (4095, 4096)	Novel Protein sim. GBank gij4589656[dbjBAA76850.1] - (AB023223) KIAA1006 protein [Homo sapiens]		UNCLASSIFIED	264909
2049	88094690 (4097, 4098)	Novel Protein sim. GBank gij4589656[dbjBAA76850.1] - (AB023223) KIAA1006 protein [Homo sapiens]		UNCLASSIFIED	264488, 264259, 29331824, 29331828, 35696052, 264906, 264907, 264908, 264909, 264910, 264603, 264783, 21906767, 21906768, 264629, 264634, 264637, 22279002, 264564, 264565, 264566, 264567



2050	79633835 (4089, 4100)				UNCLASSIFIED	264663	264488, 264259, 264509, 264906, 264907, 264768, 18108374, 35698423, 264563, 264566, 264486
2051	87780168 (4101, 4102)				UNCLASSIFIED		
2052	88096393 (4103, 4104)	Novel Protein sim. GBank gl 4529889 gb AAD21812.1  - (AF134728) G9A [Homo sapiens]	Contains protein domain (PF00856) - SET domain		- Kinase		264488, 263994, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264784, 264369, 264766, 264688, 264768, 264789, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35698423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264556, 264638, 264639, 18108385, 56529486, 60432113, 264563, 264584, 264566, 264488, 264567, 264488, 263994, 35696052, 264508, 264905, 264509, 264806, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264369, 264768, 264688, 264788, 264769, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35698423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264556, 264638, 264639, 18108385, 56529486, 60432113, 264563, 264584, 264566, 264488, 264567
2053	87763078 (4105, 4106)	Novel Protein sim. GBank gl 2995449 emb CAA75113  - (Y14848) midline 1 protein [Mus musculus]			UNCLASSIFIED		22278986, 22278987, 264259, 29331822, 264102, 264508, 35695917, 263972, 284482
2054	95358937 (4107, 4108)	Novel Protein sim. GBank gl 3876326 emb CAB02090  - (Z79754) similar to C2 domain [Caenorhabditis elegans]	Contains protein domain (PF00168) - C2 domain				60424179, 264094, 264259, 293331825, 60424289, 264908, 60432229, 60433356, 87168559, 265019, 264760, 264288, 264686, 21906789, 33657023, 264693, 55810764, 55811576, 264635, 56182323, 60432113
2055	88259449 (4109, 4110)	Novel Protein sim. GBank gl 5333746 gb AAD42226.1 AF15913 - (AF159133) SIR2-like protein [Oryza sativa subsp. indica]			UNCLASSIFIED		264488, 29331826, 60432289, 29331828, 60433356, 265019, 264683, 264684, 265021, 33657109, 18108374, 264637, 18108385, 87168518, 60432113, 22279000, 264584

2056	88177396 (4111, 4112)	Novel Protein sim. GBank gi 4826960 ref NP_005042.1 pQARS - glutamine-tRNA synthetase	Contains protein domain (PF00749) - tRNA synthetases class I (E and Q)	synthase	264488, 52645156, 56182575, 22278994, 35696286, 56994075, 22278996, 22278998, 22278999, 60432049, 264259, 29331824, 60432289, 29331827, 29331828, 33656970, 264104, 264906, 264908, 265006, 265008, 60170831, 264591, 60432229, 60433438, 18108348, 21906754, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 264760, 18108351, 264681, 264682, 264448, 264683, 264368, 264288, 264685, 264687, 264688, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 265022, 33657023, 18108362, 33657109, 18108366, 33657182, 27486281, 27486284, 27486285, 33657349, 264628, 18108370, 264629, 18108374, 18108377, 18108379, 35696423, 55811576, 20281152, 264636, 264952, 18108385, 18108388, 87168518, 264482, 264565, 264599, 264597 UNCLASSIFIED
2057	87877905 (4113, 4114)	Novel Protein sim. GBank gi 728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		UNCLASSIFIED	52646842, 52646365, 56182575, 35696286, 22278996, 22278997, 22278998, 264093, 52645080, 35696052, 29331828, 33656970, 265009, 52646317, 55811386, 52644296, 52644229, 21906769, 35695917, 265021, 60170615, 52644150, 33657109, 33657182, 27486261, 27486262, 35695763, 35696423, 35695855, 52644332 265007, 265008, 264591 29331825, 264682, 264686, 264691, 264693, 22279002
2058	86276896 (4115, 4116)	Novel Protein sim. GBank gi 119714 sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	
2059	79866684 (4117, 4118)				
2060	83050800 (4119, 4120)	Novel Protein sim. GBank gi 2811122 (U87318) - NaDC-2 [Xenopus laevis]		UNCLASSIFIED	56182575, 29331824, 29331826, 264910, 55811957, 18108370, 55811576

2061	95362204 (4121, 4122)	Novel Protein sim. GBank gi 2496947 sp Q09298 YQ08_CAEEL - HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II	Contains protein domain (PF000089) - Eukaryotic protein kinase domain	kinase	22278997, 22278998, 264258, 29331822, 29331824, 29331826, 29331827, 35696052, 29331828, 264908, 66712502, 29331830, 264908, 264909, 264112, 264511, 265007, 265009, 264910, 264591, 33657402, 21906754, 85658542, 265017, 265019, 264448, 264683, 264288, 264684, 264369, 264686, 264687, 18108358, 264689, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 33657109, 20281149, 18108379, 35695855, 264634, 264556, 264557, 264558, 18108382, 264559, 83373044, 18108384, 56526486, 60432113
2062	87028440 (4123, 4124)	Novel Protein sim. GBank gi 4502091 ref NP_001139.1 pANK2 - ankyrin 2, neuronal	Contains protein domain (PF00023) - Ank repeat	struct	264905, 264628, 264907, 264628, 264908, 264909, 18108374, 263978, 35695855, 264512, 264635, 60431850, 264636, 264760, 264563, 18108351, 264762, 264585, 264764, 264487, 264766
2063	87601272 (4125, 4126)	Novel Protein sim. GBank gi 4589562 db BAA76803.1  - (AB023176) KIAA0959 protein [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	oncogene	22278994, 22278999, 264259, 29331827, 264906, 264909, 52644045, 264686, 21906767, 55811957, 264692, 18108365, 263972, 55811576, 18108384, 22279002, 264482, 264563, 264564, 264484
2064	95317253 (4127, 4128)	Novel Protein sim. GBank gi 1754515 db BAA13413.1  - (D87515) aminopeptidase-B [Rattus norvegicus]		hydrolase	264488, 52646365, 56994075, 35696286, 22278997, 22278998, 264259, 29331826, 60432288, 29331827, 29331828, 35696052, 264508, 265007, 265008, 60432229, 60433438, 21906754, 265010, 265011, 87188559, 265017, 265018, 264761, 18108351, 264682, 264369, 264288, 52644229, 21906765, 21906767, 21906768, 35695917, 33657109, 18108368, 18108374, 35696423, 35695855, 52644332, 264559, 60432113, 22279000, 22279002, 264566, 264486
2065	95092238 (4129, 4130)	Novel Protein sim. GBank gi 2507144 sp Q04205 TENS_CHICK - TENSIN		kinase	264569, 18108394, 56182181, 60432289, 29331826, 264905, 264906, 264908, 60431735, 60433356, 55811386, 85658542, 265018, 55811150, 264691, 264766, 264692, 60431528, 263974, 55810764, 35695855, 264631, 264634, 264635, 60431850, 264557, 83373044, 18108388, 22279000, 22279002
2066	85793402 (4131, 4132)	Novel Protein sim. GBank gi 160171 (M58295) - circumsporozoite protein [Plasmodium yoelii]	Contains protein domain (PF000086) - Zinc finger, C2H2 type	UNCLASSIFIED	56182575, 264259, 264906, 264764, 264286, 58182323, 264567

2067	95303892 (4133, 4134)				35696286, 22278987, 22278998, 60432049, 264259, 60432289, 60433438, 264682, 264448, 264368, 264288, 18108355, 21906765, 21906768, 265022, 33657109, 35696423, 35695855, 264558, 264404, 264563, 264486
2068	84344754 (4135, 4136)			UNCLASSIFIED	264687
2069	94319177 (4137, 4138)	Novel Protein sim. GBank gij3152682 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	transcript factor	60424179, 56182575, 22278995, 22278996, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 33656870, 264509, 264905, 56182435, 265009, 60433356, 87168559, 265017, 265018, 264604, 265019, 264448, 264764, 264766, 21906765, 21906767, 21906768, 21906768, 265020, 265021, 33657023, 33657109, 263976, 264555, 264557, 56182323, 83373044, 87168518, 60432113, 22279000, 22279002
2070	85791380 (4139, 4140)	Novel Protein sim. GBank gij5712131 [gb]AAD47379.1 [AF12049] - (AF12049) DEM1 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264805, 264628, 264908, 264638
2071	86946116 (4141, 4142)	Novel Protein sim. GBank gij3551531 [dbj]BAA33016 [AB017437] avena [Gallus gallus]	Contains protein domain (PF00568) - WH1 domain		18108398, 265006, 265007, 265008, 265009, 264594, 265010, 265011, 18108351, 18108354, 18108364, 18108365, 18108368, 264634, 18108381, 18108385, 18108388, 18108391
2072	91718429 (4143, 4144)		Contains protein domain (PF00184) - Neurohypophyseal hormones, C-terminal Domain		22278995, 35696286, 22278997, 22278998, 22278999, 264480, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 265008, 33657402, 21906754, 265011, 265019, 18108351, 264682, 264368, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264690, 264692, 35696423, 264555, 264556, 264558, 22279000
2073	27825684 (4145, 4146)	Novel Protein sim. GBank gij1504026 [dbj]BAA13212 [D86978] similar to C.elegans protein [Z37093] [Homo sapiens]		UNCLASSIFIED	264556
2074	84324767 (4147, 4148)	Novel Protein sim. GBank gij4240317 [dbj]BAA74937.1 [AB020721] KIAA0914 protein [Homo sapiens]			29331822, 264909, 264511, 265009, 264594, 264595, 265010, 265011, 265017, 265018, 265019, 264448, 264683, 265020, 265021, 18108370, 264632, 83373044, 264587

2075	94314886 (4149, 4150)	Novel Protein sim. GBank gl 5138930 gb AAD40382.1  - (AF003680) transcription factor IIB [Homo sapiens]			18108394, 22278994, 22278996, 35696286, 22278998, 22278999, 264259, 29331822, 29331825, 29331827, 35696052, 29331828, 264905, 264907, 264908, 264510, 265007, 264910, 265009, 33857084, 264760, 264448, 264288, 264766, 264767, 264689, 21906766, 21906767, 21906769, 265021, 265022, 60170615, 33657023, 27486262, 27486265, 35696423, 35695855, 264631, 264634, 264639, 87168518, 22278002, 264563, 264488, 18108391
2076	87594118 (4151, 4152)				264259, 29331826, 264508, 264908, 264510, 265007, 265011, 264288, 264637, 18108385, 264592
2077	11389877 (4153, 4154)		UNCLASSIFIED	ubiquitin	29331825, 265017, 265018, 264288, 265020, 265021, 264634, 56526486
2078	87538364 (4155, 4156)	Novel Protein sim. GBank gl 4220590 dbj BAA74579  - (D87908) nuclear protein np85 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger		264768, 22278997, 265021, 264690, 264259, 264892, 29331822, 264693, 29331824, 29331828, 264508, 264509, 264908, 264907, 264628, 20281069, 264909, 265007, 265009, 264632, 264636, 264591, 264592, 264639, 264758, 264759, 33109954, 264604, 265018, 265019, 22279002, 264563, 264564, 264448, 264684, 264567, 264685
2079	88095916 (4157, 4158)	Novel Protein sim. GBank gl 4240255 dbj BAA74906.1  - (AB020690) KIAA0883 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	264892, 29331822, 264693, 29331824, 29331828, 264508, 264509, 264908, 264907, 264628, 20281069, 264909, 265007, 265009, 264632, 264636, 264591, 264592, 264639, 264758, 264759, 33109954, 264604, 265018, 265019, 22279002, 264563, 264564, 264448, 264684, 264567, 264685
2080	94136689 (4159, 4160)	Novel Protein sim. GBank gl 2408021 emb CAB16219.1  - (Z99162) putative vacuolar protein [Schizosaccharomyces pombe]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	56182575, 264092, 29331824, 29331826, 29331830, 265017, 265018, 265020, 83373044
2081	94847186 (4161, 4162)	Novel Protein sim. GBank gl 5524734 gb AAD44360.1 AF166350 - (AF166350) ST7 protein [Homo sapiens]	Contains protein domain (PF00431) - CUB domain	eph	22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 33657402, 85858542, 265011, 265018, 265019, 21906767, 21906768, 264693, 18108385, 22279000, 22279002
2082	87628629 (4163, 4164)	Novel Protein sim. GBank gl 3880558 emb CAA94234  - (Z70271) predicted using Genefinder; similar to collagen; cDNA EST yk308e7.3 comes from this gene; cDNA EST yk308e7.5 comes from this gene; cDNA EST yk385a8.3 comes from this gene; cDNA EST yk385a8.5 comes from this gene [Caeno...]		collagen	264907, 265019
2083	94141000 (4165, 4166)	Novel Protein sim. GBank gl 2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	56182575, 22278996, 22278997, 264259, 29331822, 29331825, 264509, 264112, 265009, 264593, 21906754, 265018, 265019, 264448, 264288, 264685, 21906769, 265020, 265022, 264691, 18108370, 65274791, 264631, 264555, 264563
2084	95199298 (4167, 4168)	Novel Protein sim. GBank gl 728836 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		UNCLASSIFIED	265018, 264763, 264683, 264691

2085	94869476 (4169, 4170)	Novel Protein sim. GBank gi 1655599 emb CAA69032  - (Y07752) peraphorin-S [Volvox carter]	UNCLASSIFIED	56182575, 60432289, 264908, 56182435, 87168474, 264763, 264369, 264686, 264693, 18108370, 56182323
2086	91234404 (4171, 4172)	Novel Protein sim. GBank gi 3875032 emb CAA88936  - (Z49125) similarity to Trichostrogylus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D37644 comes from this gene; cDNA EST EMBL:D36149 come...	UNCLASSIFIED	35696286, 264259, 35696052, 264906, 264907, 264908, 264909, 264910, 264759, 264604, 264762, 264768, 264769, 35695917, 263978, 35698423, 35695855, 264632, 264634, 264637, 264638, 264639, 56182323, 18108385, 264482, 264488
2087	21436337 (4173, 4174)		UNCLASSIFIED	264489
2088	94111527 (4175, 4176)	Novel Protein sim. GBank gi 3880930 emb CAA16334  - (AL021481) similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T0080...		264488, 22278994, 35696286, 22278996, 29331827, 35696052, 33657402, 21906754, 33108954, 87168474, 265017, 265018, 265019, 264448, 264683, 264369, 264685, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264682, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35698423, 35695855, 83373044, 87168518, 22279000, 264567
2089	95422801 (4177, 4178)	Novel Protein sim. GBank gi 4758118 ref NP_004623.1 pDAP3 - Death associated protein 3	cadherin	18108392, 264488, 52644507, 18108394, 18108397, 52646842, 18108398, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 264093, 264094, 60432049, 264259, 29331822, 20281099, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656870, 29146498, 29146499, 264102, 264106, 264107, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 66712502, 264828, 52644045, 264909, 56182435, 264110, 264112, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264592, 264593, 60433356, 33657402, 60433438, 264595, 55812038, 264758, 21906754, 33657084, 55811386, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 55811150, 264762, 18108351, 264682, 264448, 264763, 264764, 264683, 264369, 18108354, 264298, 264685, 264766, 264686, 264687, 264768, 52644229, 264688, 18108358, 56181562, 264769, 18108359, 264889, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 55811957, 29148628, 29148784, 35695917, 265020, 265021, 265022, 60170615, 264690

2080	88222470 (4179, 4180)				22278995, 22278998, 22278999, 264259, 29331826, 35696052, 264910, 33657402, 60433438, 33109954, 87168474, 87168559, 265018, 265019, 264681, 264684, 264686, 264687, 264688, 264689, 21908765, 21908766, 21908767, 21908769, 35695917, 265022, 60170615, 33657023, 35698423, 35695855, 264952, 18108387, 22279000, 263994, 264905, 264908, 264511, 264512, 265008, 264910, 55811386, 264288, 264768, 56181562, 21906765, 21906768, 21906768, 265022, 264628, 264563, 264567
2091	95309161 (4181, 4182)	Novel Protein sim. GBank gi 4580997 gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	
2092	88223605 (4183, 4184)			homeobox	22278997, 22278999, 66712502, 87168559, 264683, 265021, 264486
2093	87406073 (4185, 4186)	Novel Protein sim. GBank gi 2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264905, 264806, 264907, 264908, 264510, 265006, 265007, 265009, 264910, 264596, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264690, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564
2094	91230929 (4187, 4188)	Novel Protein sim. GBank gi 4929551 gb AAD34036.1 AF15179 - (AF151799) CGI-40 protein [Homo sapiens]		MHC	35696286, 265017, 265018, 265019, 18108388
2095	95351526 (4189, 4190)	Novel Protein sim. GBank gi 363238 pir J457284 - spermatid perinuclear RNA-binding protein Spnr - mouse	Contains protein domain (PF00035) - Double-stranded RNA binding motif	dna_ma_bind	35696286, 52644045, 265006, 265007, 265008, 87168559, 18108351, 21906769, 29148784, 265020, 33657023, 27486262, 18108374, 18108388
2096	94119760 (4191, 4192)	Novel Protein sim. GBank gi 3834423 (AF070689) - cytoplasmic dynein intermediate chain isoform DIC1a [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase_associated	264488, 264489, 65274572, 56182575, 22278998, 22278997, 22278999, 264259, 60432289, 29331826, 35696052, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 52644045, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264592, 60433356, 60433438, 264758, 264596, 55812038, 21906754, 264601, 264602, 264605, 264762, 264681, 18108351, 264764, 264683, 264288, 264887, 264768, 264769, 264689, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 52644150, 264691, 264692, 33657023, 264693, 27486281, 35695783, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264637, 263981, 264638, 264639, 264563, 264483, 264565, 264566, 264486, 264567

2097	95322772 (4193, 4194)	Novel Protein sim. GBank gil5174501[ref NP_006051.1 pLYF1 - zinc finger protein, subfamily 1A, 1 (Ikaros)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	65274572, 264511, 265010, 264600, 265017, 264448, 264288, 265021, 60170815, 264892, 33557109, 18108370, 264636, 264483 56994075, 264259, 264288, 265020, 264563
2098	87780340 (4195, 4196)	Novel Protein sim. GBank gil4758208[ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	
2099	95412927 (4197, 4198)	Novel Protein sim. GBank gil2695659 (AF026954) - pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDP1 [Bos taurus]		phosphatase	65274572, 264905, 65274444, 264691, 264636, 264555
2100	95332856 (4199, 4200)	Novel Protein sim. GBank gil3881189[emb CAB16514  - (Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C08829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4...	Contains protein domain (PF00025) - ADP-ribosylation factor family	nuc_recpt	56182575, 22278995, 22278986, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 29146498, 264909, 265008, 265009, 264910, 264591, 60432229, 60433356, 33657402, 264758, 21908754, 85658542, 87168474, 265017, 265018, 265019, 264681, 18108351, 264762, 264448, 264369, 264288, 18108355, 264686, 21908765, 21908767, 21908768, 21906769, 265020, 265021, 33657023, 18108374, 35696423, 264558, 83373044, 87168518, 60432113, 22279000, 22279002 264091, 29331824, 264105, 265007, 265010, 18108380
2101	87782604 (4201, 4202)	Novel Protein sim. GBank gil4589468[db BAA76761.1  - (AB012808) mBOCT [Mus musculus]		UNCLASSIFIED	
2102	87770461 (4203, 4204)	Novel Protein sim. GBank gil3874149[emb CAA97423.1  - (Z73103) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264489, 35696286, 264259, 35696052, 264508, 264905, 264907, 264908, 264909, 264511, 264512, 264591, 264593, 60433356, 264758, 264601, 264805, 264760, 18108351, 264448, 264764, 264288, 264767, 264768, 21908769, 35695917, 18108374, 264634, 264555, 264559, 264563, 264482, 264486
2103	95413576 (4205, 4206)	Novel Protein sim. GBank gil4240159[db BAA74858.1  - (AB020842) KIAA0835 protein [Homo sapiens]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcriptfactor	65274572, 56994075, 22278999, 264259, 29331824, 29331825, 35696052, 29331828, 66712502, 265009, 60170831, 264595, 33109954, 85658542, 87168559, 265017, 265019, 264448, 21908765, 21908768, 265022, 33657023, 27486262, 33657349, 35695763, 60431528, 18108374, 55811576, 56182323, 18108387, 87168518, 60432113, 264584
2104	85776161 (4207, 4208)			UNCLASSIFIED	264592, 264604, 22279000



2105	94848080 (4209, 4210)	Novel Protein sim. GBank gii1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE10F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8....		UNCLASSIFIED	264488, 56182575, 22278994, 56894075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264508, 264805, 264509, 264807, 29331830, 52844045, 264510, 264511, 265007, 264512, 265009, 60170831, 60432229, 33657402, 60433356, 264595, 60433438, 264758, 33657084, 87168474, 265010, 87168559, 265017, 265018, 265019, 264762, 18108351, 264884, 18108354, 264288, 264686, 52644229, 18108359, 21806765, 21806766, 21806767, 21806768, 21806769, 35695917, 265020, 265022, 60170815, 32644150, 264692, 33657023, 264693, 33657109, 60431528, 18108374, 65274791, 35895855, 264635, 60170394, 264639, 264558, 18108385, 18108387, 56526486, 87168518, 60432113, 264584, 264566, 264567
2108	83385475 (4211, 4212)				265006, 265019
2107	79822662 (4213, 4214)	Novel Protein sim. GBank gij3881524[embjCAA93883] - (Z70038) ZK1087.4 [Caenorhabditis elegans]			264906, 264639
2108	94233976 (4215, 4216)	Novel Protein sim. GBank gij3176689 (AC003671) - Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb Z35927 from S. cerevisiae. [Arabidopsis thaliana]		UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264758, 265011, 264600, 264601, 264764, 264766, 264767, 264768, 264769, 264693, 264629, 35695855, 264632, 264634, 264635, 264638, 264639, 83373044, 264486
2109	80478719 (4217, 4218)			UNCLASSIFIED	18108348, 264768, 18108370, 18108374, 264555, 264556, 264557, 264558
2110	87729075 (4219, 4220)	Novel Protein sim. GBank gij481043[pirj]S37671 - bai2 protein - human		UNCLASSIFIED	264564
2111	87818419 (4221, 4222)			UNCLASSIFIED	
2112	87293783 (4223, 4224)	Novel Protein sim. GBank gij2143639[pirj]I56542 - calmodulin-binding protein - rat	Contains protein domain (PF00069) - struct		264768, 35695917, 264630, 264567, 264488
2113	76941388 (4225, 4226)	Novel Protein sim. GBank gij4426629[gbj]AAD20459 - (AF100960) protocadherin [Rattus norvegicus]	Eukaryotic protein kinase domain		264508, 264906, 264591, 264682, 22279002
2114	87889342 (4227, 4228)	Novel Protein sim. GBank gij3327184[dbj]BAA31660 - (AB014585) KIAA0685 protein [Homo sapiens]	Contains protein domain (PF00028) - cadherin		265006
2115	80993785 (4229, 4230)	Novel Protein sim. GBank gij4757890[refNP_004328.1]pC8OR - chromosome 8 open reading frame 1		UNCLASSIFIED	66714117, 29331826, 29331827, 60433438, 55812038, 265017, 265019, 264689, 21908769, 55811957, 265020, 265021, 33657109, 60170394, 264558
					65274572, 264688, 264691, 264692, 60432113

2116	88259387 (4231, 4232)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	3586286, 2227899, 56182181, 29331824, 29331825, 29331827, 35696052, 284907, 56182435, 265008, 264591, 55812038, 55811386, 87168558, 264288, 264369, 21906769, 29148829, 33657023, 35695763, 55811576, 35696423, 18108385
2117	87788904 (4233, 4234)	Novel Protein sim. GBank gij2330021 (AF019250) - kinesin-related protein; KRP; Costal2 [Drosophila melanogaster]		struct	29331824, 264511, 265009, 33109954, 285017, 265018, 264288, 264689, 265020, 264692, 58526486, 264482
2118	87078894 (4235, 4236)	Novel Protein sim. GBank gij1078307 [prij]B56573 - nuclear pore complex glycoprotein p62 - African clawed frog		glycoprotein	264259, 264905, 264907, 264908, 264510, 264511, 265009, 264910, 265010, 264602, 264288, 264788, 264693, 263967, 263972, 264638, 264559
2119	86999317 (4237, 4238)	Novel Protein sim. GBank gij4321407 [gb]AAD15748 [Homo sapiens]		UNCLASSIFIED	264683, 18108385
2120	87788395 (4239, 4240)	Novel Protein sim. GBank gij4885527 [re]NP_005480.1 [pNSP3 - novel SH2-containing protein 3]	Contains protein domain (PF00017) - eph Src homology domain 2		264091, 264259, 29331828, 29331828, 265017, 264604, 264288, 264685, 265020, 264691, 18108370, 55810764, 264555, 264636, 60432113
2121	80021375 (4241, 4242)	Novel Protein sim. GBank gij4757728 [re]NP_004886.1 [pAGTA - angiotensin/Vasopressin receptor AII/AVP-like]		UNCLASSIFIED	264601, 264766, 263978
2122	91230831 (4243, 4244)	Novel Protein sim. GBank gij4929551 [gb]AAD34036.1 [AF15179 - (AF151799) CGI-40 protein (Homo sapiens)]			18108394, 56182575, 22278997, 29331822, 29331824, 29331826, 29331828, 29331828, 264907, 56182435, 265007, 264910, 265010, 265018, 264686, 265020, 55811576, 264555, 264637, 18108382, 83373044, 18108383, 18108384, 56528486, 264585, 284587
2123	86767898 (4245, 4246)	Novel Protein sim. GBank gij2224551 [dbj]BAA20764 - (AB002303) KIAA0305 [Homo sapiens]	Contains protein domain (PF01363) - struct F YVE zinc finger		18108396, 264757, 265011, 18108351, 264691, 264634, 18108385
2124	83005951 (4247, 4248)	Novel Protein sim. GBank gij568945 [dbj]BAA83011.1 - (AB028982) KIAA1059 protein [Homo sapiens]	Contains protein domain (PF00801) - transport PKD domain		29331822, 264906, 264907, 264591, 284639, 284563
2125	95354041 (4249, 4250)	Novel Protein sim. GBank gij728831 [sp]P39188 [ALU1_HUMAN - III] ALU SUBFAMILY J WARNING ENTRY IIII	UNCLASSIFIED		264259, 264508, 264907, 264511, 85658542, 264763, 21906765, 35695917, 264636, 264486
2126	95084231 (4251, 4252)	Novel Protein sim. GBank gij453926 [emb]CAB39853.1 - (AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]	UNCLASSIFIED		264488, 264489, 29331827, 35696052, 264905, 264509, 264908, 264909, 264510, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264596, 264758, 264601, 264603, 265018, 264604, 264605, 264760, 264681, 264762, 264683, 264764, 264684, 264288, 264685, 264689, 60170615, 33657023, 33657109, 55810764, 284635, 264636, 264637, 264638, 284639, 83373044, 264564, 264566

2127	81118652 (4253, 4254)	Novel Protein sim. GBank glt4868435gb/AAD31315.1 AF143236) apoptosis related protein APR-2 (Homo sapiens)			35696286, 29331826, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 264512, 265007, 265009, 264910, 264758, 265011, 264600, 264601, 264604, 264762, 264763, 264766, 264687, 264768, 264769, 264689, 35695917, 264690, 264691, 264692, 264693, 264629, 18108374, 35695855, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264567, 56182575, 35696286, 56182181, 29331824, 60432289, 35696052, 264905, 264907, 66712502, 264908, 264909, 264510, 264512, 265009, 264910, 264591, 55812038, 265018, 264764, 264288, 264369, 264687, 264768, 55811957, 264692, 18108368, 264628, 264632, 264634, 264635, 264637, 56182323, 264639, 18108384, 18108388, 264563, 264567
2128	87414262 (4255, 4256)				66714117, 264828, 264595, 55812038, 55811150, 55811957, 264693, 18108374, 263978, 65274791, 18108381, 83373044, 22279000 263981
2129	95102089 (4257, 4258)		UNCLASSIFIED		
2130	95417144 (4259, 4260)	Novel Protein sim. GBank glt2649255 (AE001012) - conserved hypothetical protein [Archaeoglobus fulgidus]	UNCLASSIFIED		
2131	85723065 (4261, 4262)	Novel Protein sim. GBank glt1086886 (U41276) - Similar to potassium channel protein. [Caenorhabditis elegans]		Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	35696052, 264909, 264768, 35695917
2132	95361096 (4263, 4264)	Novel Protein sim. GBank glt5689373jdb BAA82973.1  - (AB028944) KIAA1021 protein [Homo sapiens]		Contains protein domain (PF00122) - E1-E2 ATPase	264488, 22278999, 264259, 29331827, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264910, 264591, 264592, 264595, 264758, 21906754, 33109954, 87168474, 265011, 264600, 264601, 264605, 265019, 264760, 18108351, 264681, 264762, 264764, 264288, 264684, 264766, 264686, 264687, 264768, 264769, 264688, 21908769, 264690, 52644150, 264691, 264693, 18108370, 264628, 264629, 18108372, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264636, 264555, 264637, 18108380, 264639, 264558, 56182323, 56526486, 264564, 264565, 264566, 264567

2133	95351539 (4265, 4266)	Novel Protein sim. GBank gij4220489 (AC006069) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60424179, 52646365, 52646842, 56994075, 3699286, 22278997, 22278988, 60432049, 56182181, 66714117, 60424269, 29331826, 29331828, 35696052, 264905, 264906, 264907, 66712502, 29331830, 56182435, 265006, 264512, 265008, 60431735, 60433356, 33657402, 55812038, 33109954, 21906754, 55811386, 265010, 264603, 265017, 265018, 265019, 55811150, 18108351, 264682, 264369, 264288, 52644229, 56181562, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 33657023, 33657109, 60431528, 18108374, 35696423, 65274791, 35695855, 264634, 60431850, 18108380, 56182323, 83373044, 18108385, 18108387, 60432113, 22279002, 264563, 264566
2134	95412697 (4267, 4268)	Novel Protein sim. GBank gij387535 [emb] (CAB09415) - (Z96047) DY3.6 [Caenorhabditis elegans]			56181688, 35696286, 21906754, 55811388, 265011, 265017, 18108351, 264785, 264786, 264688, 21906768, 35695917, 265020, 33657023, 264628, 35695855, 264632, 264555, 264556, 264557, 264558, 18108382, 22279002
2135	88079813 (4269, 4270)	Novel Protein sim. GBank gij568955 [db] (BAA3063.1) - (AB029034) KIAA1111 protein [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	22278998, 29331828, 35696052, 264906, 264908, 264910, 265009, 264591, 264758, 52646317, 265011, 87168559, 264801, 18108351, 264448, 264683, 264684, 264689, 18108359, 264691, 33657023, 264692, 35695763, 264629, 35695855, 264631, 264635, 264636, 264637, 56182323, 264639, 22279002, 264564
2136	84346479 (4271, 4272)	Novel Protein sim. GBank gij2662167 [db] (BAA23715) - (AB007903) KIAA0443 [Homo sapiens]		UNCLASSIFIED	264639
2137	87637716 (4273, 4274)	Novel Protein sim. GBank gij4884110 [emb] (CAB43262.1) - (AL050090) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264559, 264909, 33109954, 264783, 21906768, 60170394, 18108385, 264563
2138	87395446 (4275, 4276)	Novel Protein sim. GBank gij5174779 [gb] (AAD0696.1) - (U87804) 50 kDa protein [Caulobacter crescentus]		ATPase_associated	264259, 29331828, 35696052, 264909, 265006, 265017, 265018, 18108351, 264288, 21906768, 33657023, 33657109, 264628, 18108374, 35695855, 264634, 264555, 264556, 264557, 264558, 264559
2139	94843882 (4277, 4278)	Novel Protein sim. GBank gij385082 [emb] (CAA77135) - (Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana glauca]			264905, 264910, 264591, 55812038, 55811386, 85658542, 264760, 18108351, 18108359, 55811957, 265020, 265021, 33657023, 18108364, 55811576, 83373044, 18108385, 56526486, 264482

2140	87645655 (4270, 4280)	Novel Protein sim. GBank gi 4417293 gb AAD20418  - (AC007019) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264488, 264259, 29331824, 264104, 264109, 264509, 265006, 264759, 265018, 264448, 264288, 21906766, 55811957, 265021, 33657023, 27488265, 35696423, 264636, 264558, 264557, 264559, 264566
2141	79623986 (4281, 4282)		UNCLASSIFIED	265020, 264693
2142	80041222 (4283, 4284)		UNCLASSIFIED	263978
2143	94140051 (4285, 4286)	Novel Protein sim. GBank gi 2135766 pir IS53382 - mucin 5AC (clone JER47) - human (fragment)	UNCLASSIFIED	22278997, 29331827, 264907, 265020, 60432113
2144	94320114 (4287, 4288)	Novel Protein sim. GBank gi 2078493 (U43200) - antifreeze glycopetide AFGP polypeptide precursor [Boreogadus seida]	UNCLASSIFIED	65274572, 264259, 29331824, 29331827, 264906, 264908, 264591, 265011, 87168559, 264600, 265019, 264288, 264768, 21906765, 21906767, 55811576, 35696423, 85274791, 22279002
2145	20564305 (4289, 4290)		UNCLASSIFIED	263978
2146	87010515 (4291, 4292)	Novel Protein sim. GBank gi 1255871 (U53341) - short region of weak similarity to bovine membrane receptor p63 (PIR:S28503) [Caenorhabditis elegans]	UNCLASSIFIED	264909, 60433356, 264688
2147	80432911 (4293, 4294)	Novel Protein sim. GBank gi 3080398 emb CAA18718.1  - (AL022603) putative protein [Arabidopsis thaliana]	UNCLASSIFIED	264907, 264768, 264769, 18108385
2148	80048811 (4295, 4296)	Novel Protein sim. GBank gi 728837 sp P38194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	UNCLASSIFIED	264593
2149	87362022 (4297, 4298)	Novel Protein sim. GBank gi 119863 sp P20693 FCE2_MOUSE - LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE RECEPTOR) (FC-EPSILON-RII) (CD23)	glycoprotein	29331824, 29331826, 35696052, 264758, 87168474, 265018, 52644150, 33657109
2150	94140059 (4299, 4300)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	22278998, 29331822, 29331824, 29331828, 264764, 264769, 21906766, 264486
2151	95353241 (4301, 4302)	Novel Protein sim. GBank gi 5689407 dbj BAA82987.1  - (AB028958) KIAA1035 protein [Homo sapiens]		22278996, 56894075, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 29331828, 264508, 264511, 60433356, 264758, 264596, 33109954, 60174639, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264288, 264689, 21906765, 21906766, 21906768, 265020, 60170615, 33657109, 33657182, 33657349, 18108370, 264635, 264557, 60170394, 18108385, 87168518, 22279000
2152	79321640 (4303, 4304)	Novel Protein sim. GBank gi 3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	kinase	18108397, 18108398, 265007, 264591, 265011, 18108351, 18108368, 18108374, 18108388

2153	88313371 (4305, 4306)	Novel Protein sim. GBank gij4758704ref[NP_004216.1]pMASL - MFH-amplified sequences with leucine-rich tandem repeats 1	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264488, 263994, 52646842, 22278896, 22278898, 22278899, 264259, 29331822, 35680032, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264758, 87168474, 87188558, 265017, 265018, 264760, 264288, 264369, 264766, 264687, 264769, 52644229, 21906766, 21906768, 35695917, 33657023, 33657109, 35695855, 264631, 264632, 264635, 264636, 264639, 18108385, 264483, 264564, 264486
2154	87408034 (4307, 4308)	Novel Protein sim. GBank gij225150[prj1209265U - chorton protein B11 [Bombyx mori]]		UNCLASSIFIED	5694075, 264094, 265009, 265019, 264288, 21906767, 35695917
2155	87424072 (4309, 4310)			UNCLASSIFIED	18108392, 18108398, 22278896, 264259, 29331824, 265008, 265010, 265011, 265017, 265019, 264288, 264688, 265020, 264693, 264628, 56182323
2156	84295205 (4311, 4312)	Novel Protein sim. GBank gij3970966 (AC004974) - spa-1-like; similar to AF026504 (PID:g2555183) [Homo sapiens]			265007, 264684
2157	87316344 (4313, 4314)	Novel Protein sim. GBank gij1076211[pirjS50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii]		UNCLASSIFIED	264591
2158	86444218 (4315, 4316)	Novel Protein sim. GBank gij4650844[dbjBAA77027.1] - (AB026180) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain		264596
2159	80083729 (4317, 4318)	Novel Protein sim. GBank gij2879925[dbjBAA24826] - (AB007897) KIAA0437 [Homo sapiens]			29331822, 264112, 265009, 264691, 33657023, 264634
2160	16283674 (4319, 4320)	Novel Protein sim. GBank gij1504006[dbjBAA13202] - (D86966) simlarto human ZFY protein. [Homo sapiens]		UNCLASSIFIED	265008
2161	87739131 (4321, 4322)			UNCLASSIFIED	65274572, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 265007, 264910, 264591, 264592, 264593, 55812038, 264596, 264758, 265011, 264600, 264762, 264763, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 264689, 265020, 264691, 264628, 264629, 263978, 264632, 264634, 264557, 264638, 264639, 18108385, 264563, 264586, 264587
2162	94318528 (4323, 4324)			UNCLASSIFIED	56182575, 22278898, 264093, 264683, 33657023, 65274620, 60432113
2163	95417158 (4325, 4326)	Novel Protein sim. GBank gij3876537[embCAA98270] - (Z73974) cDNA EST yk29115.3 comes from this gene; cDNA EST yk29115.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	
2164	80568456 (4327, 4328)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	collagen	264603, 264637, 264565

2165	94329169 (4329, 4330)	Novel Protein sim. GBank gj1086794 (U41107) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	56894075, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 29331830, 56182435, 265009, 21908754, 33657084, 265011, 265019, 264448, 264288, 264369, 21906765, 21906768, 21906769, 265020, 265021, 264691, 264692, 33657023, 65274620, 35695855, 264556, 60170394, 83373044, 60432113, 22278002, 264567, 52645156, 22278994, 22278998, 66714117, 29331828, 52644045, 265018, 265019, 264369, 21906765, 21906767, 21906768, 21906769, 265021, 265022, 264693, 27486282, 35695763, 18108376, 56526486, 87168518, 264567
2166	87618934 (4331, 4332)	Novel Protein sim. GBank gj2706522[embjCAA75816] - (Y15895) ubiquitin activating enzyme [Drosophila melanogaster]	ubiquitin		56182575, 35696286, 29331824, 29331826, 29146498, 56182435, 265008, 265009, 264592, 264593, 33657402, 33109954, 265011, 265017, 265018, 18108351, 264369, 21908764, 21908765, 21908768, 29148627, 21908769, 52644150, 33657109, 35696423, 18108381, 18108384, 18108385, 60432113, 264567
2167	87718864 (4333, 4334)	Novel Protein sim. GBank gj2224713[dbjBAA20840] - (AB002384) KIAA0386 [Homo sapiens]		UNCLASSIFIED	66714117, 29331827, 264907, 264511, 264591, 265018, 264764, 264683, 264766, 264768, 264566
2168	86899334 (4335, 4336)	Novel Protein sim. GBank gj4321407[gb AAD15748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	Contains protein domain (PF00664) - ABC transporter transmembrane region.	transport	264628, 264555, 264559
2169	87886937 (4337, 4338)	Novel Protein sim. GBank gj5106521[gb AAD39741.1]AF10536 - (AF105365) K-CI cotransporter KCC4 [Homo sapiens]		UNCLASSIFIED	65274572, 56182575, 22278997, 22278998, 264259, 29331825, 264509, 264906, 56182435, 60433438, 55812038, 264596, 55811386, 265019, 264762, 264763, 264448, 264764, 264684, 264288, 264766, 264685, 56181562, 264689, 55811957, 265020, 264535, 264691, 33657109, 60431528, 18108374, 35696423, 55811576, 65274791, 264634, 264638, 264558, 87168518, 60432113, 264564
2171	80194050 (4341, 4342)			UNCLASSIFIED	264369, 265020, 264558
2172	85452460 (4343, 4344)			UNCLASSIFIED	264259, 264558
2173	87036740 (4345, 4346)	Novel Protein sim. GBank gj4309681[gb AAD15478] - (AC006930) R33423.1 [Homo sapiens]		UNCLASSIFIED	264369
2174	95003288 (4347, 4348)	Novel Protein sim. GBank gj2493778[sp Q09456]YQ35_CAEEL - PUTATIVE CUTICLE COLLAGEN C09G5.5			264908, 35695855, 264555, 264557

2175	94325850 (4349, 4350)	Novel Protein sim. GBank gij1263287 (U47855) - fibroin-3 [Araneus diadematus]		UNCLASSIFIED	264488, 35696286, 20281099, 29331826, 604322289, 35696052, 264109, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264591, 264594, 264595, 264596, 264758, 55812038, 265011, 264600, 264603, 264760, 264762, 264448, 264764, 264288, 264766, 264686, 264687, 21908768, 55811957, 35695917, 265020, 265022, 264691, 264692, 33857023, 264693, 264628, 264629, 55811576, 35696423, 65274791, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264558, 18108385, 60432113, 264563, 264564, 264565, 264566, 264488, 264567
2176	88223392 (4351, 4352)	Novel Protein sim. GBank gij728837 sp P39194 ALU7_HUMAN - !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!	Contains protein domain (PF00805) - oncogene Pentapeptide repeats (8 copies)	oncogene	52644507, 52646842, 22278994, 35696286, 22278996, 22278999, 29331826, 29331827, 35696052, 29331828, 33856970, 29331830, 264910, 33857402, 264758, 52644298, 87188559, 265018, 264889, 21908765, 21906767, 21906769, 35695917, 52644150, 264690, 33657023, 33657109, 52645129, 33657182, 27486261, 27486262, 33857349, 18108376, 18108377, 35695855, 87188518, 60432113, 264404, 22279000, 264488
2177	94128942 (4353, 4354)	Novel Protein sim. GBank gij5454072 ref NP_006416.1 pSLU7 - step II splicing factor SLU7		kinase	18108392, 22278997, 22278999, 264093, 33657402, 265019, 264448, 264766, 264689, 21906767, 21906768, 21906769, 265021, 33657023, 18108370, 18108374, 60432113, 22279002
2178	87601557 (4355, 4356)	Novel Protein sim. GBank gij473407 (U08215) - NST-1 [Mus musculus]	Contains protein domain (PF00012) - eph Hsp70 protein	eph	264488, 22278996, 22278999, 29331824, 29331825, 29331826, 29331827, 52644296, 87169474, 18108370, 35695855, 22279002
2179	87316275 (4357, 4358)			UNCLASSIFIED	60424269, 264760, 264628, 264632



2180	95351397 (4358, 4360)	Novel Protein sim. GBank gi 3122317 sp P90648 KMH_B_DICDI - MYOSIN HEAVY CHAIN KINASE B (MHCK B)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52644507, 22278994, 35696266, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 33656970, 264508, 264509, 264908, 264908, 29331830, 264909, 264510, 265006, 265007, 33657402, 55812038, 21906754, 87168474, 87168559, 265017, 265018, 265019, 264763, 264682, 264683, 264684, 264288, 264686, 21906765, 21906766, 21906769, 265020, 265021, 265022, 52644150, 33657023, 33657109, 27486265, 33657349, 18108374, 35696423, 35696555, 263981, 60170394, 18108385, 56526486, 87168518, 60432113, 22279000, 264482, 264566, 264567, 264486, 29331827, 264369, 18108376, 264564
2181	85764930 (4361, 4362)	Novel Protein sim. GBank gi 3024689 sp Q15542 T2D4_HUMAN - TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT (TAFII-100) (TAFII100)		kinase	
2182	87637731 (4363, 4364)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278996, 22278997, 22278998, 264259, 29331822, 56182435, 264112, 264764, 264286, 21906767, 21906768, 21906769, 33657109, 18108376, 60170394, 22279000, 22279002 264760
2183	85460649 (4365, 4366)	Novel Protein sim. GBank gi 3873408 gb AAC77482.1  - (U17129) unknown [Rhodococcus erythropolis]		Inf	29331822, 29331825, 29331826, 56182435, 265011, 264685, 264686, 21906768, 18108370, 264629, 264631, 264636, 264557
2184	87760690 (4367, 4368)	Novel Protein sim. GBank gi 3114713 (AF061346) - Edp1 protein [Mus musculus]			29331824, 264907, 66712502, 264757, 265019, 264288, 264692, 56526486
2185	87828463 (4369, 4370)	Novel Protein sim. GBank gi 5106956 gb AAC39906.1 AF113615 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]		ATPase-associated	264259, 29331822, 29331824, 29331826, 56182435, 264592, 55812038, 264760, 264766, 55811957, 33657023, 55811576, 56182323, 264563
2186	87739227 (4371, 4372)	Novel Protein sim. GBank gi 2664625 emb CAA16972  - (AL021811) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	35696052, 264905, 264906, 264907, 264908, 264510, 264511, 265008, 264910, 264758, 265019, 264762, 264681, 264766, 264769, 35695917, 264692, 35696423, 264631, 264635, 264637, 18108388, 264566, 264486, 18108398, 56994075, 264259, 29331824, 29331825, 66714117, 29331827, 264906, 29331830, 265018, 265020, 265021, 56182323, 264559, 22279000, 22279002
2187	87388173 (4373, 4374)			histone	
2188	87771708 (4375, 4376)	Novel Protein sim. GBank gi 5107818 gb AAD40129.1 AF149413 - (AF149413) contains similarity to histone deacetylases; Pfam PF00850. Score=13.3, E=5e-10, N=1 [Arabidopsis thaliana]		Contains protein domain (PF01596) - O-methyltransferase	22278996, 264259, 29331826, 21906764, 264369, 264288, 263867
2189	85693573 (4377, 4378)	Novel Protein sim. GBank gi 3452357 (AF075724) - unknown [Legionella pneumophila]			

2180	87639197 (4378, 4380)	Novel Protein sim. GBank gij132575[sp]P29315[RINI_RAT - RIBONUCLEASE INHIBITOR]		nucleaseinhib	22278996, 22278998, 29331822, 29331824, 29331826, 265008, 264910, 60170831, 55812038, 52844296, 265010, 265018, 264685, 264688, 56181562, 21908769, 35695917, 265022, 60170394, 22279000
2191	95198928 (4381, 4382)	Novel Protein sim. GBank gij5327002[emb]CAB46272.1] - (Y18503) XAP-5-like protein [Homo sapiens]			29331825, 29331826, 29331830, 264510, 264511, 264910, 264593, 264594, 264556, 264559
2192	11126316 (4383, 4384)	Novel Protein sim. GBank gij462600[sp]P34400[Mi10_CAEEL - MIG-10 PROTEIN]	Contains protein domain (PF00169) - PH domain		264558
2193	94140073 (4385, 4386)	Novel Protein sim. GBank gij5420389[emb]CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	56181686, 29331825, 29331827, 264508, 264909, 265008, 264592, 60432229, 264288, 264684, 264766, 35695917, 33657023, 60431802, 60431528, 55810764, 55811576, 65274781, 35695855, 60431850, 56182323, 60432113
2184	21418714 (4387, 4388)	Novel Protein sim. GBank gij2773341 (AF040954) - putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]			264592
2195	88083023 (4389, 4390)	Novel Protein sim. GBank gij2832763[emb]CAA15685.1] - (AL009191) /prediction=(method:; /prediction=(method:; /match=(desc:; /match=(desc:; /molif=(desc: [Drosophila melanogaster]		UNCLASSIFIED	22278996, 22278999, 35696052, 265006, 21908754, 265017, 35695917, 265021, 265022, 35695855
2196	95091631 (4391, 4392)	Novel Protein sim. GBank gij5262487[emb]CAB46699.1] - (AL080076) hypothetical protein [Homo sapiens]		collagen	56182575, 35696286, 22278997, 22278999, 264259, 29331822, 66714117, 60432289, 29331827, 35696052, 29331828, 264508, 52844045, 56182435, 264510, 265007, 265008, 265009, 60433438, 55812038, 265010, 265011, 264448, 264288, 264686, 264687, 52644229, 21906765, 21908766, 21908767, 35695917, 265022, 264691, 33657023, 264693, 18108370, 18108376, 35696423, 55811578, 65274791, 35695855, 264636, 56182323, 18108385
2197	95073613 (4393, 4394)	Novel Protein sim. GBank gij4929567[gb]AAD34044.1]AF151807 CGI-49 protein [Homo sapiens]			264768, 264769, 21906765, 21906766, 21908767, 29148627, 55811857, 35696286, 265020, 22278998, 265021, 264259, 33657023, 264693, 29331824, 35696052, 29331828, 18108370, 35695855, 264113, 265008, 264910, 60432229, 56182323, 33657402, 264758, 83373044, 21906754, 265018, 265019, 22279002, 264482, 264448, 264565, 264288, 264369
2198	88080914 (4395, 4396)	Novel Protein sim. GBank gij3548787 (AC005622) - R30953_1 [Homo sapiens]		UNCLASSIFIED	

2199	88054355 (4397, 4398)	Novel Protein sim. GBank gij2739372 (AC002505) - hypothetical protein [Arabidopsis thaliana]				264105, 264110, 264112, 264688, 55811957, 33657023, 264692, 263967, 20281071, 56526486
2200	87405385 (4398, 4400)	Novel Protein sim. GBank gij3043634[dbj BAA25481] - (AB011127) KIAA0555 protein [Homo sapiens]	struct			29331824, 264763, 264768
2201	94316872 (4401, 4402)	Novel Protein sim. GBank gij3913470[sp O57314 DHXB_ANAPL - PUTATIVE STEROID DEHYDROGENASE SPM2]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase		29331824, 35696052, 264905, 264907, 33657402, 55811386, 265017, 265018, 265019, 264288, 21906768, 35695917, 265020, 265022, 33657023, 33657109, 27486261, 18108370, 35696423, 35695855, 264555, 264556, 83373044, 87168518, 60432113
2202	91672385 (4403, 4404)	Novel Protein sim. GBank gij5262665[emb CAB45767.1] - (AL080186) hypothetical protein [Homo sapiens]	UNCLASSIFIED			264489, 264259, 29331824, 60432289, 35696052, 264905, 264909, 264592, 265017, 265018, 265019, 18108351, 264762, 264448, 264369, 264288, 264768, 21906768, 21908766, 264690, 264691, 264692, 33657109, 264634, 264636, 264555, 264639, 264558, 264559, 83373044, 18108385, 264404, 22279002, 264482
2203	87761832 (4405, 4406)	Novel Protein sim. GBank gij1172845[sp P46629 RB25_RABIT - RAS-RELATED PROTEIN RAB-25]	Contains protein domain (PF00071) - Ras family	glycoprotein		52646365, 56994075, 264259, 29331822, 29331826, 29331827, 29331828, 264910, 265010, 265011, 87168559, 265018, 265019, 264605, 264288, 21906769, 35695917, 33657023, 264692, 33657109, 35695763, 18108376, 264638, 22279000, 264566, 264567
2204	88088671 (4407, 4408)	Novel Protein sim. GBank gij121036[sp P29348 GBT3_RAT GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA 3 SUBUNIT (GUSTOCIN ALPHA-3 CHAIN)]	Contains protein domain (PF00503) - G-protein alpha subunit	UNCLASSIFIED		
2205	84147589 (4409, 4410)	Novel Protein sim. GBank gij4589480[dbj BAA76768.1] - (AB023141) KIAA0924 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind		18108394, 18108397, 56182575, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264906, 265007, 265008, 265009, 60432229, 265010, 265011, 265018, 264683, 264288, 264369, 264686, 21906766, 21908768, 21908769, 264690, 264691, 264693, 18108368, 55811576, 65274791, 264634, 18108381, 18108384, 60432113, 22279002, 264563, 264566
2206	20620008 (4411, 4412)		UNCLASSIFIED			264591
2207	87787870 (4413, 4414)	Novel Protein sim. GBank gij4557753[ref NP_000372.1 pMID1 - midline 1 protein]	Contains protein domain (PF00622) - SPRY domain			29331822, 56182181, 28331827, 35696052, 52844045, 265006, 265019, 56181562, 55811957, 265021, 33657023, 35695763, 35695855, 60170394, 60432113, 264568
2208	86100830 (4415, 4416)					264908, 265019, 18108351, 21908769
2209	87800420 (4417, 4418)	Novel Protein sim. GBank gij3986746 (AF105228) - tuftelin [Bos taurus]		struct		264112, 265009, 264691, 18108365, 18108374, 264634, 20281166

2210	57152407 (4418, 4420)	Novel Protein sim. GBank gij728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	264603
2211	87341720 (4421, 4422)	Novel Protein sim. GBank gij728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		oncogene	264685, 264686, 18108365, 22278002, 264482
2212	91223924 (4423, 4424)	Novel Protein sim. GBank gij3776027 emb CAA09214  - (AJ010475) RNA helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278995, 22278997, 22278999, 264082, 264094, 29331822, 66714117, 29331828, 29331828, 264907, 52644045, 265009, 60170831, 21906754, 87168559, 265017, 265019, 18108351, 264683, 18108354, 264369, 264766, 264687, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 33657109, 18108370, 18108374, 264638, 56182323, 18108384, 18108387, 87168518, 264565
2213	91219309 (4425, 4426)	Novel Protein sim. GBank gij5420387 emb CA846679.1  - (AJ243459) proteophosphoglycan [Leishmania major]			56182575, 22278998, 22278997, 35696052, 264905, 66712502, 264908, 264828, 56182435, 264112, 265008, 60431735, 60433438, 21906754, 265010, 265011, 285017, 265018, 265019, 18108351, 264765, 21906765, 21906768, 21906769, 265020, 265021, 264693, 264629, 263974, 263976, 18108379, 55811576, 264556, 264637, 264558, 83373044, 22278002, 264482, 264483

2214	95361453 (4427, 4428)	Novel Protein sim. GBank gil4504325[re]NP_000173.1[pHADH - hydroxyacyl- Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha su	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	264488, 52644507, 18108394, 56182575, 22278994, 22278995, 35696286, 56994075, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 52645080, 29331822, 29147620, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 20281100, 264509, 264907, 66712502, 264908, 29331830, 52644045, 56182435, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 264593, 60433356, 60433438, 33109954, 33657084, 52644288, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 18108351, 264448, 264682, 264763, 264288, 264687, 52644228, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 264532, 60170815, 264690, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 33657182, 27486262, 27486264, 27486265, 35695763, 18108370, 264629, 60431528, 18108374, 18108376, 55810764, 35696423, 35695855, 264634, 264636, 52644332, 264638, 264558, 60170394, 18108381, 56182323, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22278002, 264482, 264564, 264565, 264566, 264909, 265006, 264555, 264558, 87168518
2215	95419208 (4428, 4430)	Novel Protein sim. GBank gil1947160 (AF000298) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans]		
2216	87614046 (4431, 4432)	Novel Protein sim. GBank gil1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]		264693
2217	80589404 (4433, 4434)	Novel Protein sim. GBank gil5031707[re]NP_005503.1[pGARP - glycoprotein A repetitions predominant]	UNCLASSIFIED	
2218	85518254 (4435, 4436)	Novel Protein sim. GBank gil3878636[emb]CAA88953] - (Z49128) similar to cAMP-dependant protein kinase; cDNA EST EMBL: T00719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk492f4.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00560) - Leucine Rich Repeat	264288, 33657109, 264556
2219	87614048 (4437, 4438)	Novel Protein sim. GBank gil1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35696423, 264563
			Contains protein domain (PF01963) - TraB family	264682, 264683, 264688, 264689, 264693, 18108370, 18108376

2220	95354165 (4438, 4440)	Novel Protein sim. GBank gij4507261 ref NP_003145.1 pSTAT - statheir			264488, 18108394, 18108395, 35686286, 264259, 284097, 60432289, 264509, 264905, 264906, 284907, 29331830, 264908, 264909, 264510, 284511, 265007, 264512, 264910, 265008, 264593, 264594, 60433356, 264595, 55812038, 284758, 85858542, 265010, 264601, 264603, 265019, 264605, 264760, 264762, 284448, 284784, 284389, 264766, 18108357, 264768, 264687, 18108358, 264769, 55811957, 264690, 264691, 33657023, 264692, 18108362, 18108368, 264628, 264829, 18108374, 263978, 264634, 264635, 264636, 264637, 264638, 18108385, 264483, 264568, 264486, 264567
2221	88060827 (4441, 4442)	Novel Protein sim. GBank gj3549154 (AC005625) - R27328_1 [Homo sapiens]			
2222	84425892 (4443, 4444)			UNCLASSIFIED	264908, 265020, 35695855
2223	95091849 (4445, 4446)			UNCLASSIFIED	265010, 264685, 264690, 264693, 264628, 263974, 263976, 55811576, 264555, 264638, 83373044, 264483
2224	87388515 (4447, 4448)	Novel Protein sim. GBank gj3876005 emb CAA84799  - (Z35719) cDNA EST EMBL:D67419 comes from this gene; cDNA EST EMBL:C13853 comes from this gene; cDNA EST EMBL:C11578 comes from this gene; cDNA EST yk234a7.3 comes from this gene; cDNA EST yk234a7.5 comes from this gene; cDNA ES ...	Contains protein domain (PF01958) - Domain of unknown function	UNCLASSIFIED	264259, 264509, 56182435, 265006, 265008, 265009, 264757, 21806754, 18108351, 264693, 18108374, 18108385
2225	85749484 (4449, 4450)	Novel Protein sim. GBank gj1255847 (U53338) - C05E11.1 gene product [Caenorhabditis elegans]		transport	22278994, 22278995, 22278999, 52644045, 264600, 265019, 21806785, 21806789
2226	86978953 (4451, 4452)	Novel Protein sim. GBank gj4826524 emb CAB42852.1  - (AL049848) hypothetical protein [Homo sapiens]			264259, 29331822, 29331824, 29331825, 29331827, 264508, 284908, 285007, 284691, 264634, 264486
2227	87721135 (4453, 4454)			UNCLASSIFIED	22278999, 265006, 265008, 18108354, 29148629, 29148784, 27486281, 18108374, 264637, 18108384
2228	91227337 (4455, 4456)	Novel Protein sim. GBank gj1808976 (U16800) - ribonucleoprotein [Xenopus laevis]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	- dna_rna_bind	264091, 264092, 264094, 29331822, 29331825, 68714117, 264693, 263972, 284639, 83373044, 264583
2229	88060931 (4457, 4458)	Novel Protein sim. GBank gj3549155 (AC005625) - R27328_2 [Homo sapiens]		UNCLASSIFIED	

2230	85342915 (4459, 4460)	Novel Protein sim. GBank gij226154[prfj1412350A - DNA polymerase [Human adenovirus type 2]	UNCLASSIFIED	264488, 264768, 52644507, 264769, 21906765, 21906768, 21906767, 21906769, 22278995, 35695917, 22278996, 22278997, 22278998, 22278999, 265021, 264259, 52645129, 29331827, 264508, 264509, 264907, 18108370, 18108374, 35696423, 35695855, 265007, 264910, 264555, 33657402, 21906754, 18108387, 265010, 265018, 265019, 264760, 264288, 264587, 264563
2231	88060937 (4461, 4462)	Novel Protein sim. GBank gij3549154 (AC005625) - R27328_1 [Homo sapiens]	UNCLASSIFIED	
2232	87762581 (4463, 4464)	Novel Protein sim. GBank gij5281316[gbpAAD41478.1][AF133124] transcription factor IIC63 [Homo sapiens]	transcription factor	18108394, 56182575, 22278995, 35696286, 22278997, 22278999, 264259, 29331827, 35696052, 264907, 56182435, 265006, 265007, 265008, 264910, 264758, 55812038, 264503, 265018, 265019, 18108351, 264682, 264764, 264683, 264369, 264288, 264688, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 29148829, 35695917, 264690, 52644150, 264691, 33657023, 264693, 18108370, 18108374, 55811576, 35695855, 264639, 18108385, 264564, 264906, 33657402, 265018, 264288, 264686, 265020, 264635, 18108385
2233	87755292 (4465, 4466)	Novel Protein sim. GBank gij4248733[gbpAAD13780] - (AF109377) IdIBp [Mus musculus]		56182435, 264368, 264688, 21906765, 265020, 264693, 264556, 56526486
2234	87771817 (4467, 4468)	Novel Protein sim. GBank gij1708559[spP54352][EAS_DROME - ETHANOLAMINE KINASE (EASILY SHOCKED PROTEIN)]	kinase	
2235	91012318 (4469, 4470)	Novel Protein sim. GBank gij4972734[gbpAAD34762.1] - (AF132174) unknown [Drosophila melanogaster]	UNCLASSIFIED	22278997, 264563
2236	88003131 (4471, 4472)	Novel Protein sim. GBank gij1082675[pilrjB53814 - p20 protein - human]	Contains protein domain (PF00400) - WD domain, G-beta repeat Contains protein domain (PF00011) - Hsp20/alpha crystallin family	264569, 264687, 264768, 265022, 264259, 60432049, 264681, 29331826, 60432289, 20281149, 264906, 264907, 264511, 265008, 265009, 264634, 264635, 264636, 264555, 264556, 264557, 264558, 60433356, 264595, 264559, 60433438, 60432113, 264761, 264762, 264763, 264764
2237	91012318 (4473, 4474)	Novel Protein sim. GBank gij4972734[gbpAAD34762.1] - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat kinase	264488, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 22278995, 22278996, 22278997, 22278998, 265020, 265021, 22278999, 264259, 29331824, 29331826, 29331827, 35695763, 18108376, 35695855, 265007, 60432229, 33657402, 60433358, 60433438, 83373044, 18108385, 21906754, 18108387, 60432113, 22279000, 265019, 22279002, 264482, 18108351, 264288

2238	84988857 (4475, 4476)		Contains protein domain (PF00286) - Viral coat protein	264509, 264907, 264629, 264634, 264564
2239	87798688 (4477, 4478)			28331825, 265008, 264369, 33657109, 18108370, 18108374, 264557, 264559, 264488, 65274572, 56182575, 35698286, 22278997, 22278999, 264259, 29331827, 35698052, 264508, 52844045, 56182435, 284511, 265007, 265008, 265009, 60433356, 60433438, 55812038, 21906754, 33657084, 55811386, 265018, 265019, 18108351, 264683, 264288, 264768, 264687, 264688, 264769, 21906765, 21906768, 21906769, 35695917, 265021, 265022, 60170615, 52644150, 33657023, 33657182, 33657349, 35695763, 18108370, 35696423, 35695855, 87168518, 22279000
2241	80091951 (4481, 4482)			264693, 264629
2242	81228075 (4483, 4484)	Novel Protein sim. GBank gij2484312 sp P70541 E2BG_RAT - TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)	UNCLASSIFIED synthase	22278995, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 264509, 265007, 265009, 264598, 21906754, 265010, 265011, 265017, 265018, 265019, 264448, 264369, 264288, 52844229, 21906785, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657109, 27486262, 27486264, 18108374, 35695855, 264634, 264637, 56182323, 83373044, 56526486, 87168518, 264564 265008 264604
2243	78902026 (4485, 4486)	Novel Protein sim. GBank gij2291143 (AF016417) - Similar to BZIP transcription factor [Caenorhabditis elegans]	UNCLASSIFIED	
2244	85723527 (4487, 4488)	Novel Protein sim. GBank gij470340 (U00043) - similar to beta-mannosyltransferase [Caenorhabditis elegans]	UNCLASSIFIED	
2245	85318545 (4489, 4490)		Contains protein domain (PF00534) - Glycosyl transferases group 1	52645156, 22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331827, 264907, 264512, 60433438, 264758, 21906754, 265011, 264603, 264764, 264687, 21906767, 21906768, 21906769, 55811957, 265022, 264691, 264629, 35698423, 264638, 18108387, 60432113, 22279000, 22279002, 264566



2246	94848710 (4481, 4492)	Novel Protein sim. GBank gi 4986086 dbj BAA78326.1  - (AB028069) activator of S phase Kinase [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	65274572, 22278895, 35696286, 22278896, 22278897, 22278899, 264259, 35696052, 264106, 264905, 264907, 265008, 265007, 265008, 60433438, 33109954, 87168559, 265018, 265019, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 265022, 265022, 27486264, 18108370, 18108374, 65274791, 35695855, 60432113
2247	87862542 (4493, 4494)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	52645156, 52646365, 52645080, 35686052, 33656970, 52646317, 33657084, 265017, 21906768, 21906769, 35695917, 33657109, 52645129, 33657182, 27486261, 27486262, 33657349, 27486285, 18108387
2248	95412986 (4495, 4496)	Novel Protein sim. GBank gi 4758502 ref NP_004123.1 pHABP - hyaluronan-binding protein 2	Contains protein domain (PF00089) - Trypsin	cathepsin	264488, 264259, 264907, 29331830, 264909, 265007, 265009, 264595, 21906754, 65274444, 264603, 265019, 264762, 264448, 264288, 264688, 21906768, 55811957, 265021, 264691, 18108374, 264634, 264635, 264636, 264555, 264638, 264557, 264558, 264559, 18108383, 83373044, 18108385, 264488
2249	94865662 (4497, 4498)	Novel Protein sim. GBank gi 4038461  (AF107772) - TcST11 [Trypanosoma cruzi]	Contains protein domain (PF00515) - TPR Domain	eph	264768, 264628, 264636, 264637
2250	79827508 (4498, 4500)	Novel Protein sim. GBank gi 3738140 emb CAA21241  - (AL031852) valyl-tRNA synthetase, mitochondrial precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	264908, 18108374
2251	87385863 (4501, 4502)	Novel Protein sim. GBank gi 3218467 emb CAA07090.1  - (AJ006528) putative phosphatase [Gallus gallus]		UNCLASSIFIED	264259, 35696052, 264508, 56182435, 265009, 264592, 264593, 264760, 264448, 264884, 264288, 264690, 264628, 55811576, 264555, 264556, 264557, 264558, 264559, 264566
2252	87735867 (4503, 4504)	Novel Protein sim. GBank gi 4929325 gb AAD33953.1 AF14531 - (AF145316) vacuolar proton pump delta polypeptide [Homo sapiens]	Contains protein domain (PF01813) - ATP synthase subunit D	synthase	264092, 264094, 264259, 29331822, 66714117, 29331828, 264102, 264103, 264104, 264105, 264109, 264112, 264511, 265007, 60433356, 265010, 18108351, 21906767, 21906768, 264691, 263974, 263977, 264488, 264567
2253	91010703 (4505, 4506)			UNCLASSIFIED	65274572, 265019

2254	95320031 (4507, 4508)	Novel Protein sim. GBank gi 4502847 ref NP_001271.1 pCIRB - cold inducible RNA- binding protein	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	264569, 18108394, 18108398, 56182575, 58994075, 35698286, 22278999, 264084, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 35698052, 264106, 264508, 264509, 264806, 264807, 29331830, 66712502, 264908, 264909, 264510, 265006, 264511, 265007, 265008, 265009, 60170831, 60432229, 60433356, 60433438, 264758, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264764, 264288, 264369, 264768, 264686, 264768, 264769, 21908765, 21908787, 55811957, 264691, 33657023, 264692, 18108362, 65274620, 263969, 264628, 18108370, 60431528, 263972, 264629, 18108372, 18108377, 18108378, 55811576, 35698423, 35698555, 264630, 264634, 264635, 264636, 264656, 263981, 264638, 56182323, 60170394, 264558, 18108381, 18108382, 83373044, 18108385, 87168518, 60432113, 22279002, 264482, 264564, 264565, 264488, 264587, 18108391
2255	91010546 (4509, 4510)	Novel Protein sim. GBank gi 5541865 emb CAB51072.1  - (AL086858) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	struct	65274572, 56182575, 22278997, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264508, 264905, 264906, 264907, 66712502, 264908, 56182435, 264510, 264511, 265008, 264583, 264595, 21906754, 33109954, 87168474, 285011, 265017, 265019, 264682, 264764, 264369, 264288, 264768, 264685, 264686, 264768, 21906765, 21906768, 21906768, 21906769, 265020, 60170815, 52844150, 264690, 264692, 264693, 33657109, 33657349, 264632, 264636, 52644332, 56182323, 22279000, 22279002 264768, 264689, 18108374
2256	87020531 (4511, 4512)	Novel Protein sim. GBank gi 3327174 dbj BAA31655  - (AB014580) KIAA0680 protein [Homo sapiens]		UNCLASSIFIED	
2257	80088235 (4513, 4514)			UNCLASSIFIED	22278996, 22278998, 264681, 21906765, 21906768, 264567
2258	88090516 (4515, 4516)	Novel Protein sim. GBank gi 3025446 (AC004528) - R32184_2 [Homo sapiens]	Contains protein domain (PF00060) - Ligand-gated ion channel	misc_channel	264908, 264592, 264764

2259	95364155 (4517, 4518)	Novel Protein sim. GBank gi 4894140 emb CAB43278.1  - (AL050110) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108396, 65274572, 56182575, 22278997, 22278998, 264259, 28331822, 29331827, 264905, 68712502, 284908, 264909, 56182435, 265007, 285008, 60432229, 33657084, 87168559, 18108351, 264448, 264683, 264288, 264369, 56181582, 265021, 60170615, 264690, 33857109, 60431528, 18108374, 52644332, 56182323, 18108385, 22279000, 22279002, 264482
2260	88084119 (4519, 4520)	Novel Protein sim. GBank gi 3080663 (AC004614) - similar to f-spondin proteins AB006086 (PID:g2529225) [Homo sapiens]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	oxidase	56182575, 265020, 264905, 264906, 264908, 35696423, 264511, 264635, 55812038, 264758, 265018, 265019, 264605, 264760, 264563
2261	88074157 (4521, 4522)	Novel Protein sim. GBank gi 3334528 emb CAA16138 - (AL021306) predicted using FGENEH [Homo sapiens]		UNCLASSIFIED	
2262	91639282 (4523, 4524)	Novel Protein sim. GBank gi 4877759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]			56182575, 22278999, 29331822, 29331825, 60432288, 29331827, 35696052, 264508, 66712502, 52644045, 56182435, 265008, 265008, 265009, 60433356, 55812038, 265010, 265017, 265019, 264288, 264369, 21906765, 21906767, 55811957, 35695917, 52644150, 33657023, 33857109, 55811578, 65274791, 56182323
2263	87602495 (4525, 4526)	Novel Protein sim. GBank gi 3341697 (AC003672) - hypothetical protein [Arabidopsis thaliana]			22278994, 22278997, 264907, 264828, 52644150, 18108361, 264693, 18108374
2264	87756525 (4527, 4528)	Novel Protein sim. GBank gi 1657601 (U66220) - unknown [Nannocystis exedens]		UNCLASSIFIED	264686, 264488, 264768, 264769, 264691, 264508, 264905, 264509, 264906, 264907, 264908, 264908, 35695855, 264510, 264511, 264512, 265007, 265009, 264638, 264639, 264757, 264758, 18108385, 265011, 264760, 264564, 264565, 264764, 264566, 264486, 264768
2265	85918663 (4529, 4530)	Novel Protein sim. GBank gi 477072 pir J448018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264689, 264910, 264764
2266	8773458 (4531, 4532)	Novel Protein sim. GBank gi 3150479 (AF067212) - partial CDS [Caenorhabditis elegans]	Contains protein domain (PF01305) - Ribosomal protein L15 amino terminal region	ribosomal prot	22278995, 22278997, 22278999, 264259, 265008, 265007, 265009, 60433438, 21906754, 265010, 265011, 265017, 264448, 264683, 264288, 264689, 21906765, 21906768, 35695917, 265021, 18108374, 264638, 22279000, 22279002, 264566, 264487

2267	8735838 (4533, 4534)	Novel Protein sim. GBank glj3560229[embjCAA20697.1] - (AL031530) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35698286, 264259, 29331824, 29331825, 35698052, 29331828, 264805, 264508, 264907, 264908, 264909, 264512, 265009, 264910, 264593, 33657402, 265010, 265018, 264762, 264448, 264288, 264369, 264768, 52644229, 35695917, 264691, 33657023, 18108382, 33657109, 35698423, 264834, 18108381, 87168518, 264568
2268	85893867 (4535, 4536)	Novel Protein sim. GBank glj728832[spP39189]ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	cadherin		264488, 264259, 264509, 264595, 265010, 265017, 264766, 18108385, 264486
2269	88177877 (4537, 4538)	Novel Protein sim. GBank glj103418[pir]S17885 - Tcd37 protein - fruit fly (Drosophila melanogaster)	UNCLASSIFIED		56182575, 60432048, 265007, 265009, 264591, 87168559, 264605, 18108351, 21808784, 265020, 264828, 60431528, 264638, 18108385, 18108387, 60432113, 264763
2270	80410327 (4539, 4540)				
2271	91010392 (4541, 4542)		Cyto450		264809, 56182435, 265008, 55812038, 55811957, 33657023, 264693, 33657109, 55810784, 55811576, 56182323
2272	84208220 (4543, 4544)	Novel Protein sim. GBank glj4176370 (AC005058) - similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	UNCLASSIFIED	Contains protein domain (PF00462) - Glutaredoxin	264905, 264908
2273	95014271 (4545, 4546)				52645156, 22278998, 22278999, 60432048, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264809, 265008, 264593, 60433438, 21908754, 265018, 264689, 21908765, 21908766, 21908767, 21908769, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27488264, 18108378, 35696423, 35695855, 264630, 52644332, 264558, 56182323, 22279002
2274	91640217 (4547, 4548)	Novel Protein sim. GBank glj1480112[embjCAA67961] - (X99642) HP1-BP74 protein [Mus musculus]	histone linker histone H1 and H5 family	Contains protein domain (PF00538) -	52645156, 22278997, 22278999, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 52644045, 264511, 265008, 265009, 60170831, 264591, 21908754, 33109954, 265011, 265018, 18108351, 264448, 264288, 264684, 264768, 21908765, 21908766, 21908767, 21908768, 52644150, 264693, 18108384, 35695763, 52644150, 264693, 18108384, 35695763, 18108374, 35698423, 264634, 264557, 264638, 52644332, 83373044, 18108385, 56526486, 87168518, 22278002
2275	86082501 (4549, 4550)	Novel Protein sim. GBank glj3165406 (AC004755) - fos37502_2 [Homo sapiens]	transport	Contains protein domain (PF00122) - E1-E2 ATPase	
2276	11287447 (4551, 4552)		UNCLASSIFIED		264555, 264556

2277	88084123 (4553, 4554)	Novel Protein sim. GBank gij2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1359906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278989, 35696052, 265008, 265019, 264369, 265020, 265022, 55810764, 264404, 22279002
2278	94133078 (4555, 4556)	Novel Protein sim. GBank gij2618702 (AC002510) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	18108394, 22278987, 28331826, 60433356, 60433438, 21906754, 285018, 33857023, 264639, 83373044, 264585
2279	80419375 (4557, 4558)	Novel Protein sim. GBank gij119714spIP13983JEXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	264766, 264565
2280	94239723 (4559, 4560)				
2281	85293048 (4561, 4562)	Novel Protein sim. GBank gij4240299[dbj]BAA74928.1] - (AB020712) KIAA0805 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transport	265008, 33109954, 285010, 285019, 265020, 264092, 264259, 29331822, 29331824, 29331826, 35696052, 264107, 264906, 264909, 52644045, 265006, 33857402, 60433356, 264758, 285011, 265019, 264681, 264683, 264684, 264686, 21906765, 21906767, 21906768, 21906769, 60170615, 264690, 52644150, 18108382, 264692, 18108368, 18108374, 263978, 264631, 18108381, 264559, 18108385, 56526486, 22279000, 264566, 264567
2282	87602829 (4563, 4564)	Novel Protein sim. GBank gij1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]		UNCLASSIFIED	264488, 264259, 29331822, 29331824, 29331827, 29331828, 29331830, 33657402, 60433438, 87168474, 265018, 18108351, 21906787, 21906769, 55811957, 33657023, 52645129, 33657109, 33657182, 27486262, 263972, 55811576, 87168518, 20281169
2283	95362386 (4565, 4566)	Novel Protein sim. GBank gij2495728spIQ92556]Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)		UNCLASSIFIED	60424179, 56182575, 22278994, 35696286, 22278997, 22278999, 29331822, 29331824, 56182181, 29331825, 29331827, 35696052, 29146498, 264905, 66712502, 264908, 265007, 265009, 60432229, 264593, 60431735, 60433356, 33109954, 33657084, 55811386, 87168474, 265010, 265011, 265018, 265019, 55811150, 264683, 264369, 264288, 264688, 21906765, 21906767, 21906768, 29146827, 21906769, 55811957, 265020, 265022, 33657182, 27486261, 18108370, 264628, 18108374, 55810764, 18108378, 55811576, 35696423, 35695855, 264630, 60431850, 263981, 18108382, 83373044, 18108385, 18108387, 60432113, 22279000, 264482, 264567

2284	95414955 (4587, 4588)	Novel Protein sim. GBank gi 2498797 sp Q64311 PNAD_MOUSE - PROTEIN N- TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN- AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNA4)			60424179, 52644507, 18108394, 52646842, 22278994, 35698286, 22278996, 22278997, 22278999, 264259, 60432049, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331830, 52644045, 56182435, 33657402, 60433438, 33109954, 21908754, 85658542, 67168559, 265018, 265019, 55811150, 264682, 264369, 21906765, 21906766, 21906767, 21908789, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 33657023, 33657182, 27486262, 27486264, 27486265, 18108376, 55810784, 35698423, 35695855, 60431850, 87168518, 60432113, 264482, 264584
2285	87781484 (4568, 4570)	Novel Protein sim. GBank gi 3342234 (U93809) - nuclear antigen EBNA-1 [Carcopillhedne herpesvirus 15]		collagen	35696052, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264595, 264760, 18108351, 264682, 264763, 264685, 264766, 264686, 264768, 264683, 264629, 35695855, 264631, 264634
2286	87737825 (4571, 4572)	Novel Protein sim. GBank gi 3873414 (U00043) - similar to D. melanogaster trithorax protein [Caenorhabditis elegans]		kinase	35696286, 58182435, 60170831, 264591, 60432229, 264592, 264593, 264594, 264595, 55812038, 264596, 87168474, 35695917, 264692, 55811576, 264555, 264557
2287	82886696 (4573, 4574)	Novel Protein sim. GBank gi 630805 p ri S42731 - collagen alpha 1 chain - sea urchin (Hemicentrotus putcherrimus) (fragment)	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	UNCLASSIFIED	264682
2288	84133083 (4575, 4576)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		tm7	22278995, 56994075, 22278997, 22278998, 264259, 60432289, 264508, 264512, 265008, 33657402, 265017, 265018, 265019, 18108351, 264448, 21906765, 21906766, 21908767, 21906768, 33657023, 264557, 22279000, 22279002
2289	88084133 (4577, 4578)	Novel Protein sim. GBank gi 2887497 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	
2290	88084137 (4579, 4580)	Novel Protein sim. GBank gi 2887497 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264683
2291	84295281 (4581, 4582)	Novel Protein sim. GBank gi 3253120 (AC005175) - R31449_3 [Homo sapiens]		struc1	18108394, 264907, 265006, 265009, 33109954, 52646317, 265010, 18108351, 264681, 264686, 264692, 18108370, 18108374, 18108385

2292	94328834 (4583, 4584)	Novel Protein sim. GBank gij4803672[emb]CAB42643.1]- (A1133789) nuclear transport receptor [Homo sapiens]		UNCLASSIFIED	56182575, 35686286, 56894075, 29331824, 29331825, 35686052, 56182435, 60433438, 55812038, 33109954, 87168474, 87168559, 265018, 18108351, 264763, 264448, 264369, 264288, 56181562, 264769, 21906765, 21906766, 21906767, 21906769, 265021, 265022, 33657023, 264693, 65274620, 33657109, 27486264, 264628, 55810764, 55811576, 35695855, 56182323, 56526486, 87168518, 22279000, 264567
2293	87759213 (4585, 4586)	Novel Protein sim. GBank gij3252981 (AF068921) - Ras- binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - struct Leucine Rich Repeat		264488, 18108397, 35696286, 264092, 264259, 29331822, 29331828, 264806, 264908, 264511, 264512, 265009, 264810, 18108351, 264764, 264369, 264288, 264885, 264766, 265020, 265022, 264534, 35696423, 264631, 264637, 18108381, 56182323, 264639, 18108385, 264404, 264563, 264565
2294	86693580 (4587, 4588)	Novel Protein sim. GBank gij2062680 (U88964) - HEM45 [Homo sapiens]	Contains protein domain (PF00929) - Exonuclease	nuclease	22278997, 22278998, 22278999, 264259, 29331822, 60432289, 29331828, 35696052, 265018, 264684, 264288, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264692, 33657109, 18108376, 35696423, 35695855, 264634, 22279000, 22279002, 264563, 264486
2295	95312200 (4589, 4590)			UNCLASSIFIED	22278996, 60432289, 264682, 264683, 264689, 18108374
2296	80030781 (4591, 4592)				263974, 263978
2297	94321251 (4593, 4594)	Novel Protein sim. GBank gij5689501[dbj]BAA83034.1]- (AB029005) KIAA1082 protein [Homo sapiens]		transcriptfactor	264488, 65274572, 56182575, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331828, 35696052, 264807, 264908, 52644045, 56182435, 264112, 265006, 265007, 264910, 265009, 60433356, 33657402, 264595, 55812038, 21906754, 265011, 265018, 265019, 264448, 264764, 264288, 264766, 21906785, 21906787, 21906788, 21906769, 55811857, 265020, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 55811576, 56182323, 60170394, 83373044, 18108385, 56526486, 264564, 264486

2298	85312207 (4595, 4598)	Novel Protein sim. GBank gij3875051[emb]CAB02849) - (Z81050) predicted using GeneFINDER; similar to collagen; cDNA EST EMBL:D65584 comes from this gene; cDNA EST EMBL:D69048 comes from this gene; cDNA EST yk368b12.3 comes from this gene; cDNA EST yk368b12.5 comes from this gene ...		collagen	60424178, 56181686, 22278995, 35696286, 22278996, 22278998, 22278999, 264490, 264259, 28331822, 29331824, 66714117, 60424269, 35696052, 29331828, 68712502, 56182435, 264510, 265006, 60433438, 21908754, 33109954, 55811386, 265010, 265018, 55811150, 264762, 18108351, 264682, 264683, 264288, 264684, 264686, 264688, 56181562, 264689, 21906767, 29148629, 55811957, 29148784, 35695917, 265020, 18108362, 33657023, 18108364, 33657109, 60431602, 18108370, 60431528, 18108374, 55810764, 35698423, 35695855, 264630, 264634, 60431850, 18108380, 56182323, 264558, 83373044, 18108385, 60432113, 22278000, 264482, 264567, 264488
2299	80193720 (4587, 4588)	Novel Protein sim. GBank gij2443888 (AC002284) - Unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264369, 264488, 22278998, 22278999, 264259, 29331824, 66714117, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 265008, 264910, 285009, 264758, 285010, 87168559, 264600, 265018, 264760, 264762, 18108351, 264764, 264766, 264788, 264789, 21908766, 21908767, 35695917, 265021, 264691, 33657023, 35695763, 18108370, 18108374, 35698423, 35695855, 264631, 264636, 264638, 18108385, 22278002, 264563
2301	91235725 (4601, 4602)	Novel Protein sim. GBank gij2143637[pir]I84505 - calcium-dependent actin-binding protein - rat		struct	264908, 264758, 265017, 21908765, 83373044, 264563
2302	88084141 (4603, 4604)	Novel Protein sim. GBank gij2887497 (AC004144) - R34001.1 [Homo sapiens]		UNCLASSIFIED	52644045, 265019, 264288, 33657023, 18108370, 18108385
2303	94141439 (4605, 4606)	Novel Protein sim. GBank gij4884194[emb]CAB43220.1 - (AL049948) hypothetical protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	264259, 60432049, 264907, 264909, 264910, 60432229, 33657402, 265011, 265018, 264762, 264448, 264769, 264637, 264638, 83373044, 264486
2304	94840434 (4607, 4608)	Novel Protein sim. GBank gij2494162[pir]Q10005[YRY1, CAEL - HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR		UNCLASSIFIED	264259, 29331824, 21906767, 33657182, 33657348
2305	90935811 (4609, 4610)	Novel Protein sim. GBank gij4972696[gb]AAD34738.1 - (AF132150) unknown [Drosophila melanogaster]			65274572, 22278996, 264908, 265006, 21908769, 264691, 264488



2306	95334940 (4611, 4612)	Novel Protein sim. GBank gi4929565 gb AAD34043.1 AF15180 - (AF151806) CGI-48 protein (Homo sapiens)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	264488, 22278995, 22278996, 35686286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35686052, 284508, 264905, 264907, 29331830, 264908, 284909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 33657402, 21906754, 85658542, 265010, 265011, 264601, 265017, 265018, 264604, 265019, 18108351, 284448, 264288, 264768, 264769, 21906765, 21906766, 21906767, 21906768, 29148629, 29148784, 35685917, 265020, 265021, 265022, 33657023, 264682, 18108370, 18108374, 18108376, 35686423, 35685855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108382, 18108385, 18108387, 264563, 284568, 284486 264828
2307	78415283 (4613, 4614)	Novel Protein sim. GBank gi4758732 ref NP_004522.1 pMOCS - molybdenum cofactor synthesis 2		UNCLASSIFIED	264828
2308	87608409 (4615, 4616)	Novel Protein sim. GBank gi4758732 ref NP_004522.1 pMOCS - molybdenum cofactor synthesis 2		synthase	35686286, 264259, 29331822, 29331824, 264112, 264512, 264757, 21906754, 264288, 264690, 27485264, 264631, 264634, 264404
2309	95357218 (4617, 4618)	Novel Protein sim. GBank gi3878059 emb CAB17070  - (299942) cDNA EST EMBL:D73444 comes from this gene; cDNA EST EMBL:D70905 comes from this gene; cDNA EST EMBL:D72208 comes from this gene; cDNA EST EMBL:D75030 comes from this gene; cDNA EST EMBL:D72944 comes from this gene; cDN...		glycoprotein	18108397, 22278996, 22278997, 22278998, 22278999, 60432049, 29331822, 29331826, 60432289, 68712502, 60432228, 60433356, 60433438, 65274444, 265010, 264600, 264681, 264448, 264683, 264288, 21906766, 21906768, 265020, 284691, 264692, 264693, 65274620, 65274791 264508
2310	79601668 (4619, 4620)	Novel Protein sim. GBank gi2137337 pit 48281 - gene	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	18108397, 56182575, 22278996, 56994075, 264259, 29331824, 29331827, 264508, 264907, 56182435, 264510, 264511, 265006, 264512, 265007, 265008, 265009, 60433438, 33109954, 265010, 265011, 264603, 265017, 18108351, 264762, 284683, 264288, 264369, 264686, 33657023, 20281149, 20281069, 264628, 283972, 55811578, 35696423, 20281071, 264632, 264636, 18108385, 18108387, 87168518, 22278000, 264563, 264486
2311	87721189 (4621, 4622)	mCBP protein - mouse		transcriptfactor	

2312	87549681 (4623, 4624)	Novel Protein sim. GBank gij2911264 (AC002550) - Unknown gene product [Homo sapiens]			56182575, 56994075, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 52644045, 60432229, 60433356, 55812038, 33109954, 21906754, 87168474, 265018, 18108351, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 60170815, 33657023, 27486281, 27486284, 35696423, 35695855, 18108385, 22279000, 22279002
2313	80042533 (4625, 4626)	Novel Protein sim. GBank gij3043626[dbj BAA25477] - (AB011123) KIAA0551 protein [Homo sapiens]			263981
2314	94313401 (4627, 4628)	Novel Protein sim. GBank gij5596714[embj CAB51401.1] - (AL035398) dJ796117.2 (CGI-51) [Homo sapiens]		UNCLASSIFIED	52844507, 52646365, 52646842, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 60432289, 29331828, 29331827, 29331828, 35696052, 33656870, 52644045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 265017, 265018, 265019, 264288, 264369, 21906765, 21906766, 21906768, 35695917, 52644150, 33657023, 33657109, 52645129, 33657349, 35695763, 18108374, 35896423, 35695855, 52644332, 22279000, 22279002, 264563, 264567
2315	80430119 (4629, 4630)			UNCLASSIFIED	264905, 264906, 264767, 264768, 264693, 55811576, 264635, 56182323, 18108385
2316	94312181 (4631, 4632)	Novel Protein sim. GBank gij5531827[gb AAD44488.1] - (AF078856) p47 [Homo sapiens]	Contains protein domain (PF00769) - UBX domain	glycoprotein	52644507, 52645156, 52646365, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264906, 264907, 29331830, 52644045, 56182435, 264511, 265007, 265008, 265009, 60170831, 60433438, 21906754, 52646317, 33109954, 33657084, 52644286, 87168474, 265010, 87168559, 265017, 265018, 265019, 264681, 264763, 264448, 264683, 264389, 52644229, 21906764, 264689, 21906769, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 18108362, 52645129, 33657182, 33657349, 35695763, 18108370, 18108376, 35696423, 35695855, 264631, 264556, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113, 22279000, 264566, 264567

2317	87020571 (4633, 4634)			UNCLASSIFIED	22278998, 60432049, 264910, 60432229, 264686, 264687, 264688, 264689, 264558, 18108385
2318	79959879 (4635, 4636)			UNCLASSIFIED	265008, 264910
2319	95101781 (4637, 4638)	Novel Protein sim. GBank gij5262613[emb CAB45746.1] - (AL080155) hypothetical protein [Homo sapiens]			264486, 264569, 18108396, 52646365, 22278994, 22278995, 22278996, 56994075, 35686286, 22278997, 22278998, 264259, 52645080, 26331825, 26331826, 26331827, 26331828, 26331830, 56182435, 60170831, 60432229, 60431735, 33657402, 21906754, 52644298, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 264369, 52644229, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 27486284, 33657349, 35685763, 18108370, 18108376, 18108378, 35686423, 264558, 83373044, 18108385, 56526486, 87168518, 264564, 264565, 264566
2320	91622426 (4639, 4640)	Novel Protein sim. GBank gij728837[sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	22278994, 60432049, 60432289, 26331827, 264511, 265008, 52646317, 265017, 265019, 21906765, 18108372, 18108387, 22279002
2321	94320377 (4641, 4642)	Novel Protein sim. GBank gij3873837[emb CAB02700] - (Z81029) Similarity to S.pombe hypothetical protein C1D4.09C (SW:Q10154); cDNA EST EMBL: T00543 comes from this gene; cDNA EST EMBL: T01062 comes from this gene; cDNA EST EMBL: T01321 comes from this gene; cDNA EST EMBL: T02288 com...		UNCLASSIFIED	264488, 264687, 18108394, 264689, 21906765, 18108397, 18108398, 21906767, 21906768, 65274791, 22278995, 35695855, 22278998, 265021, 265022, 264510, 265006, 264511, 264512, 265008, 60170815, 264555, 264636, 264556, 18108361, 264259, 60432229, 33657023, 264557, 264558, 264693, 60433356, 264559, 60433438, 29331824, 18108365, 18108348, 18108384, 29331825, 18108385, 33109954, 29331827, 56526486, 29146499, 265011, 60432113, 265017, 265018, 264508, 264563, 264482, 264509, 18108351, 264448, 264907, 264682, 18108370, 264683, 264908, 264288, 264909, 18108354, 264486, 264567
2322	97803165 (4643, 4644)	Novel Protein sim. GBank gij5678957[emb CAB51685.1] - (AL108630) BACR7A4.y [Drosophila melanogaster]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	22278996, 264907, 264511, 264757, 18108351, 264768, 264638

2323	94840445 (4645, 4646)	Novel Protein sim. GBank gi 2494162 sp Q10005 YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H8.1 IN CHROMOSOME II PRECURSOR	Contains protein domain (PF00226) - eph DnaJ domain	22278994, 22278995, 22278997, 60432049, 264259, 29331822, 33656970, 264509, 56182435, 264511, 265008, 60433358, 60433438, 55812038, 33109954, 21908754, 85658542, 87168474, 265011, 87188559, 265017, 265019, 264760, 264681, 18108351, 264369, 264288, 18108355, 264687, 264688, 21906765, 21906767, 21906768, 55811957, 35695917, 265021, 33657023, 18108362, 27486262, 55811576, 264631, 264555, 83373044, 87168518, 60432113, 22279002 264592, 264593, 265020 265020
2324	86633607 (4647, 4648)	Novel Protein sim. GBank gi 5419865 emb CAB46377.1  - (AL086732) hypothetical protein [Homo sapiens]	ATPase-associated	
2325	88165074 (4649, 4650)	Novel Protein sim. GBank gi 231885 sp P29881 CP4C_BLADI - CYTOCHROME P450 4C1 (CYP1VC1)	Contains protein domain (PF00067) - Cytochrome P450	265006, 264759, 35695855, 56182323
2326	84390962 (4651, 4652)	Novel Protein sim. GBank gi 231885 sp P29881 CP4C_BLADI - CYTOCHROME P450 4C1 (CYP1VC1)	UNCLASSIFIED	
2327	88081648 (4653, 4654)	Novel Protein sim. GBank gi 4240227 dbj BAA74892.1  - (AB020676) KIAA0869 protein [Homo sapiens]	UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 265007, 264512, 264910, 264758, 265010, 264768, 264768, 264768, 33657023, 264693, 264628, 264631, 264634, 264638, 264639, 264486
2328	83388428 (4655, 4656)	Novel Protein sim. GBank gi 1245105 U48463  - glutamine repeat protein-1 [Mus musculus]	UNCLASSIFIED	60433438, 264595, 265017, 264766, 264692, 264629, 264635, 264638, 264638, 56182323, 60432113, 264566
2329	87604478 (4657, 4658)	Novel Protein sim. GBank gi 1169343 sp P42209 DIF6_MOUSE - DIFF6 PROTEIN	Contains protein domain (PF00735) - Cell division protein	265017, 264685, 60432113, 264088 265009
2330	87335396 (4659, 4660)	Novel Protein sim. GBank gi 5679136 gb AAD46874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]	transport	
2331	86980463 (4661, 4662)	Novel Protein sim. GBank gi 5679136 gb AAD46874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]	ATPase-associated	33696286, 22278998, 29331824, 60424268, 265006, 265008, 265018, 264448, 264764, 21908765, 35695917, 35695855, 264636, 22279000, 264566
2332	87784182 (4663, 4664)	Novel Protein sim. GBank gi 2104452 emb CAB08779  - (Z95397) unknown [Schizosaccharomyces pombe]	UNCLASSIFIED	56182575, 56984075, 29331826, 29331828, 264107, 33657402, 87168559, 264683, 35695917, 265021, 33657023, 263976
2333	88206958 (4665, 4666)	Novel Protein sim. GBank gi 3679885 emb CAA92691.1  - (Z68318) cDNA EST CEMSD62F comes from this gene; cDNA EST EMBL.C07930 comes from this gene; cDNA EST EMBL.C08493 comes from this gene; cDNA EST yk415e8.3 comes from this gene; cDNA EST yk415e8.5 comes from this gene; cDNA EST...	UNCLASSIFIED	
2334	94319788 (4667, 4668)	Novel Protein sim. GBank gi 4968270 gb AA852261.2  - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase). Score=57.4, E- value=1e-13, N=1 [C...	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	56182575, 29331825, 21906768, 264636, 83373044

2335	80046103 (4669, 4670)	Novel Protein sim. GBank gl 3283350 (AF062378) - calmodulin-binding protein SH-1 [Mus musculus]	Contains protein domain (PF00612) - IQ calmodulin-binding motif	struct	18108351, 21906769, 264555
2336	95196121 (4671, 4672)	Novel Protein sim. GBank gl 1929055 (emb CAA72805) - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]		kinase	264907, 35695917, 18108379
2337	95345810 (4673, 4674)	Novel Protein sim. GBank gl 495063 (emb CA839181.1) - (Z85886) dJ108K1.1.3 (similar to yeast suppressor protein SRP40) [Homo sapiens]	UNCLASSIFIED		35695286, 22278999, 56182181, 29331825, 60424269, 56182435, 33657402, 55812038, 55811386, 265017, 265018, 265019, 21906768, 35695917, 264691, 33657023, 33657109, 263972, 35696423, 35695855, 60432113
2338	67634045 (4675, 4676)	Novel Protein sim. GBank gl 2224688 (db BAA20829) - (AB002372) KIAA0374 [Homo sapiens]	Contains protein domain (PF00323) - Mammalian defensin	UNCLASSIFIED	18108394, 29331822, 66714117, 60432289, 264908, 56182435, 265009, 60433438, 264596, 265010, 265019, 18108354, 264288, 264369, 55811957, 265021, 33657023, 263976, 55811576, 264632, 56182323, 264639
2339	85863319 (4677, 4678)	Novel Protein sim. GBank gl 3673550 (emb CAA22127) - (AL033534) serine-rich protein [Schizosaccharomyces pombe]	UNCLASSIFIED		35695286, 264592, 264369, 264691, 264558
2340	90837716 (4679, 4680)				
2341	87775281 (4681, 4682)				
2342	95334968 (4683, 4684)	Novel Protein sim. GBank gl 3874563 (emb CA802797) - (Z81042) similar to Yeast hypothetical protein YEE6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	65274572, 22278994, 35695286, 22278997, 22278999, 264259, 29331822, 60432289, 29331826, 29331830, 265009, 33657402, 33109954, 265017, 265018, 264768, 264665, 21906769, 35695917, 264691, 264692, 35696423, 87188518, 22279000
2343	87775448 (4685, 4686)	Novel Protein sim. GBank gl 4929741 (gb AAD34131.1) AAF15189 - (AF151894) CGI-136 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264259, 264908, 264809, 264682, 22279000, 264488, 65274572, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 35696052, 264905, 264509, 29331830, 265008, 60170831, 60432229, 60433358, 87168474, 265017, 265018, 265019, 264448, 264389, 264288, 21906765, 21906766, 55811957, 35695917, 265020, 265022, 52644150, 33657023, 65274620, 33657109, 18108370, 18108376, 55810784, 35696423, 55811576, 264556, 264558, 18108385, 60432113, 264563, 264564, 264565, 264566, 264567, 264907, 264512, 265011, 264683
2344	79953198 (4687, 4688)				
2345	94319789 (4689, 4690)	Novel Protein sim. GBank gl 2506307 (sp P13944) ICA1C - COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR (FIBROCHIMERIN)	Contains protein domain (PF00092) - von Willebrand factor type A domain	UNCLASSIFIED	264758, 264488, 264259, 66712502, 264759, 83373044, 264568

2346	94131820 (4691, 4692)	Novel Protein sim. GBank gll1255411 (U53153) - one short region of weak similarity to S. cerevisiae protease A inhibitor 3 (SP:P01094) and another short region of weak similarity to S. cerevisiae glucose repression mediator protein (SP:P14922) [Caenorhabditis elegans]	Contains protein domain (PF00515) - TPR Domain	proteaseinhib	35696286, 22278998, 264259, 35698052, 29331828, 33857402, 60433356, 33109854, 87168559, 264603, 265019, 18108351, 264681, 264685, 21906766, 265021, 33657109, 55811576, 35695855, 264637, 52644332, 264557, 83373044, 22279000, 22279002
2347	85330367 (4693, 4694)				22278997, 264511, 264683, 264694, 264768, 264687, 264688, 264691, 264692, 55811576
2348	95196133 (4695, 4696)	Novel Protein sim. GBank gll1929056[emb]CAA72805] - (Y12090) putative 3,4-dihydroxy-2-butanone Kinase [Lycopersicon esculentum]		kinase	18108394, 35698286, 264259, 35698052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265011, 264601, 264762, 18108351, 264764, 264288, 264766, 264768, 264689, 35695917, 264693, 264628, 18108370, 264629, 18108374, 35696423, 264631, 264635, 264636, 264637, 264638, 264639, 83373044, 18108385, 264587, 264488
2349	87776502 (4697, 4698)	Novel Protein sim. GBank gll4884109[emb]CAB43254.1] - (AL050062) hypothetical protein [Homo sapiens]			35698052, 29146489, 264908, 264369
2350	88260594 (4699, 4700)				22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 33109954, 21906754, 265010, 87168559, 265018, 265019, 264761, 264681, 264288, 18108357, 21906766, 21906767, 264681, 264682, 35695855, 87168518, 22279000, 22279002, 264482
2351	86888042 (4701, 4702)	Novel Protein sim. GBank gll728832[sp]P39189[ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII]		kinase	56182575, 264909, 265006, 264558
2352	87337196 (4703, 4704)	Novel Protein sim. GBank gll731637[sp]P38760[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264259, 264448
2353	91638784 (4705, 4706)	Novel Protein sim. GBank gll1346955[sp]P48809[RB27_DROME - HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	29331826, 55812038, 265019, 264692, 264636
2354	87337196 (4707, 4708)	Novel Protein sim. GBank gll731637[sp]P38760[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	29331824, 264908, 265006, 265008

2355	91638786 (4709, 4710)	Novel Protein sim. GBank gij4938503[emb]CAB43861.1] - (AL078465) hnRNP-like protein [Arabidopsis thaliana]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	56994075, 22278986, 35696286, 22278999, 264259, 29331825, 29331826, 29331828, 29146498, 264905, 264908, 265006, 264758, 87168474, 265010, 265017, 264687, 21908765, 21908767, 21908769, 264691, 264692, 263987, 18108370, 87168518, 22279000
2356	95327688 (4711, 4712)	Novel Protein sim. GBank gij5138920[gb]AAD40377.1] - (AF082135) PTD014 [Homo sapiens]			52644507, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35696052, 29331828, 264908, 66712502, 264512, 265007, 265008, 60170831, 60432229, 60433356, 60433438, 264758, 52646317, 33109954, 21908754, 55811386, 87168474, 265017, 265018, 264605, 265019, 264681, 264682, 264448, 264369, 264288, 264686, 264768, 21908765, 21908766, 21908767, 21908768, 21908769, 265021, 60170615, 33657109, 27488284, 35695763, 55810764, 18108379, 35696423, 55811576, 35695855, 60170394, 56182323, 83373044, 18108385, 56526486, 264404, 60432113, 22279000, 264482, 264563, 264566, 264486, 264567
2357	87775458 (4713, 4714)	Novel Protein sim. GBank gij4928741[gb]AAD34131.1[AF15189] CGI-136 protein [Homo sapiens]		UNCLASSIFIED	264488, 264769, 18108394, 264259, 29331822, 18108370, 18108374, 264510, 265017, 264482, 264563, 264762, 264565, 264566, 264389, 18108354
2358	87777078 (4715, 4716)	Novel Protein sim. GBank gij4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 22278999, 264509, 264905, 264592, 18108351, 264681, 264682, 264769, 32833986, 18108374, 264556, 18108385, 264482
2359	87755859 (4717, 4718)	Novel Protein sim. GBank gij1086830 (U41264) - coded for by C. elegans cDNA yk2018.5; coded for by C. elegans cDNA yk44g1.5; coded for by C. elegans cDNA yk12b7.5; coded for by C. elegans cDNA yk36g6.5; coded for by C. elegans cDNA yk2018.5; coded for by C. elegans cDNA yk16g12....		UNCLASSIFIED	35696286, 22278998, 264905, 264511, 265007, 265008, 60433438, 264288, 264686, 21908769, 265020, 264692, 35695855, 264558, 56526486, 264563
2360	80046125 (4719, 4720)	Novel Protein sim. GBank gij3881545[emb]CAA93779] - (Z69804) cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	22278997, 29331826, 263981, 22279000
2361	94232181 (4721, 4722)	Novel Protein sim. GBank gij746487 (U23514) - No definition line found [Caenorhabditis elegans]			22278995, 22278999, 264512, 265009, 264757, 21908765, 65274620, 18108370, 60431528, 18108374, 264635, 60170394, 264482

2362	91721193 (4723, 4724)	Novel Protein sim. GBank glij1171093jsp1P19706IMYSB_ACACA - MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN II)		UNCLASSIFIED	22278998, 264259, 28331822, 28331824, 60432289, 284509, 264512, 60432228, 60433356, 264448, 284682, 264683, 264369, 21906765, 21906768, 21906769, 60432113, 22279000, 22279002
2363	95006035 (4725, 4726)	Novel Protein sim. GBank glij854065[emb]CAA583371 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264807, 264628, 264635
2364	94827104 (4727, 4728)	Novel Protein sim. GBank glij5839830jgijAAD45886.1(AF14601) - (AF146018) hydroxypyruvate reductase [Homo sapiens]	Contains protein domain (PF00388) - Disomer specific 2-hydroxyacid dehydrogenases	reductase	264488, 18108394, 264887, 18108398, 22278998, 58994075, 35898286, 22278987, 22278998, 264259, 66714117, 28331825, 35898052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 264511, 265006, 264512, 265007, 265008, 33657402, 264758, 21906754, 87188474, 265010, 87188559, 264603, 265017, 265018, 265019, 264780, 264782, 18108351, 284448, 264764, 264683, 264684, 264288, 18108355, 264786, 18108358, 264689, 18108359, 21906765, 21906766, 21906767, 35895917, 285020, 265021, 265022, 60170615, 52644150, 264691, 33657023, 264692, 18108384, 33657109, 18108388, 18108370, 18108374, 35898423, 35895855, 264635, 264556, 264557, 264638, 60170394, 83373044, 18108383, 18108384, 18108385, 18108386, 56526486, 264482, 264564, 264486
2365	94140746 (4729, 4730)	Novel Protein sim. GBank glij1840045 (U49082) - transporter protein [Homo sapiens]		transport	22278998, 22278998, 22278999, 264907, 264909, 264910, 33657402, 264758, 264600, 264766, 264687, 264689, 21906765, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 83373044, 264566
2366	94312388 (4731, 4732)			UNCLASSIFIED	52644507, 264259, 28331824, 28331825, 28331826, 28331827, 28331828, 284907, 28331830, 264909, 264511, 265008, 33657402, 264595, 52646317, 265017, 265018, 265019, 264605, 264685, 264766, 264689, 21906766, 21906768, 35895917, 265020, 265021, 265022, 52644150, 35895855, 52644332, 18108385, 18108387, 264564, 264566
2367	94140910 (4733, 4734)	Novel Protein sim. GBank glij1065457 (U40410) - C54G7.4 gene product [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	35898286, 21908768, 55810764, 65274791, 264567
2368	94322180 (4735, 4736)				264628



2369	94314334 (4737, 4738)	Novel Protein sim. GBank gij5360901[dbj BAA82158.1] - (AB029343) a-helix coiled-coil rod homologue [Homo sapiens]		struct	52644507, 52646842, 35696286, 264092, 264094, 52645080, 35696052, 264107, 29331830, 52644045, 265008, 265007, 265009, 52644298, 52644229, 284689, 21906765, 21906766, 35695917, 265020, 52644150, 263967, 33657109, 27486265, 35695783, 18108370, 263974, 18108374, 18108376, 52644332, 263981, 18108385, 264508, 264909, 264596
2370	79804120 (4739, 4740)			UNCLASSIFIED	264369
2371	57280408 (4741, 4742)			UNCLASSIFIED	263967, 263981
2372	87642413 (4743, 4744)			UNCLASSIFIED	29331826, 265010, 265019, 35695917, 284634, 60432113
2373	87418611 (4745, 4746)	Novel Protein sim. GBank gij4589582[dbj BAA76813.1] - (AB023186) KIAA0989 protein [Homo sapiens]		UNCLASSIFIED	265006, 265007, 265008, 265009, 265011, 264766, 35695917, 35695855, 263981, 264557, 264565
2374	94123665 (4747, 4748)	Novel Protein sim. GBank gij5105131[dbj BAA80445.1] - (AF000061) 246aa long hypothetical ribonuclease PH [Aeropyrum pernix]		UNCLASSIFIED	60432048, 29331824, 264807, 52644045, 264512, 60433356, 21906754, 52644298, 87188559, 264448, 21906765, 21906768, 21906769, 33657023, 18108368, 55811576, 52644332
2375	87731355 (4749, 4750)	Novel Protein sim. GBank gij135115[sp P47758 SRPB_MOUSE - SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)]		UNCLASSIFIED	264259, 29331830, 264909, 264910, 265008, 60433438, 21908754, 265017, 265018, 265019, 264682, 264288, 264685, 21906767, 263972, 35695855, 87188518, 60432113
2376	87613744 (4751, 4752)	Novel Protein sim. GBank gij2645435 (AF007780) - CHD3 [Drosophila melanogaster]	Contains protein domain (PF00682) - PHD-finger	UNCLASSIFIED	18108394, 65274572, 22278997, 22278999, 264095, 29331822, 29147620, 29331824, 66714117, 29331825, 29331826, 29331828, 33656970, 29146498, 29148499, 264509, 265006, 265007, 265008, 265009, 60170831, 265010, 265011, 265018, 55811150, 18108351, 264764, 264288, 21908767, 21908768, 29148627, 29148629, 265021, 33657023, 33657109, 18108370, 18108374, 18108378, 35696423, 264558, 83373044, 18108385, 18108388, 55526486, 22279000, 22279002, 264563
2377	95319689 (4753, 4754)	Novel Protein sim. GBank gij5257005[gb AAD41239.1] - (AF083249) Rb binding protein homolog [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	UNCLASSIFIED	65274572, 56182575, 35696286, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 60432289, 29331827, 56182435, 264510, 265009, 60433356, 87168474, 265011, 265018, 264288, 21908765, 33657023, 264557, 56182323, 83373044, 18108385, 22279002, 264482
2378	94137032 (4755, 4756)	Novel Protein sim. GBank gij1072198 (U40942) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	265017, 264288, 21908768
2379	65444324 (4757, 4758)	Novel Protein sim. GBank gij3337357 (AC004481) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	

2380	88023062 (4759, 4760)	Novel Protein sim. GBank gi 4502839 ref NP_001845.1 pCOL1 - collagen, type XI, alpha 1	Contains protein domain (PF01410) - collagen Fibrillar collagen C-terminal domain	264908, 264910, 265011
2381	87608241 (4761, 4762)	Novel Protein sim. GBank gi 4455609 emb CAB38555  - (AL031846) dJ742C18.5 (novel Chromobox protein) [Homo sapiens]	Contains protein domain (PF00385) - helixase 'chromo' (CHR)romatin Organization Modifier domain	56182575, 264091, 264093, 264259, 29331825, 264105, 264906, 60433356, 21906754, 265017, 265019, 264683, 264288, 264685, 264686, 264687, 264691, 264692, 264693, 55811576, 264636, 264567
2382	91235982 (4763, 4764)	Novel Protein sim. GBank gi 4325130 gb AAD17276  - (AF119716) dMI-2 protein [Drosophila melanogaster]	Contains protein domain (PF00628) - transport PHD-finger	29331824, 60432289, 264805, 264596, 21906754, 264769, 265022, 264693, 263967, 33657109, 264629, 264631, 264556, 83373044, 60432113, 264482
2383	87442841 (4765, 4766)	Novel Protein sim. GBank gi 1902982 gb BAA19005  - (D89049) lectin-like oxidized LDL receptor [Bos taurus]	Contains protein domain (PF00059) - glycoprotein Lectin C-type domain	265009, 21906765, 21906766
2384	95354766 (4767, 4768)	Novel Protein sim. GBank gi 2462851  (AF016252) - Spinophilin [Rattus norvegicus]	Contains protein domain (PF00595) - struct PDZ domain (Also known as DHR or GLGF)	264488, 52644507, 52645156, 52646365, 35696286, 22278998, 52645080, 29331824, 29331826, 35696052, 29331828, 264906, 264828, 52644045, 265008, 265009, 265009, 33109954, 33657084, 52644296, 265011, 285017, 265018, 264683, 52644229, 21906765, 21906767, 21906768, 265020, 52644150, 33657023, 264693, 65274620, 52645129, 33657108, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108374, 35695855, 264634, 264555, 264556, 264557, 52644332, 264558, 264559, 18108385, 22279000, 22279002
2385	95419485 (4769, 4770)		UNCLASSIFIED	264488, 52644507, 52645156, 264887, 52646365, 22278995, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331826, 35696052, 52644045, 265008, 265007, 265008, 265009, 264910, 60432228, 60433356, 52646317, 21906754, 265019, 264448, 264683, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 265021, 265022, 264690, 264691, 264692, 65274620, 33657109, 18108370, 264631, 52644332, 22279000, 22279002, 264563, 264565, 264567
2386	94742648 (4771, 4772)	Novel Protein sim. GBank gi 4929699 gb AAD34110.1 AF15187 - (AF151873) CGI-115 protein [Homo sapiens]	glycoprotein	264488, 22278995, 22278996, 22278997, 264259, 29146498, 264112, 264511, 60170831, 60432228, 264595, 60433438, 87168474, 87168559, 264682, 21906765, 21906766, 21906767, 21906769, 26148629, 35695917, 265021, 264690, 33657109, 264628, 18108376, 83373044, 60432113, 22279000, 264564, 264566, 264487

2387	14987980 (4773, 4774)			UNCLASSIFIED	264634
2388	11424604 (4775, 4776)			UNCLASSIFIED	264595
2389	95310650 (4777, 4778)	Novel Protein sim. GBank gi 4758058 ref NP_004372.1 pCREB - cAMP responsive element binding protein-like 1	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED - dna_rna_bind	264488, 22278988, 22278999, 264509, 264905, 264908, 264907, 264908, 264909, 265008, 264511, 264512, 264910, 264591, 21908754, 264601, 264604, 264761, 18108351, 264764, 264288, 264768, 264768, 264769, 21906765, 21906768, 264692, 264693, 35698423, 264635, 264636, 264555, 83373044, 22278000, 264486
2390	94320812 (4778, 4780)	Novel Protein sim. GBank gi 1644239 dbj BAA122231 - (D84103) mitochondrial DNA polymerase gamma [Homo sapiens]	Contains protein domain (PF00476) DNA polymerase family A	polymerase	52644507, 56182575, 22278995, 35698286, 22278998, 22278997, 22278999, 29331822, 29331825, 29331826, 35696052, 264905, 52644045, 265009, 264758, 264759, 33109954, 52644298, 85658542, 265011, 265017, 265018, 264605, 52644229, 21906765, 21906767, 21906768, 21906769, 35695917, 52644150, 33657023, 33657109, 33657349, 35695763, 18108370, 18108374, 18108376, 35698423, 35695855, 264555, 52644332, 56182323, 60170394, 83373044, 58528486
2391	80036194 (4781, 4782)			UNCLASSIFIED	263976
2392	94245016 (4783, 4784)	Novel Protein sim. GBank gi 4240169 dbj BAA74863.1  - (AB020847) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nuclease	35696286, 35696052, 264508, 264905, 264509, 264908, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 265009, 264591, 264758, 264600, 264604, 264762, 264448, 264764, 264369, 264766, 264768, 264769, 264689, 35695917, 264629, 18108374, 263978, 35698423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 60170394, 264639, 264565, 264486

2393	95302833 (4785, 4786)	Novel Protein sim. GBank gi 4506667 ref NP_000983.1 pRPLP - ribosomal protein, large, P0	Contains protein domain (PF00466) - Ribosomal protein L10	- ribosomal prot	18108392, 60424179, 264489, 18108394, 18108397, 22278995, 56994075, 35898286, 22278996, 22278997, 22278999, 264093, 60432049, 264259, 29331822, 29147620, 20281099, 29331824, 29331825, 68714117, 60432289, 29331826, 29331827, 29331828, 35896052, 29146499, 264508, 264509, 264905, 264907, 264908, 66712502, 52644045, 264828, 264809, 56182435, 264112, 264113, 264510, 265008, 264511, 265007, 265008, 265009, 264910, 264591, 264593, 60433356, 264595, 60433438, 52646317, 33109954, 21906754, 55811386, 265010, 265011, 265017, 265018, 265019, 264681, 264762, 18108351, 264763, 284682, 264764, 264683, 264369, 264288, 18108354, 264766, 264686, 264687, 264688, 264689, 18108359, 21908765, 21908766, 21908767, 21908768, 21908769, 55811857, 29148629, 29148784, 35895917, 265021, 265022, 33657023, 264692, 264693, 18108364, 33657109, 18108368, 27486261, 27486262, 33657349, 35895763, 18108370, 263972, 264629, 18108374, 263977, 18108376, 263978, 55810764, 35898423, 35895855, 264634, 60431850, 264555, 264637, 264557, 263981, 264558, 18108381, 60170394, 35896286, 22278997, 22278998, 56182181, 35896052, 265008, 264592, 55811388, 265010, 265011, 265017, 265019, 264448, 264683, 264288, 21908765, 21908768, 21908769, 55811857, 35895917, 33657023, 65274620, 33657182, 33657349, 35895763, 18108374, 18108376, 55810764, 55811576, 35898423, 60170394, 18108385, 264584, 264586, 264567
2394	94323266 (4787, 4788)	Novel Protein sim. GBank gi 4159888 (AC004908) - zinc finger protein from gene of uncertain exon structure; similar to Q99676 (PID:g3025333) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	- dna_ma_bind	264259, 29331824, 264910, 264288, 265021, 83373044, 18108387, 264563, 264568
2395	95287212 (4789, 4790)	Novel Protein sim. GBank gi 5712756 gb AAD47636.1 AF16079 - (AF160798) calcium transporter CaT1 [Rattus norvegicus]		- dna_ma_bind	

2396	95096700 (4791, 4792)	Novel Protein sim. GBank gi 106322 pir B34087 - hypothetical protein (L1H 3' region) - human	Contains protein domain (PF00560) - Leucine Rich Repeat	nuclease	52646365, 18108387, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264108, 264907, 29331830, 66712502, 264110, 60170831, 264591, 33657402, 60433438, 55812038, 33109954, 21908754, 33657084, 87168474, 265017, 265018, 265019, 264760, 264448, 264288, 264786, 52644229, 21906766, 21906767, 265020, 265021, 60170815, 264692, 33657023, 65274620, 52645129, 33657182, 27486262, 27486264, 27486265, 264629, 18108374, 35696423, 35696855, 264631, 264556, 52644332, 264558, 83373044, 18108388, 87168518, 22279002, 264482
2397	87280854 (4793, 4794)				52644507, 52645156, 56182575, 264259, 29147620, 264905, 264907, 264908, 264909, 264910, 264758, 52644296, 264603, 264604, 264762, 264681, 264764, 18108357, 264769, 21906768, 264693, 264628, 264635, 264638, 264639, 264584
2398	88047689 (4795, 4796)	Novel Protein sim. GBank gi 3258609 (AC005178) - H53 GS1 [Homo sapiens]		UNCLASSIFIED	
2399	87738965 (4797, 4798)	Novel Protein sim. GBank gi 786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 60432289, 264906, 29331830, 56182435, 264112, 264910, 33109954, 21906764, 87168474, 264600, 265017, 265018, 265019, 264764, 264765, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265022, 60170815, 33657023, 18108370, 18108374, 264558, 60170394, 264558, 87168518, 22279000, 22279002, 264564, 264566, 264487
2400	91214116 (4799, 4800)	Novel Protein sim. GBank gi 2352822 gb AAB69285.1  - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	21906766, 52646842, 56994075, 33657182, 27486262, 52644296, 265017

2401	91214118 (4801, 4802)	Novel Protein sim. GBank gij2352822[gjAAB69285.1] - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	52644507, 52645156, 52644229, 264688, 21906764, 21906765, 52646365, 52646842, 21906766, 21906767, 21906768, 22278995, 35695917, 56994075, 35696286, 22278996, 22278997, 265020, 22278998, 22278999, 264259, 33657023, 52645080, 264693, 29331824, 33657109, 52645129, 29331826, 33657182, 29331827, 35696052, 27486261, 27486262, 33656970, 33657349, 27486265, 35695763, 264106, 264905, 35696423, 35695855, 265006, 265007, 265008, 265009, 264637, 52644332, 55812038, 52646317, 18108385, 52644296, 87168474, 265010, 87168559, 80432113, 265017, 265018, 265019, 264563, 264288, 264907, 264908, 264909, 264566
2402	91221408 (4803, 4804)	Novel Protein sim. GBank gij4689258[gjAAD27832.1] (AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]			
2403	94135432 (4805, 4806)	Novel Protein sim. GBank gij4929575[gjAAD34048.1] (AF15181 - (AF151811) CGI-53 protein [Homo sapiens]	Contains protein domain (PF00062) - C-type lysozyme/alpha-lactalbumin family		22278999, 35696052, 265018, 264686, 264693, 83373044, 264567
2404	95312605 (4807, 4808)	Novel Protein sim. GBank gij2315786 (AF016685) - similar to short chain-type dehydrogenases [Caenorhabditis elegans]	Contains protein domain (PF00106) - short chain dehydrogenase family	dehydrogenase	35696286, 29331826, 35696052, 265008, 265018, 21906769, 264584
2405	94311851 (4809, 4810)	Novel Protein sim. GBank gij464179[gjBAA03581] - (D14853) polypeptide [Hepatitis C virus]		UNCLASSIFIED	35696286, 29331822, 265007, 21906754, 265017, 265018, 265019, 264763, 264369, 21906765, 35695917, 265020, 265021, 52644150, 264693, 35695855, 264632, 52644332, 22279002
2406	88094501 (4811, 4812)	Novel Protein sim. GBank gij2773363 (AF041382) - microtubule binding protein D-CLIP-190 [Drosophila melanogaster]	Contains protein domain (PF01302) - CAP-Gly domain	struct	52646842, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 284092, 264093, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264102, 264106, 264908, 52644045, 265007, 265008, 265009, 264910, 264592, 60433356, 60433438, 33109954, 265010, 265011, 265018, 265019, 264369, 264685, 264688, 21906768, 21906769, 52644150, 264693, 52645129, 264628, 35696423, 264632, 56182323, 264639, 22279000, 22279002, 264553, 264685, 264686
2407	79465005 (4813, 4814)			UNCLASSIFIED	
2408	87391503 (4815, 4816)	Novel Protein sim. GBank gij423442[pri]S33513 - gene Fif protein - mouse		UNCLASSIFIED	264910, 265010, 264448, 264557

2409	94741770 (4817, 4818)	Novel Protein sim. GBank gi 1176801 sp P45968 YNZ8_CAEEL - HYPOTHETICAL 20.8 KD PROTEIN T08A5.6 IN CHROMOSOME III		UNCLASSIFIED	22278995, 22278996, 22278997, 264097, 29331822, 29331824, 29331827, 29148498, 52644045, 60433438, 33657084, 87168474, 264760, 21906767, 29148627, 29148629, 52644150, 33657023, 263967, 20281069, 18108374, 20281071, 56182323, 83373044, 18108385, 87168518 22278998, 264259
2410	87604860 (4819, 4820)	Novel Protein sim. GBank gi 4966262 gb AAC48052.2  - (U64849) Contains similarity to Pfam domain: PF00646 (F- box), Score=28.7, E-value=4.3e-05, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00080) - Copper/zinc superoxide dismutase (SODC)		
2411	87534633 (4821, 4822)	Novel Protein sim. GBank gi 3114713 (AF061346) - Edp1 protein [Mus musculus]		Inf	29331824, 29331827, 29331828, 264764, 264389, 33657109, 56182323
2412	87778332 (4823, 4824)	Novel Protein sim. GBank gi 5410336 gb AAD43038.1  - (AF106685) myelin gene expression factor 2 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	22278998, 29331827, 264907, 265011, 265017, 265018, 265019, 18108351, 21906766, 265020, 33657109, 264559, 18108365
2413	84133820 (4825, 4826)	Novel Protein sim. GBank gi 5262705 emb CAB45778.1  - (AL080214) hypothetical protein [Homo sapiens]	Contains protein domain (PF00038) - Intermediate filament proteins	struct	264488, 264259, 29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264510, 264511, 264512, 265008, 265009, 264910, 265011, 264682, 264764, 264766, 264686, 264768, 264688, 265021, 33657023, 18108370, 264628, 35695855, 264632, 264634, 264635, 264636, 83373044, 264563, 264564, 264585, 264586, 264567, 264486 52645156, 52646842, 52646365, 18108398, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 29331830, 264909, 60433356, 33657402, 264594, 52646317, 21906754, 33657084, 265010, 87168559, 265017, 265018, 265019, 264369, 264684, 264687, 264688, 56181562, 21906764, 264689, 21906765, 21906766, 21906767, 29148627, 21906769, 265020, 265021, 60170615, 33657023, 264693, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 18108370, 60431528, 264629, 18108374, 18108376, 55810764, 264636, 52644332, 264638, 264558, 56182323, 83373044, 18108385, 87168518, 22279002
2414	84312590 (4827, 4828)	Novel Protein sim. GBank gi 1082340 pir J52863 - DNA- binding protein R kappa B - human		ubiquitin	

2415	86086002 (4828, 4830)	Novel Protein sim. GBank gj[423915]pir[A45439 - myosin I heavy chain - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	struct	264259, 264908, 60433356, 33657402, 21906754, 265018, 264687, 264689, 21906769, 55811957, 265021, 264690, 264691, 33657023, 264693, 35698423, 56182323, 56526466
2416	94118356 (4831, 4832)	Novel Protein sim. GBank gj[3025445 (AC004528) - R32184_1 [Homo sapiens]			264638
2417	87733334 (4833, 4834)	Novel Protein sim. GBank gj[1084944]pir[S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins		264094, 29331822, 29331824, 29331827, 264369
2418	94234348 (4835, 4836)	Novel Protein sim. GBank gj[1176572]sp[P45895]YNA4_CAEEL - HYPOTHETICAL 91.0 KD PROTEIN PAR2.4 IN CHROMOSOME III	Contains protein domain (PF00411) - Ribosomal protein S11	UNCLASSIFIED	56994075, 264091, 264259, 29331824, 29331825, 60432289, 29331828, 264905, 264907, 264511, 265009, 60432229, 21906754, 87168559, 265019, 264682, 21906768, 21906769, 265020, 265021, 33657023, 65274620, 18108370, 55811576, 264634, 60170394, 18108385, 22279000, 22279002, 264588
2419	82374249 (4837, 4838)	Novel Protein sim. GBank gj[284006]pir[S18732 - autoantigen, 84K - human		struct	264569, 264762, 264448, 264691, 264631, 264634, 264555, 264556, 264638, 264558
2420	9484244 (4839, 4840)	Novel Protein sim. GBank gj[107621]pir[S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	29331824, 29331825, 29331828, 60432229, 33109954, 85658542, 87168474, 265018, 264288, 265020, 264564
2421	87805345 (4841, 4842)	Novel Protein sim. GBank gj[2224567]dbj[BAA20772] - (AB002311) KIAA0313 [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	UNCLASSIFIED	264909, 264768, 264638
2422	88084714 (4843, 4844)	Novel Protein sim. GBank gj[4505153]ref[NP_002392.1]pMEKK - MAP/ERK kinase kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	18108392, 18108394, 18108398, 264906, 265006, 265010, 18108351, 18108374, 18108385
2423	88058390 (4845, 4846)	Novel Protein sim. GBank gj[4505153]ref[NP_002392.1]pMEKK - MAP/ERK kinase kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 604332049, 29331822, 29331826, 60432289, 29331828, 265008, 265009, 60433356, 21906754, 265017, 265018, 265019, 21906766, 21906768, 21906769, 265020, 265021, 20281149, 263971, 60432113
2424	94854047 (4847, 4848)	Novel Protein sim. GBank gj[2988398 (AC004381) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278997, 60432048, 264259, 29331828, 29331828, 264905, 66712502, 29331830, 60433356, 265011, 265019, 264766, 21906768, 55811957, 264692, 33657023, 33657109, 55811576, 56182323, 83373044, 18108385, 18108388, 60432113, 22279000
2425	87415981 (4849, 4850)	Novel Protein sim. GBank gj[2077632]dbj[BAA19878] - (D88556) Protein Kinase [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264634
2426	87613945 (4851, 4852)	Novel Protein sim. GBank gj[2039368]gbj[AAB33003.1] - (U94619) circulating cathodic antigen [Schistosoma mansoni]		UNCLASSIFIED	22278998, 22278998, 264259, 264102, 264512, 265008, 21808767, 18108370, 18108374, 263976



2427	87622893 (4853, 4854)	Novel Protein sim. GBank gi 4680695 gb AAD27737.1 AF13296 - (AF132962) CGI-28 protein [Homo sapiens]	Contains protein domain (PF00573) - Ribosomal protein L4/L1 family	ribosomalprot	264259, 20281099, 35686052, 265008, 264594, 265011, 264760, 18108351, 264682, 264683, 264369, 264684, 264686, 264687, 264689, 21908766, 264691, 264692, 18108374, 18108377, 264557, 264639, 18108385
2428	85732889 (4855, 4856)	Novel Protein sim. GBank gi 1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]			22278986, 22278989, 35686052, 21906754, 264288, 21906765, 21906768, 21906769, 35695917, 265020, 263972, 22279002
2429	87769276 (4857, 4858)	Novel Protein sim. GBank gi 601331 (M94316) - neurofilament-H [Oryctolagus cuniculus]	Contains protein domain (PF00711) - Beta defensins	UNCLASSIFIED	22278989, 29331824, 264906, 264909, 264511, 265009, 21906754, 265017, 265018, 265019, 264448, 264883, 264288, 21906765, 21906768, 265021, 264693, 18108381
2430	86948827 (4859, 4860)			UNCLASSIFIED	264112, 264691
2431	87049884 (4861, 4862)	Novel Protein sim. GBank gi 3860729 emb CAA14630  - (AJ235270) CELL DIVISION PROTEIN FTSJ (fts.j) [Rickettsia prowazekii]	Contains protein domain (PF01728) - FtsJ cell division protein		29331826, 29331827, 35696052, 29146499, 264905, 264908, 264681, 264288, 264689, 21908765, 264692, 35696423
2432	80083033 (4863, 4864)	Novel Protein sim. GBank gi 3876367 emb CAA93287  - (Z69360) Weak similarity to Eimeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89266 comes from this gene; cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans]		protease	264634, 264558
2433	80055092 (4865, 4866)	Novel Protein sim. GBank gi 2224593 dbj BAA20784  - (AB002324) KIAA0326 [Homo sapiens]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	transcriptfactor	264569, 264905, 265018, 264762, 264683, 264691, 264556, 264557, 264639, 264558
2434	19520148 (4867, 4868)			UNCLASSIFIED	264563
2435	20759044 (4869, 4870)	Novel Protein sim. GBank gi 1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	264555
2436	68044008 (4871, 4872)	Novel Protein sim. GBank gi 3641352 (AF091234) - putative transcription factor [Mus musculus]		UNCLASSIFIED	265008, 264758, 265010, 264689, 27486261, 263972, 18108374, 18108381
2437	83363424 (4873, 4874)	Novel Protein sim. GBank gi 3641352 (AF091234) - putative transcription factor [Mus musculus]		UNCLASSIFIED	29331828, 265007, 265009, 265017, 264760, 264885, 264693, 264565
2438	94143473 (4875, 4876)	Novel Protein sim. GBank gi 3860014 (AF091088) - unknown [Homo sapiens]	Contains protein domain (PF01256) - Uncharacterized protein family UPF0031	UNCLASSIFIED	29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 265008, 264512, 264910, 265009, 264591, 33657402, 21906754, 265011, 264760, 264764, 264885, 264686, 264768, 35695917, 33657023, 264693, 264631, 264632, 56182323, 264558, 83373044, 264563, 264564, 264565, 264566, 264567

2439	94850650 (4877, 4878)	Novel Protein sim. GBank gii4263519 gb AAD15345  - (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]	Contains protein domain (PF01423) - Sm protein	UNCLASSIFIED	60424179, 18108397, 56182575, 56181686, 56894073, 22278996, 35686286, 22278997, 22278999, 284259, 52845080, 29331822, 56182181, 29331824, 60424268, 68714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35686052, 29146498, 264509, 264905, 264906, 52844045, 60431735, 33109954, 21906754, 33657084, 55811388, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264768, 52644229, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35685917, 33657023, 33657109, 33657182, 27486262, 27486264, 33657349, 27486265, 35685763, 18108370, 60431528, 263977, 55810764, 35686423, 65274791, 35895855, 60431850, 56182323, 60432113, 22279000, 22279002, 264587
2440	87641733 (4879, 4880)			UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 35686052, 264508, 264907, 264510, 265018, 265019, 264448, 264369, 265020, 265021, 56182323, 264639, 22279002
2441	87623914 (4881, 4882)	Novel Protein sim. GBank gii3024889 sp P56524 Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)		UNCLASSIFIED	264488, 264629, 18108374, 264564
2442	87273590 (4883, 4884)	Novel Protein sim. GBank gii4506013 ref NP_002703.1 pPPP1 - protein phosphatase 1, regulatory subunit 7	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	22278996, 22278999, 28331822, 264768, 264693
2443	84305949 (4885, 4886)	Novel Protein sim. GBank gii1170659 sp Q02875 KID1_RAT - RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17)	Contains protein domain (PF01352) - KRAB box	transcription factor	264906
2444	88086345 (4887, 4888)	Novel Protein sim. GBank gii4758824 ref NP_004280.1 pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	264259, 18108382, 18108383, 18108385, 22279000
2445	87338636 (4889, 4890)	Novel Protein sim. GBank gii2135950 p p S58222 - PQ-rich protein - human			264259, 35686052, 264369, 18108361
2446	88059293 (4891, 4892)	Novel Protein sim. GBank gii4753887 emb CAA05409.2  - (AJ002424) p85 protein [Rattus norvegicus]	Contains protein domain (PF00095) - WAP-type (Whey Acidic Protein) 'four-disulfide core'	proteaseinhib	265011, 264689, 33657023, 263981, 18108385
2447	94845148 (4893, 4894)	Novel Protein sim. GBank gii4885813 ref NP_005409.1 pST5  - suppression of tumorigenicity 5	cadherin		56182575, 264259, 29331824, 29331825, 29331827, 60433356, 60433438, 264758, 265018, 264692, 65274620, 60431528, 65274791, 56182323

2448	87749680 (4895, 4896)			UNCLASSIFIED	22278996, 22278997, 22278998, 29331826, 35696052, 264107, 264110, 87168474, 87168559, 18108351, 21906767, 21906768, 27486262, 263976
2449	87869075 (4897, 4898)	Novel Protein sim. GBank gij128837[sp]P39194[ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII]		cadherin	264259, 264828, 265007, 264595, 265021, 56526488
2450	86597784 (4899, 4900)			UNCLASSIFIED	264906
2451	91014563 (4901, 4902)	Novel Protein sim. GBank gij1710021[sp]P35280[RB24_MOUSE - RAS-RELATED PROTEIN RAB-24 (RAB-16)]	Contains protein domain (PF00071) - Ras family	glycoprotein	264093, 29331822, 29331824, 29331825, 86714117, 29331826, 29331828, 35696052, 264907, 66712502, 29331830, 264910, 265009, 264758, 265017, 265018, 264762, 264448, 264288, 21906767, 265021, 33657023, 264693, 33857109, 263969, 83373044, 18108385
2452	91230509 (4903, 4904)	Novel Protein sim. GBank gij1504034[dj]BAA13216] - (D86980) KIAA0227 [Homo sapiens]		isomerase	264102, 264112, 264688, 263972, 18108374, 83373044, 264563
2453	84201088 (4905, 4906)	Novel Protein sim. GBank gij2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369908) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	ngfrecp	264509, 264512, 18108385
2454	95310691 (4907, 4908)	Novel Protein sim. GBank gij1076802[pir]S49915 - extensin like protein - maize	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263394, 66714117, 29331827, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 264591, 264759, 265010, 265011, 264603, 264604, 264760, 264761, 264762, 18108351, 264764, 264765, 264766, 264686, 264768, 264769, 264534, 264691, 264692, 33657023, 264693, 33657109, 264628, 263978, 35695855, 264634, 264635, 264637, 264638, 264639, 83373044, 18108385, 264563, 264564, 264488
2455	95288301 (4909, 4910)	Novel Protein sim. GBank gij543817[sp]P35585[AP47_MOUSE - CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)]	Contains protein domain (PF00828) - Adaptor complexes medium subunit family	glycoprotein	264488, 22278996, 264259, 35696052, 264905, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264758, 265019, 264760, 264681, 18108351, 264683, 264764, 18108354, 264766, 264768, 264769, 264689, 21906766, 21906767, 21906769, 29148629, 35695917, 265020, 265022, 33657023, 33657109, 18108370, 264628, 264629, 264631, 264632, 264635, 56182323, 60170394, 18108385, 264563, 264564, 264566, 264567
2456	88166700 (4911, 4912)	Novel Protein sim. GBank gij2588630 (AC003079) - Ankyrin- like; 54% similar to 2022340A (NID:g1092123) in exons spanning 43874 to 11551 of clone. [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	264693

2457	94118375 (4913, 4914)	Novel Protein sim. GBank gl 3025447 (AC004528) - R32184_3 [Homo sapiens]		UNCLASSIFIED	55181686, 264805, 264907, 264511, 264596, 55811386, 264682, 264684, 264685, 264687, 264691, 33657023, 264693, 35695855, 264636, 264555, 56182323, 264558, 56526488, 264563
2458	85875304 (4915, 4916)	Novel Protein sim. GBank gl 2384942 (AF022985) - Similar to collagen [Caenorhabditis elegans]		UNCLASSIFIED	264691, 264693, 264634, 264559
2459	87551913 (4917, 4918)	Novel Protein sim. GBank gl 5441942[gb AAD3187.1 AC00499 - (AC004997) supported by mouse EST AA538043 (NID:g2284036) [Homo sapiens]	Contains protein domain (PF00037) - Zinc finger, C3HC4 type (RING finger)	transport	27486265
2460	94315289 (4919, 4920)	Novel Protein sim. GBank gl 4929701[gb AAD3411.1 AF15187 - (AF151874) CGI-116 protein [Homo sapiens]		kinase	63274572, 35686268, 22278996, 22278987, 60432049, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33856970, 29146499, 264102, 264108, 60433438, 265017, 265018, 265019, 264288, 21908765, 21908766, 21908769, 35685917, 265020, 264691, 33657023, 27486261, 18108374, 35685855, 87168518, 60432113
2461	87645147 (4921, 4922)	Novel Protein sim. GBank gl 4426962[gb AAD20833] - (AF128062) Arf-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264259, 29331828, 264910, 18108351, 18108370, 18108374
2462	86988002 (4923, 4924)	Novel Protein sim. GBank gl 5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			284909, 264758, 264684, 18108374, 264637, 18108385
2463	84388543 (4925, 4926)	Novel Protein sim. GBank gl 5052516[gb AAD38588.1 AF14561 - (AF145613) BcDNA, GH03108 [Drosophila melanogaster]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264681, 264566
2464	91219957 (4927, 4928)	Novel Protein sim. GBank gl 5410300[gb AAD43021.1] - (AF100757) COP9 complex subunit 4 [Homo sapiens]	Contains protein domain (PF01399) - protease PCI domain		264489, 52646842, 22278995, 35686286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35686052, 29331828, 264509, 52644045, 264510, 264511, 264512, 265008, 60170831, 264593, 52646317, 33109954, 33657084, 265017, 265018, 265019, 264762, 264448, 264764, 264288, 264766, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 18108370, 18108381, 60170394, 18108385, 22279002, 264486

2465	95357483 (4929, 4930)	Novel Protein sim. GBank gi 4508401 ref NP_002871.1 pRAF1 - v-raf-1 murine leukemia viral oncogene homolog 1	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	oncogene	18108392, 52644507, 52645156, 52646365, 22278994, 22278995, 35696286, 22278998, 22278998, 284259, 29331822, 29331824, 29331825, 60424289, 60432289, 29331827, 35696052, 29331828, 264907, 29331830, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264810, 33657402, 60433438, 55812038, 21908754, 33109954, 265010, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264369, 264288, 264685, 264787, 21908765, 21908787, 21908768, 55811957, 35695917, 265020, 265021, 60170815, 52644150, 33657023, 52845129, 33657109, 27486261, 27486264, 35695763, 264628, 263972, 18108374, 35695855, 264636, 264637, 60170394, 56526486, 87168518, 60432113, 264563, 264564, 264566, 264487 264369
2466	85681386 (4931, 4932)	Novel Protein sim. GBank gi 4321619 gb AAD15788.1  - (AF051098) seven transmembrane domain orphan receptor (Mus musculus)			
2467	88059465 (4933, 4934)	Novel Protein sim. GBank gi 3513300 (AC005595) - F16601_1, partial CDS [Homo sapiens]		UNCLASSIFIED	56894075, 264908, 21906768, 33657023
2468	87614696 (4935, 4936)	Novel Protein sim. GBank gi 2143455 pr j 58106 - gene DMR-N9 protein - mouse (fragment)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	29331824, 52644045, 265008, 264910, 265019, 21906785, 21906789, 265021 264288, 264628
2469	86294397 (4937, 4938)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1  - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264592, 264692, 264555, 264556, 264557, 264558, 264559, 18108385, 264482
2470	80223831 (4939, 4940)	Novel Protein sim. GBank gi 5419892 emb CAB46424.1  - (AL096749) DKFZp434G153 [Homo sapiens]		UNCLASSIFIED	65274572, 35696286, 29331827, 265007, 264592, 33109954, 265018, 265019, 264288, 55811957, 265020, 264693, 55811576, 58182323
2471	91013681 (4941, 4942)			UNCLASSIFIED	
2472	85060811 (4943, 4944)	Novel Protein sim. GBank gi 4928747 gb AAD34134.1 AF15189 - (AF151897) CGI-139 protein [Homo sapiens]		UNCLASSIFIED	264092, 60432049, 29331825, 60433356, 265010, 265011, 18108351, 264764, 264288, 264692, 65274620, 18108370, 18108372, 18108374, 264634, 18108385
2473	95421509 (4945, 4946)	Novel Protein sim. GBank gi 4539008 emb CAB39630.1  - (AL049481) putative protein [Arabidopsis thaliana]			60424178, 65274572, 22278999, 60424289, 29331828, 265008, 60433356, 60433438, 265010, 18108351, 264448, 264288, 264687, 264689, 265021, 264692, 65274620, 60431528, 65274791, 264556, 56182323, 60432113
2474	94315616 (4947, 4948)	Novel Protein sim. GBank gi 3252827 (AC004382) - Unknown gene product [Homo sapiens]			65274572, 56894075, 264259, 29331826, 60170831, 265017, 265018, 265019, 264683, 264369, 265020, 264693, 264563, 264564

2475	94321693 (4949, 4950)	Novel Protein sim. GBank gij1216486 (U48652) - HT protein [Crice(tulus griseus)]	Contains protein domain EGF-like domain	Ig1	264259, 29331822, 265006, 265007, 265010, 265011, 264448, 264288, 264369, 264685, 264686, 18108357, 264768, 18108382, 264693, 18108370, 18108374, 18108379, 35696423, 83373044, 18108383, 18108385, 264564, 264565, 264567
2476	94315618 (4951, 4952)	Novel Protein sim. GBank gij3252827 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264259, 60424269, 66714117, 264905, 265006, 264511, 265008, 265009, 264758, 265010, 265011, 18108351, 264681, 264369, 264288, 264689, 21908767, 265020, 18108374, 264639, 18108382, 83373044, 18108385, 87168518
2477	20718974 (4953, 4954)			UNCLASSIFIED	263978
2478	17659165 (4955, 4956)			UNCLASSIFIED	265017
2479	94314569 (4957, 4958)	Novel Protein sim. GBank gij1644232[dbj][BAA11082] - (D67066) N-WASP [Bos taurus]		Im7	56994075, 22278999, 21908754, 264682, 21906785
2480	95295805 (4959, 4960)			UNCLASSIFIED	264905, 264907, 264765
2481	94718481 (4961, 4962)	Novel Protein sim. GBank gij5689469[dbj][BAA83018.1] - (AB028989) KIAA1066 protein [Homo sapiens]		collagen	63274572, 56182575, 22278997, 264094, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 56182435, 265008, 264910, 33657402, 55612038, 264758, 265010, 265011, 265017, 265018, 264760, 264762, 18108351, 264784, 264288, 264766, 264686, 264768, 21908768, 55811957, 265020, 264691, 264692, 264693, 264629, 55811576, 264630, 264634, 264635, 264636, 264637, 264556, 264558, 56182323, 83373044, 60432113, 22279002
2482	87393165 (4963, 4964)	Novel Protein sim. GBank gij321249[pir][S28407 - guanine nucleotide-exchange activator CDC25 homolog - mouse		UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 264508, 264905, 264509, 264906, 264907, 264908, 264511, 264591, 264768, 264693, 264631, 264632, 264636, 264638, 264639, 264563
2483	87731593 (4965, 4966)			UNCLASSIFIED	264488, 22278995, 264093, 264095, 60432049, 60433356, 60433438, 264448, 264288, 263967, 18108370, 18108385, 18108388, 264482
2484	94187774 (4967, 4968)	Novel Protein sim. GBank gij728831[sp][P39188][ALU1_HUMAN - IIII] ALU SUBFAMILY J WARNING ENTRY IIII		kinase	264563
2485	87786556 (4969, 4970)	Novel Protein sim. GBank gij1185397 (U25281) - SH3 domain binding protein [Rattus norvegicus]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 60432289, 29331827, 265007, 264910, 264593, 264600, 264603, 264604, 265019, 264448, 264288, 264685, 264686, 264769, 264689, 35695917, 265022, 264692, 264693, 56182323

2486	87748978 (4971, 4972)	Novel Protein sim. GBank gi 2662167 dbj BAA23715  - (AB007903) KIAA0443 [Homo sapiens]			265017, 264555
2487	95343105 (4973, 4974)	Novel Protein sim. GBank gi 464559 sp P35287 RB14_RAT RAS-RELATED PROTEIN RAB-14	Contains protein domain (PF00071) - Ras family	glycoprotein	22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331822, 35696052, 264106, 264905, 264907, 29331830, 264909, 265006, 264511, 265008, 265009, 60433438, 21906754, 33109954, 87168559, 265018, 264681, 264288, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 264534, 33857023, 264692, 33857109, 263972, 18108377, 35696423, 35695855, 60170394, 18108385, 56526486, 22279000, 22279002, 264563, 264482, 264565, 20281169, 18108391
2488	87652451 (4975, 4976)			UNCLASSIFIED	264910, 264448, 264288, 264684, 264691, 264634
2489	82990585 (4977, 4978)	Novel Protein sim. GBank gi 4886439 emb CAB43355.1  - (AL050253) hypothetical protein [Homo sapiens]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complementrecept	264686, 264693, 55811576, 22279002
2490	88069609 (4979, 4980)	Novel Protein sim. GBank gi 2586624 (AC003083) - Rap2 interacting protein-like; similar to U7394.1 (PID:g1816018) [Homo sapiens]		UNCLASSIFIED	264907, 265008, 22279002
2491	81242116 (4981, 4982)	Novel Protein sim. GBank gi 726832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		Im7	264259, 29331826, 265008, 264762, 18108370, 18108376, 18108379
2492	85308202 (4983, 4984)	Novel Protein sim. GBank gi 3355303 (AF001549) - Unknown gene product [Homo sapiens]		transcriptfactor	264488, 22278998, 22278999, 29331828, 264591, 33109954, 265017, 55811150, 21906764, 21906768, 264692, 60431528, 87168518, 60432113, 22279000

2483	95422415 (4885, 4886)	Novel Protein sim. GBank gij4240307[dbj][BAA74932.1] - (AB020716) KIAA0909 protein [Homo sapiens]	Contains protein domain (PF01424) - struct R3H domain	18108394, 264887, 65274572, 56182575, 22278995, 56994075, 60432049, 29331822, 29331824, 29331825, 29331826, 29331827, 29146488, 264508, 264905, 264508, 264906, 264907, 29331830, 264909, 264510, 265008, 264511, 265007, 264512, 265008, 265009, 264910, 21906754, 265011, 264600, 265017, 265018, 264604, 264605, 265019, 55811150, 264762, 18108351, 264681, 264448, 264683, 264369, 264288, 18108355, 18108357, 264687, 21908765, 21908766, 21908767, 21908768, 21908769, 265020, 264691, 264692, 33857023, 33857349, 18108370, 18108374, 18108376, 55810764, 18108379, 65274791, 264630, 264632, 264634, 264635, 264636, 264555, 264637, 264557, 264558, 264639, 264559, 83373044, 18108385, 87168518, 60432113, 22279000, 22279002, 264482, 264566, 264486
2484	30793118 (4887, 4888)			264907, 264601
2485	84234551 (4889, 4890)	Novel Protein sim. GBank gij5420389[emb][CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED collagen
2486	80018765 (4891, 4892)	Novel Protein sim. GBank gij4808220[emb][CAB42832.1] - (AL022315) dJ117715.1 (PUTATIVE novel protein) [Homo sapiens]		263894, 22278997, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 265009, 264595, 264604, 264448, 264682, 264764, 264288, 264685, 264768, 264769, 264689, 265020, 264692, 65274820, 264629, 55810764, 35696423, 55811576, 264636, 264637, 18108385, 22279000, 264564, 264567, 264486
2487	91723554 (4893, 4894)			29147620, 264905, 265006, 265007, 18108348, 18108362, 18108370, 18108374, 264555, 264556, 18108381, 18108383, 18108388
2488	87724633 (4895, 4896)	Novel Protein sim. GBank gij1200503 (U47924) - B [Homo sapiens]		UNCLASSIFIED
2489	94685125 (4897, 4898)	Novel Protein sim. GBank gij3510234 (AC005581) - R31237_1, partial CDS [Homo sapiens]		52644507, 22278996, 22278999, 29331824, 29331828, 33857402, 21906754, 87168474, 265019, 264369, 264689, 21906765, 21906766, 21906767, 21906768, 265020, 33857023, 18108376, 18108387
2490				29331827, 264512, 264910, 264288, 18108374, 35695855
2491				264909, 55812038, 264631, 264637, 264558



2500	94848324 (4988, 5000)	Novel Protein sim. GBank gi 3881275 emb CAA21725  - (AL032655) predicted using GeneFinder; similar to Inositol monophosphatase family; cDNA EST YK255e11.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00459) - Inositol monophosphatase family	transport	52644507, 52845156, 22278995, 56994075, 35696286, 22278998, 264259, 52845080, 29331824, 29331825, 66714117, 60432289, 29331828, 29331827, 35696052, 29331828, 264508, 264509, 284510, 284512, 33657402, 60433438, 21906754, 52644296, 87168474, 87168559, 264603, 284681, 284448, 264683, 264288, 264369, 52844229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 284693, 33657182, 35695763, 35695423, 35695855, 52644332, 83373044, 18108387, 87168518, 22279002
2501	94303896 (5001, 5002)	Novel Protein sim. GBank gi 4929615 gb AAD34088.1 AF151831 - (AF151831) CGI-73 protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	- dna_rna_bind	65274572, 56182575, 35696286, 22278998, 56984075, 22278997, 60432049, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264905, 264908, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264910, 264591, 60432229, 33657402, 60433356, 264595, 55812038, 264758, 284596, 87168474, 87168558, 264600, 264601, 264602, 265017, 264604, 265018, 264605, 265019, 18108351, 264448, 264369, 264288, 264766, 18108357, 21908765, 21906766, 21906767, 21906769, 29148629, 35695917, 264692, 33657023, 284629, 35696423, 55811576, 35695855, 264630, 264634, 264635, 264555, 264638, 264558, 60170384, 83373044, 18108385, 18108387, 87168518, 60432113, 22279002, 264568
2502	90993716 (5003, 5004)	Novel Protein sim. GBank gi 3041847 (AC004542) - OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID:gi129308) [Homo sapiens]	Contains protein domain (PF01237) - Oxysterol-binding protein	UNCLASSIFIED	65274572, 264907, 56182435, 265007, 264592, 264760, 18108351, 264448, 264369, 264288, 264684, 264686, 55811957, 265021, 264892, 33657109, 263973, 55811576, 264635, 264555, 264556, 264557, 264558, 56182323, 264559, 87168518, 264563, 264482
2503	87878345 (5005, 5006)	Novel Protein sim. GBank gi 2196874 emb CAA72638  - (Y11896) BRX protein [Mus musculus]			264905, 264907, 264512, 265008, 265011, 18108351, 264448, 264288, 29148627, 264693, 18108370, 18108374, 18108385

2504	87868708 (5007, 5008)	Novel Protein sim. GBank gi 550420 emb CAA48220  - (X68101) trg [Rattus norvegicus]			264488, 52644507, 52645156, 52646842, 22278994, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264908, 264908, 52644045, 265009, 60433356, 33657402, 60433438, 264595, 33109954, 87168474, 265017, 265019, 264448, 264288, 264766, 52644228, 21906765, 21906766, 21906767, 21906768, 52644150, 264682, 27486261, 27486262, 27486264, 27486265, 35695763, 35698423, 35695855, 52644332, 58182323, 18108387, 87168518, 60432113, 22279002, 264564
2505	8760559 (5009, 5010)			UNCLASSIFIED	264605
2506	91232326 (5011, 5012)	Novel Protein sim. GBank gi 2137562 pir  49635 - mouse Dhmt protein - mouse		nuclease	264488, 52644507, 52645156, 52646365, 65274572, 22278995, 56994075, 22278998, 22278997, 22278998, 22278998, 284259, 60432048, 29331822, 29331825, 29331828, 29331828, 264509, 56182435, 264112, 264593, 60433358, 55812038, 21906754, 265011, 265017, 265018, 265019, 264605, 264762, 18108351, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906768, 21906768, 35695917, 265020, 265021, 265022, 60170615, 33657023, 27486264, 18108379, 35695855, 264637, 83373044, 18108385, 87168518, 60432113, 22279000, 264563, 264482, 264565
2507	95316233 (5013, 5014)	Novel Protein sim. GBank gi 5174489 ref NP_006035.1 pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 263994, 264592, 264585, 264369, 264686, 264768, 35695917, 35696423, 264583
2508	95315505 (5015, 5016)	Novel Protein sim. GBank gi 4826433 emb CAB42889.1  - (AL031447) dJ126A5.2.1 (novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 60432049, 264259, 29331828, 265006, 265007, 60433438, 33657084, 265010, 265017, 265018, 265019, 18108351, 264448, 18108354, 264369, 18108359, 21906765, 21906769, 55811957, 265020, 265022, 27486261, 33657349, 18108377, 35695855, 60432113, 22279002, 264583, 264585
2509	87813741 (5017, 5018)	Novel Protein sim. GBank gi 1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	265007, 265008, 18108357, 264556, 264567

2510	95421379 (5019, 5020)	Novel Protein sim. GBank gi 3293537 gb AAC25762.1  - (AF071059) zinc finger RNA binding protein [Mus musculus]		dna_ma_bind	65274572, 22278994, 22278996, 22278998, 22278999, 60432048, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 33656970, 264908, 66712502, 265007, 294910, 60170831, 60432228, 60433356, 60433438, 21906754, 87168474, 265017, 265018, 264448, 264288, 21908767, 21906768, 21906769, 55811957, 35695917, 265020, 265022, 264691, 33857023, 264693, 65274620, 33657109, 33657182, 27486262, 33657349, 18108370, 35695855, 264555, 56182323, 83373044, 60432113, 22279002, 265017, 21906764, 265020, 264692
2511	87384281 (5021, 5022)	Novel Protein sim. GBank gi 4323152 gb AAD16228.1  - (AF098863) Ets-protein Spi-C [Mus musculus]			
2512	88084771 (5023, 5024)	Novel Protein sim. GBank gi 4502075 ref NP_001135.1 pAMFR - autocrine motility factor receptor	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transport	22278999, 264259, 29331825, 29331826, 29146489, 264907, 264909, 265008, 265008, 264591, 60432229, 21906754, 264763, 264883, 264768, 18108357, 264889, 21906769, 264693, 18108370, 263972, 18108374, 264558, 22278000
2513	95357843 (5025, 5026)	Novel Protein sim. GBank gi 3004657 (AF017777) - bobby sox [Drosophila melanogaster]		UNCLASSIFIED	60424179, 52645156, 18108394, 22278994, 35696286, 58994075, 22278996, 29331822, 29331824, 60424289, 29331825, 29331827, 33656970, 60431735, 33657084, 87168559, 265017, 264448, 264369, 56181562, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108386, 33657109, 27486281, 27486282, 33657349, 18108374, 55810704, 35696423, 56182323, 264558, 18108385
2514	88094578 (5027, 5028)	Novel Protein sim. GBank gi 2258437 (AF008197) - syncoilin [Rattus norvegicus]		UNCLASSIFIED	264510
2515	87994508 (5029, 5030)	Novel Protein sim. GBank gi 3757727 emb CAA18783  - (AL022727) dJ80119.7 olfactory receptor-like protein (hsGMI-3) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	-Im7	
2516	87768908 (5031, 5032)			UNCLASSIFIED	264259, 29146498, 264905, 264288, 29148829, 35695917, 27486261, 264634
2517	87764966 (5033, 5034)	Novel Protein sim. GBank gi 4220527 emb CAA23000  - (AL035356) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264091, 29331824, 29331825, 29331826, 29331828, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 33657402, 264757, 33109954, 265017, 265018, 264605, 264760, 264762, 264763, 264766, 264768, 264769, 33657109, 33657182, 264628, 55811576, 35696423, 264631, 264634, 264637, 264638, 264639, 87168518, 22279002, 264564

2518	94147410 (5035, 5036)	Novel Protein sim. GBank gi 4929591 gb AAD34056.1 AF15181 - (AF151818) CGI-61 protein [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 264907, 264909, 264511, 265007, 60432229, 60433358, 60433438, 55812038, 265010, 265017, 264448, 264288, 264689, 21906768, 21906769, 265022, 52644150, 264693, 18108370, 263972, 264555, 56182323, 83373044, 18108385, 60432113, 264088, 264259, 68714117, 29331826, 29331827, 29331828, 264907, 68712502, 265006, 265008, 264594, 265010, 265011, 265018, 264288, 21906768, 265020, 60431528, 55811576, 65274781, 264632, 264555, 264636, 22278002, 264564
2519	94326180 (5037, 5038)	Novel Protein sim. GBank gi 4263748 gb AAD154201 - (AC004883) similar to KIAA0766; similar to PID:g3882253 [Homo sapiens]	kinase		264259, 264908, 264910, 264682, 21906769, 265020, 264563
2520	87413235 (5039, 5040)	Novel Protein sim. GBank gi 4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4	transport		264488, 264489, 263894, 65274572, 22278995, 22278998, 264259, 29331822, 29331826, 264508, 264905, 264509, 264906, 264907, 66712502, 264511, 265005, 265007, 264591, 264592, 264593, 264594, 264595, 264596, 264681, 264448, 264763, 264682, 264764, 264684, 264369, 264288, 264685, 264686, 21906768, 55811957, 264692, 264693, 27486261, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264632, 264558, 18108385, 65274727, 60432113, 264563, 264564, 264585, 264566, 264567
2521	95316244 (5041, 5042)	Novel Protein sim. GBank gi 5174489 ref NP_006035.1 pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 264489, 263894, 65274572, 22278995, 22278998, 264259, 29331822, 29331826, 264508, 264905, 264509, 264906, 264907, 66712502, 264511, 265005, 265007, 264591, 264592, 264593, 264594, 264595, 264596, 264681, 264448, 264763, 264682, 264764, 264684, 264369, 264288, 264685, 264686, 21906768, 55811957, 264692, 264693, 27486261, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264632, 264558, 18108385, 65274727, 60432113, 264563, 264564, 264585, 264566, 264567
2522	87754052 (5043, 5044)	Novel Protein sim. GBank gi 458001 gb AAD24201.1 U81002 - (U81002) TRAF4 associated factor 1 [Homo sapiens]	transport		264488, 22278997, 20281171, 21906754, 35695917, 263967, 263976, 263981, 20281169
2523	95340467 (5045, 5046)	Novel Protein sim. GBank gi 1809327 U76374 - skm-			263969
2524	95340469 (5047, 5048)	Novel Protein sim. GBank gi 1809327 U76374 - skm- BOP2 [Mus musculus]	Contains protein domain (PF01763) - MYND finger		56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 29331830, 29331824, 29331826, 29331828, 29331830, 56182435, 264512, 265008, 60170831, 33657402, 265010, 87168559, 265019, 264288, 21906765, 21906769, 35695917, 265020, 265021, 265022, 52644150, 264691, 33657023, 33657109, 27486261, 35696423, 65274791, 264559, 83373044, 56528486, 87168518, 264567

2525	94126928 (5049, 5050)	Novel Protein sim. GBank gjl2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]		kinase	264488, 22278997, 22278998, 60432049, 60432288, 29331828, 264905, 265008, 55812038, 21908754, 265019, 264369, 21908765, 21908766, 21908767, 21908769, 35695917, 265020, 265021, 33657109, 60431528, 83373044, 60432113, 22279000, 22279002, 264565
2526	95289404 (5051, 5052)	Novel Protein sim. GBank gjl4589628[dj]BAA76636.1j - (AB023209) KIAA0992 protein [Homo sapiens]	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomalprot	60424178, 264768, 264687, 264769, 264689, 65274572, 21908767, 56182575, 21908768, 21908769, 55811957, 22278994, 22278995, 35696288, 35695917, 22278996, 22278997, 265020, 22278998, 265021, 22278999, 265022, 264690, 264691, 60432049, 264259, 264097, 33657023, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 27486262, 264508, 264509, 264805, 284907, 18108370, 66712502, 60431528, 264828, 264909, 18108372, 18108374, 56182435, 18108376, 55810764, 55811576, 35696423, 35695855, 265006, 265007, 264512, 265008, 265009, 264634, 264635, 60431850, 264636, 264555, 264592, 60431735, 264638, 33657402, 56182323, 60433356, 60433438, 264595, 55812038, 264598, 264758, 83373044, 52646317, 18108385, 33657084, 18108387, 55811386, 65274727, 56526486, 87168518, 60432113, 265017, 22279000, 265018, 265019, 264584, 18108351, 264448, 264566, 264288, 264488, 264587, 264769
2527	88094580 (5053, 5054)	Novel Protein sim. GBank gjl2258437 (AF008197) - syncoilin [Rattus norvegicus]		UNCLASSIFIED	264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354
2528	88078380 (5055, 5056)	Novel Protein sim. GBank gjl2085786 (AC002086) - similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:g1399185) [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bind	55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2529	86670826 (5057, 5058)	Novel Protein sim. GBank gjl3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]		synthase	264908, 264769, 265020, 265021, 18108383
2530	80259978 (5059, 5060)				
2531	87768931 (5061, 5062)			UNCLASSIFIED	264369, 264556
2532	87419778 (5063, 5064)	Novel Protein sim. GBank gjl2864625[emb]CAA16972j - (AL021811) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	29331822, 29331824, 60432289, 264508, 264509, 264908, 265011, 264769, 21908768, 33657023, 87168518, 22279000
2533	87000255 (5065, 5066)	Novel Protein sim. GBank gjl437181 (U02289) - GTPase-activating protein [Caenorhabditis elegans]		UNCLASSIFIED	264553
				UNCLASSIFIED	264555

2534	87332322 (5087, 5088)	Novel Protein sim. GBank gi 3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]		UNCLASSIFIED	264259, 35696052, 264905, 265017, 21908769, 265020, 265022, 33657109, 22279000
2535	91225056 (5089, 5070)	Novel Protein sim. GBank gi 4488311 (emb CAB37992) - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			65274572, 35696286, 60432228, 29331828, 66712502, 265008, 60432229, 265017, 265018, 265019, 264288, 264389, 264689, 21906768, 265020, 265021, 264636, 60170394, 22279002
2536	94218540 (5071, 5072)	Novel Protein sim. GBank gi 728836 sp P39183 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		kinase	18108398, 56182575, 35696286, 22278987, 22278989, 60432049, 264259, 29331824, 29331826, 29331827, 29331828, 264905, 264511, 265009, 264910, 264596, 52646317, 18108351, 264681, 264683, 18108354, 264288, 264687, 264769, 264689, 21906765, 21906766, 21906767, 265021, 52645129, 33657109, 18108374, 18108380, 56182323, 18108381, 18108388, 87168518, 60432113, 22279000, 22279002, 264567, 18108391
2537	95422283 (5073, 5074)	Novel Protein sim. GBank gi 4557026 ref NP_003913.1 pHERC - guanine nucleotide exchange factor p532		ubiquitin	65274572, 35696286, 29331822, 29331825, 29331827, 29331828, 35696052, 264906, 66712502, 264909, 265008, 285011, 264760, 264288, 264685, 35695917, 60170615, 264681, 33657023, 65274620, 33657109, 18108374, 35696423, 35695855, 264636, 264558, 60170394, 56182323, 83373044
2538	36853454 (5075, 5076)			UNCLASSIFIED	
2539	84144916 (5077, 5078)			UNCLASSIFIED	22278996, 22278999, 29331822, 29331825, 29331828, 29148499, 264908, 264112, 60170831, 87168559, 264604, 265019, 264685, 264768, 87168518, 22279000, 264565, 264566
2540	94218545 (5079, 5080)	Novel Protein sim. GBank gi 1362647 pir J553876 - sax-regulated protein Janus A - fruit fly (Drosophila pseudoobscura)		UNCLASSIFIED	22278997, 29331828, 265008, 265009, 264758, 265010, 18108351, 264683, 264288, 21906765, 35695917, 265020, 18108374, 264597
2541	95308238 (5081, 5082)	Novel Protein sim. GBank gi 1711858 sp P54797 T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264488, 264768, 264689, 264511, 20281171, 264634, 264635, 264691, 264639, 29331824, 264603, 264604, 264905, 264907, 264908, 264768

2542	95298162 (5083, 5084)	Novel Protein sim. GBank gjl525320jblAAD0850.1(AFO83107) sirtuin type 2 [Homo sapiens]	Contains protein domain (PF00220) - Neurohypophyseal hormones, N- terminal Domain	UNCLASSIFIED	284488, 18108394, 52846385, 52846842, 65274572, 22278994, 35898286, 22278996, 284259, 52845080, 29331822, 29331824, 29331827, 35898052, 33856970, 284907, 284909, 52844045, 284510, 265008, 284512, 265007, 265008, 265009, 264910, 60431735, 52846317, 52844286, 265010, 265011, 265018, 265019, 18108351, 264683, 264288, 284685, 284687, 52844228, 284789, 21908766, 21908767, 21906769, 52844150, 33857023, 33857109, 52845129, 33857182, 27486261, 27486284, 33657349, 35695763, 18108374, 35696423, 35695855, 284631, 284634, 284635, 284558, 83373044, 18108385, 18108387, 87168518, 264583, 284584
2543	94139088 (5085, 5086)	Novel Protein sim. GBank gjl5419857(emb)CAB46374.1] - (AL086723) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)		65274572, 56182575, 22278999, 264259, 29331826, 284907, 284510, 284511, 284592, 284595, 264784, 264369, 264288, 264684, 264786, 284689, 21906765, 21908767, 21906769, 80170815, 264692, 284693, 55811576, 65274791, 284636, 284558, 18108381, 60170394, 284639, 18108385, 60432113, 22279000
2544	94218548 (5087, 5088)	Novel Protein sim. GBank gjl2498110(esp)Q63191(AEGP_RAT - APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR	Contains protein domain (PF00629) - MAM domain.	glycoprotein	18108397, 52846365, 22278997, 264258, 60432049, 29331822, 29331825, 29331826, 29331827, 29331828, 284905, 264908, 265006, 265007, 265008, 87168559, 265017, 265018, 265019, 18108351, 284448, 284688, 284687, 284689, 21906765, 265020, 265021, 18108370, 18108374, 18108376, 18108381, 18108385, 18108387, 56526486, 22279000, 284482, 284583, 264567
2545	87742845 (5089, 5090)	Novel Protein sim. GBank gjl3327046(jbl)BAA31591] - (AB014516) KIAA0616 protein [Homo sapiens]			29331825, 264906, 265009, 60170831, 265017, 264369, 21906767, 60170815, 284692, 33857109
2546	88093861 (5091, 5092)	Novel Protein sim. GBank gjl2996032 (AF054586) - brain finger protein [Rattus norvegicus]	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	29331824, 265007, 22279002

2547	94143888 (5093, 5094)	Novel Protein sim. GBank gij4928607 gb AAD34084.1 AF151827 - (AF151827) CGI-69 protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264488, 18108394, 52646842, 18108397, 56182575, 22278995, 56994075, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 35696052, 29331828, 264104, 264508, 264905, 264906, 264908, 66712502, 264909, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432228, 60431735, 264594, 60433438, 21906754, 52646317, 265010, 265011, 264600, 264601, 265018, 265019, 264760, 18108351, 264682, 264448, 264288, 264369, 264684, 264686, 264687, 56181562, 264688, 264689, 21906765, 21906768, 21906767, 21906768, 29148627, 21906769, 55811957, 265020, 265021, 265022, 264690, 264691, 18108382, 264692, 264693, 27486261, 18108370, 18108374, 55810764, 55811576, 35696423, 35695855, 264635, 264636, 264555, 264637, 263981, 264557, 18108380, 264638, 56182323, 264558, 264559, 83373044, 18108385, 87168518, 22278002, 264584, 264586, 264488
2548	88179079 (5085, 5086)			UNCLASSIFIED	264488, 18108394, 52646365, 22278994, 35696286, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 56182435, 264511, 265007, 264512, 60433356, 87168559, 264684, 264369, 52644228, 265021, 33657023, 264692, 18108374, 52644332, 264557, 18108380, 18108381, 18108382, 18108384, 18108385, 60432113, 22279000, 22279002, 264583, 264567
2549	94186883 (5087, 5098)	Novel Protein sim. GBank gij728837 sp P39194 ALU7_HUMAN - III  ALU SUBFAMILY SQ WARNING ENTRY III	Contains protein domain (PF00412) - LIM domain containing proteins	struct	56182575, 22278996, 22278997, 22278998, 22278999, 264259, 264508, 264908, 29331830, 265009, 265010, 265018, 264688, 21906764, 21906765, 21906766, 21906767, 21906769, 265020, 265021, 52644150, 264691, 18108388, 60431602, 18108376, 35696423, 56182323, 18108387, 264567
2550	87778584 (5089, 5100)	Novel Protein sim. GBank gij2143886 pir j 52523 - nucleoporin p82 homolog - rat (fragment)		UNCLASSIFIED	56182575, 29331822, 264105, 264512, 18108351, 35695917, 264637, 264638



2551	95308400 (5101, 5102)	Novel Protein sim. GBank gij4337103gibjAAD18079) - (AF129756) NG28 [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	UNCLASSIFIED	18108396, 65274572, 22278995, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 264905, 56182435, 265007, 60433438, 55812038, 21906754, 65274444, 265017, 265018, 264605, 265019, 264288, 21906766, 21906768, 21906769, 265020, 60170615, 264693, 33657109, 35696423, 264638, 56182323, 83373044, 22279000
2552	95332620 (5103, 5104)			UNCLASSIFIED	56182575, 35696286, 29331824, 29331826, 35696052, 29331828, 264508, 264907, 56182435, 265008, 264591, 33109954, 264760, 55811957, 35695917, 33657023, 33657109, 18108374, 55811578, 35696423, 35695855, 56182323, 264558
2553	95308243 (5105, 5106)	Novel Protein sim. GBank gij1711658spjP54797IT10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264686, 264488, 263976, 264768, 29331826, 35696052, 35696423, 264601, 264511, 264602, 264910, 264634, 264760, 264555, 264782, 264908, 264592, 264891, 264566, 264908, 264684, 264567, 264909, 264768, 22278997, 29331822, 264508, 21906769, 33657023, 33657109, 56182323
2554	87761520 (5107, 5108)	Novel Protein sim. GBank gij72883spjP39192IALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII		cadherin	
2555	87627551 (5109, 5110)	Novel Protein sim. GBank gij4884319jembjCAB43260.1) - (AL050084) hypothetical protein [Homo sapiens]		nuclease	29331824, 263972
2556	87645533 (5111, 5112)	Novel Protein sim. GBank gij4106984 (AC003038) - R30923_1 [Homo sapiens]	Contains protein domain (PF00514) - Armadillo/beta-catenin-like repeats	UNCLASSIFIED	22278998, 264509, 33657402, 264683, 264684, 264786, 264689, 33657023, 33657109, 35695855, 264558, 264567, 264595
2557	79437803 (5113, 5114)	Novel Protein sim. GBank gij1191101spjP03211EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	
2558	87617591 (5115, 5116)			UNCLASSIFIED	22278997, 29331824, 66714117, 29331825, 264906, 264511, 265018, 264448
2559	88096382 (5117, 5118)	Novel Protein sim. GBank gij4538998jembjCAB39619.1) - (AL049481) AIG1-like protein [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 29331822, 29331828, 60433356, 265011, 264288, 264765, 264766, 264769, 21906765, 21906766, 60432113, 264482
2560	87894530 (5119, 5120)	Novel Protein sim. GBank gij5051399jembjCAB44995.1) - (AL078630) 573K1.3 (mm17M1-4 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor LIKE protein)) [Mus musculus]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)		
2561	88176575 (5121, 5122)	Novel Protein sim. GBank gij5326825gibjAAD42056.1)AF044953 (NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens])		UNCLASSIFIED	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 265007, 60432228, 87168559, 265017, 265018, 265019, 264689, 21906768, 21906769, 35695917, 265020, 33657023, 33657109, 18108374, 264634, 264559, 18108385, 87168518, 22279002

2562	87645539 (5123, 5124)	Novel Protein sim. GBank gl 4106984 (AC003036) - R30923_1 [Homo sapiens]		UNCLASSIFIED	56994075, 22278986, 22278987, 22278989, 264259, 29331822, 60432288, 33657402, 60433356, 21908765, 55811957, 60170815, 33657023, 264693, 35695855, 87168518, 264488, 35686286, 22278989, 264259, 29331822, 29331824, 35696052, 264508, 264907, 264908, 264909, 52644045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21908767, 21908768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35698423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264568, 264486
2563	88095487 (5125, 5126)	Novel Protein sim. GBank gl 486447 emb CAB43371.1  - (AL050270) hypothetical protein [Homo sapiens]		UNCLASSIFIED	29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2564	80502763 (5127, 5128)	Novel Protein sim. GBank gl 1352944 sp P47179 YJSP_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR		sulfotransferase	29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2565	85530906 (5129, 5130)	Novel Protein sim. GBank gl 828012 pir JAS3933 - myosin I myr. 4 - rat	Contains protein domain (PF00063) - struct	UNCLASSIFIED	68714117, 264909, 283978, 264632
2566	80224956 (5131, 5132)	Novel Protein sim. GBank gl 828012 pir JAS3933 - myosin I myr. 4 - rat	Myosin head (motor domain)	struct	18108370, 35695855, 284556, 264558, 18108383
2567	86143590 (5133, 5134)	Novel Protein sim. GBank gl 466009 sp P34548 YNJ4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III		synthase	265020, 60170615
2568	91233098 (5135, 5136)	Novel Protein sim. GBank gl 466009 sp P34548 YNJ4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III			60424179, 18108394, 56181686, 56994075, 22278989, 264490, 264259, 29331822, 56182181, 29331824, 60424269, 29331825, 29331826, 29331828, 264509, 29331830, 265007, 265008, 265009, 33657402, 265010, 265011, 265019, 264448, 264683, 264288, 18108354, 264769, 21908766, 21908767, 35695917, 265021, 33657023, 18108362, 33657109, 33657182, 35695763, 60431528, 55810784, 18108379, 83373044, 18108385, 60432113, 264482

2569	95313764 (5137, 5138)	Novel Protein sim. GBank gi 2599560 gb AAB84166.1  - (AF029974) basic leucine zipper protein LZIP [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	18108394, 56182575, 56181686, 22278995, 22278996, 56894075, 35868286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 56182161, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35896052, 264905, 264908, 56182435, 265008, 265009, 264910, 60432229, 264592, 60433356, 60433438, 21906754, 87168558, 265017, 265018, 265019, 264682, 264448, 264288, 21906765, 21906768, 21906767, 21906769, 29148627, 21906769, 35895917, 265021, 265022, 5264150, 264690, 264691, 264692, 264693, 65274620, 263967, 35895763, 20281069, 263674, 18108374, 55810764, 35896423, 35895855, 264558, 18108381, 56182323, 18108382, 83373044, 18108385, 58526486, 87168518, 22279000, 22279002, 264566
2570	84136754 (5139, 5140)	Novel Protein sim. GBank gi 4758954 ref NP_004567.1 pPPP2 - protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	Contains protein domain (PF01240) - Protein phosphatase 2A regulatory subunit PR55	phosphatase	22278996, 29331822, 29331824, 66714117, 29331825, 60432289, 29331827, 35898052, 264907, 264510, 265007, 265009, 264758, 33109954, 265019, 264686, 264689, 265020, 265021, 264691, 264692, 264693, 18108374, 35895855, 264634, 56182323, 264639, 60170394, 83373044, 22279002, 264482
2571	87733750 (5141, 5142)	Novel Protein sim. GBank gi 732218 sp P34609 YO60_CAEEL - HYPOTHETICAL 128.8 KD PROTEIN ZK1098.10 IN CHROMOSOME III		struct	264508, 264905, 264907, 264628, 18108351, 264555, 264556, 264557, 264558, 264559
2572	87627560 (5143, 5144)	Novel Protein sim. GBank gi 4894319 emb CAB43260.1  - (AL050084) hypothetical protein [Homo sapiens]		UNCLASSIFIED	35896286, 29331827, 35896052, 264100, 264104, 264110, 264592, 21906754, 29148627, 29148629, 263972, 263974, 18108374, 263976, 35895855, 60170394, 264559, 18108385

2573	95313928 (5145, 5146)	Novel Protein sim. GBank gi 399138 sp P02745 C1QA_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264488, 60424178, 65274572, 56182575, 56181886, 22278995, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432288, 29331826, 29331827, 29331828, 264104, 264107, 264508, 264806, 29331830, 264909, 264510, 265006, 264512, 265008, 265009, 264910, 264591, 264592, 60432229, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264759, 21906754, 87189474, 265010, 265011, 87188559, 265017, 265018, 265019, 264761, 264762, 264763, 264764, 264369, 264288, 264685, 264766, 264686, 264687, 264688, 264769, 58181562, 264689, 21906768, 21906769, 21906767, 29148827, 21906768, 21908769, 265020, 265021, 265022, 60170615, 264690, 52844150, 264691, 264692, 33657023, 65274620, 18108365, 18108368, 27486265, 60431602, 264629, 60431528, 263976, 65274791, 35895855, 20281071, 60431850, 264637, 264638, 264558, 264639, 56182323, 60170394, 83373044, 18108384, 87188518, 60432113, 264482, 264564, 264565, 264566, 264567, 22278995, 264259, 60432289, 29331827, 29331828, 33656970, 264908, 265008, 264910, 264591, 33657402, 265018, 265019, 264448, 264764, 264369, 264288, 18108357, 21906765, 21906766, 21906768, 55811957, 60170615, 264691, 33657023, 264693, 33657109, 33657182, 27486261, 27486264, 33657349, 264636, 264555, 83373044, 18108385, 264482
2574	84746814 (5147, 5148)	Novel Protein sim. GBank gi 3334982 (AC005306) - R27216_1 [Homo sapiens]	Contains protein domain (PF00851) - BTB/POZ domain	UNCLASSIFIED	264488, 264906, 264908, 264910, 264596, 264603, 264804, 264805, 264768, 21908769, 264828, 264630, 264634, 264639, 264563, 29331822, 29331824, 264767
2575	87754408 (5149, 5150)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 AF15188 - (AF151888) CGI-130 protein [Homo sapiens]		UNCLASSIFIED	264910, 264601, 264683, 264689, 264080
2576	95357881 (5151, 5152)	Novel Protein sim. GBank gi 4680881 gb AAD27730.1 AF13295 - (AF132955) CGI-21 protein [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264259, 35696052, 264906, 60433438, 264681, 18108351, 264288, 52644150, 264628, 35698423
2577	86996621 (5153, 5154)	Novel Protein sim. GBank gi 4337103 gb AAD18079  - (AF129756) NG26 [Homo sapiens]		UNCLASSIFIED	29331825, 265018, 265019, 264685
2578	87786941 (5155, 5156)			UNCLASSIFIED	264488, 264906, 264908, 264910, 264596, 264603, 264804, 264805, 264768, 21908769, 264828, 264630, 264634, 264639, 264563
2579	87282879 (5157, 5158)			UNCLASSIFIED	29331822, 29331824, 264767

2580	88168788 (5159, 5160)	Novel Protein sim. GBank gi2588628 (AC003080) - Similar to KIAA0289; 60% similarity to AB002297 (PID:g2224539) [Homo sapiens]				265007, 265018, 264762
2581	87898048 (5181, 5182)	Novel Protein sim. GBank gi4406642 [gb AAD20048] - (AF131809) Unknown [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	collagen		56994075, 29331824, 29331826, 29331828, 264905, 60433356, 60433438, 264758, 87188559, 21908769, 265022, 35695855, 263981
2582	87786789 (5163, 5164)	Novel Protein sim. GBank gi2738367 (AC002505) - putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]		eph		264488, 264907, 264908, 264910, 264764, 264684, 264766, 264636, 264555, 264585
2583	91220950 (5165, 5166)	Novel Protein sim. GBank gi4378112 [emb CAA16521.1] - (AL021578) dJ453C12.2 (similar to transcription factor RBP-L) [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	transcript factor		56181686, 264259, 264510, 264512, 264591, 264592, 264593, 264594, 264595, 264596, 264603, 264629, 55810764, 264630, 264637, 264565
2584	80430941 (5167, 5168)			UNCLASSIFIED		264908, 264910, 264768, 264693, 18108374, 55811576, 56182323
2585	80436128 (5169, 5170)	Novel Protein sim. GBank gi2736151 (AF021935) - myotonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]		kinase		264768
2586	91226136 (5171, 5172)					22278998, 264259, 29331822, 29331824, 29331827, 29331828, 264906, 265007, 265009, 264591, 60433356, 33657402, 265018, 264762, 264288, 21906766, 21906767, 21906769, 265022, 264691, 83373044, 58528486, 22279002
2587	80430943 (5173, 5174)					264908, 265019, 264768, 264693, 55811576, 56182323
2588	80074385 (5175, 5176)			UNCLASSIFIED		264564
2589	85515607 (5177, 5178)	Novel Protein sim. GBank gi3021598 [emb CAA71415] - (Y10389) nuclear protein [Xenopus laevis]		UNCLASSIFIED		35696052, 264905, 264906, 264907, 264908, 264909, 265009, 265018, 264769, 35698423, 264636
2590	87054526 (5179, 5180)	Novel Protein sim. GBank gi2104689 (U92793) - alpha glucosidase II, alpha subunit [Mus musculus]	Contains protein domain (PF01055) - Glycosyl hydrolases family 31	glucoamylase		22278995, 29331830, 265008, 265010, 265017, 264639
2591	94192167 (5181, 5182)	Novel Protein sim. GBank gi5702202 [gb AAD47199.1] (AF129166) long-chain acyl-CoA synthetase 5 [Homo sapiens]		eph		264259, 29331822, 264106, 264906, 56182435, 265007, 265008, 33109954, 264448, 55811957, 265020, 18108370, 55811576, 22279002

2592	85332648 (5183, 5184)	Novel Protein sim. GBank gi 3024988 sp Q60936 YAB1_MOUSE - HYPOTHETICAL HEART PROTEIN		transport	18108397, 56182575, 35696286, 56994076, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 284906, 264909, 265007, 285008, 264910, 60432229, 264594, 60433356, 60433438, 55812038, 18108348, 21906754, 265011, 87168559, 285017, 285018, 284764, 264369, 264288, 264766, 265021, 60170615, 33657023, 33657109, 264629, 35696423, 35695855, 264557, 264638, 60170394, 58182323, 83373044, 56526486, 87168518, 264563, 264482, 264565
2593	87754416 (5185, 5186)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 AF15188 - (AF15188) CGI-130 protein [Homo sapiens]		tm7	22278999, 29331825, 264758, 21906754, 52646317, 265010, 18108351, 264288, 264369, 21906768, 264693, 18108370, 264637, 264638, 264482
2594	95305758 (5187, 5188)	Novel Protein sim. GBank gi 4929587 gb AAD34054.1 AF15181 - (AF15181) CGI-59 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108388, 56182575, 35696286, 22278997, 264093, 264259, 29331822, 29331825, 66714117, 29331828, 264905, 264909, 52644045, 58182435, 264510, 264512, 265007, 264757, 21906754, 87168474, 285017, 264760, 264448, 264764, 264288, 284766, 264689, 21906768, 33657109, 263975, 263977, 264634, 264556, 60170394, 56182323, 56526486, 264482, 264563, 264564, 264566, 264567
2595	79561678 (5189, 5190)			UNCLASSIFIED	264692
2596	87538637 (5191, 5192)	Novel Protein sim. GBank gi K309681 gb AAD154781 - (AC006930) R33423.1 [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 265018, 264448, 285021, 80431528
2597	94784089 (5193, 5194)			UNCLASSIFIED	264905, 264509, 264908, 264762, 264766, 35695917, 35695855, 264635, 264636, 83373044, 264486
2598	88084948 (5185, 5198)	Novel Protein sim. GBank gi 1001351 dbj BAA108381 - (CG4006) hypothetical protein [Synecocystis sp.]		UNCLASSIFIED	22278998, 264259, 29331824, 87168474, 264683, 21906768, 35695817, 264691, 33657023, 33657109, 18108370, 18108374, 264584, 264585
2599	87842889 (5197, 5198)	Novel Protein sim. GBank gi 3941737 (AF109719) - BAT2 [Mus musculus]		MHC	264766, 264769, 21906768, 33657182, 35695763, 18108370, 18108374, 264635, 264636, 56526486, 22279000, 264566
2600	87787846 (5199, 5200)	Novel Protein sim. GBank gi 4263521 gb AAD153471 - (AC004044) putative WD-repeat protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	35696286, 264093, 264288, 21906769, 35696423, 35695855

2601	91243070 (5201, 5202)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	56182575, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 264908, 285007, 285008, 264591, 60433356, 33657402, 60433438, 21906754, 265011, 265018, 265019, 18108351, 264448, 264369, 21906769, 265020, 60170615, 264693, 33857109, 18108370, 18108376, 58182323, 18108381, 18108385, 22279002, 264563, 60433438, 21906754, 87168559, 264601, 264369, 264288, 21906767
2602	88180022 (5203, 5204)	Novel Protein sim. GBank gi 4406632 sp AAD200471 - (AF131801) Unknown (Homo sapiens)			
2603	94325821 (5205, 5206)	Novel Protein sim. GBank gi 3122387 sp O61211 LIGA_MOUSE - LIGATIN		UNCLASSIFIED	264488, 65274572, 22278995, 22278996, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 56182435, 264113, 265008, 265009, 60433356, 264757, 60433438, 264759, 33657084, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264683, 18108354, 264288, 264767, 264689, 21908765, 21908766, 21906767, 21908768, 21908769, 55811957, 265020, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27486262, 18108374, 35698423, 65274791, 35695855, 264555, 264636, 264637, 56182323, 83373044, 56526486, 87168518, 60432113, 22278900
2804	94676801 (5207, 5208)	Novel Protein sim. GBank gi 5454030 ref NP_008468.1 pRRP2 - RAS-related on chromosome 22		oncogene	284259, 35696052, 264508, 264906, 264907, 284908, 264909, 264510, 264512, 265008, 264910, 33657402, 264604, 264605, 264762, 264763, 264682, 264764, 264683, 264768, 264769, 264689, 33657023, 264693, 18108365, 264628, 35698423, 264631, 264632, 264634, 264635, 264637, 18108381, 264639, 83373044, 264565
2605	94316766 (5209, 5210)	Novel Protein sim. GBank gi 3628745 dbj BAA33366  - (AB013721) mlisugumin 23 [Oryctolagus cuniculus]		UNCLASSIFIED	22278998, 264480, 60432049, 264259, 60432289, 264909, 265008, 60433356, 60433438, 264758, 21906754, 265010, 265011, 265018, 264681, 18108351, 264288, 264766, 264685, 21908765, 21908766, 21906768, 21906769, 264691, 264692, 264693, 65274791, 264634, 264555, 264636, 22278996, 264510, 264512, 265009, 264766, 22279002, 264566
2606	87746408 (5211, 5212)				

2607	87627742 (5213, 5214)	Novel Protein sim. GBank gij4826628[gb AAD30202.1] - (AF135022) mediator [Homo sapiens]			29331822, 29331825, 29331826, 29331827, 29331828, 264906, 264907, 264908, 66712502, 264828, 56182435, 55812038, 265010, 265017, 265018, 265019, 264768, 264689, 21906765, 55811857, 265020, 265022, 264692, 33657023, 264693, 33657109, 18108370, 264639, 56182323
2608	81734786 (5215, 5216)	Novel Protein sim. GBank gij2226005 (U49973) - ORF2: function unknown [Homo sapiens]			264509, 264907, 264908, 264592, 264758, 264631
2609	94843791 (5217, 5218)	Novel Protein sim. GBank gij3024889[sp P56524]Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)	Contains protein domain (PF00850) - histone Histone deacetylase family		264488, 65274572, 35696286, 22278997, 22278999, 60432049, 264259, 56182181, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264907, 60433356, 60433438, 55812038, 265011, 87168559, 265017, 265018, 264448, 264765, 264288, 264766, 264689, 21906765, 21906767, 21906769, 265020, 265021, 264691, 264692, 33657109, 27486261, 18108370, 65274791, 264636, 264556, 56182323, 18108395, 56526486
2610	88177654 (5219, 5220)	Novel Protein sim. GBank gij4336855[gb AAD17989] - (AF106473) leucine-rich-domain inter-acting protein 1; LeR inter-acting protein 1; LEAP1 [Mus musculus]	transcript factor		18108394, 22278994, 56594075, 60432049, 264259, 29331822, 29331825, 60432289, 29331827, 264107, 264109, 264905, 56182435, 264112, 265008, 265007, 265008, 265009, 60433358, 60433438, 265011, 87168559, 265017, 264448, 264682, 264764, 264288, 265021, 33657023, 263967, 33657182, 27486261, 18108374, 263976, 55811576, 264638, 87168518, 60432113
2611	87428890 (5221, 5222)	Novel Protein sim. GBank gij387676[emb CAA92994] - (Z68760) predicted using GeneFinder. Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00234) - FKBP-type peptidyl-prolyl cis-trans isomerases		22278999, 265017, 264684, 21906768, 22279000
2612	87771198 (5223, 5224)	Novel Protein sim. GBank gij5679138[gb AAD46874.1]AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]	transport		265009, 264910, 264759, 265017, 21906767, 18108365, 18108388, 60432113
2613	79481498 (5225, 5226)	Novel Protein sim. GBank gij533081[gb AAD45009.1]AF16118 - (AF161181) P55T protein [Mus musculus]	UNCLASSIFIED		264685
2614	87643948 (5227, 5228)		Contains protein domain (PF00625) - Guanylate kinase		22278998, 22278999, 29331825, 264508, 264906, 21906754, 264602, 264768, 264769, 52644229, 21906765, 33657109, 27486284, 18108370, 263972, 264555, 60432113
2615	87381986 (5229, 5230)		UNCLASSIFIED		264768, 18108394, 264692, 264693, 264508, 264509, 264907, 264628, 264908, 264909, 18108377, 264511, 264512, 264910, 264635, 264595, 265010, 264404, 264563, 264764, 264685, 264766



2616	87428895 (5231, 5232)	Novel Protein sim. GBank gi 3876761 emb CAA02994  - (Z68760) predicted using GeneFinder; Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278995, 22278997, 22278998, 60432049, 60432289, 264828, 60433356, 264594, 60433438, 33109954, 87168474, 265011, 265017, 265019, 264288, 264788, 21906765, 21908767, 265020, 265021, 18108378, 18108377, 18108387, 87168518, 264482, 264587
2617	88976888 (5233, 5234)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		kinase	265010, 265019, 264369, 264693, 55811576, 22278002
2618	81231662 (5235, 5236)	Novel Protein sim. GBank gi 3319282 (AF049103) - Huntingtin interacting protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	UNCLASSIFIED	264489, 22278996, 264490, 264259, 29331822, 264102, 264509, 264908, 264907, 66712502, 29331830, 265008, 264910, 265009, 60433356, 60433438, 264758, 21908754, 265011, 87168559, 265017, 265018, 264369, 264288, 264768, 264768, 264688, 21906765, 21906766, 21906787, 35695917, 265020, 265022, 33657023, 264692, 33657109, 264628, 18108374, 35695855, 18108381, 83373044, 18108385, 18108388, 56528486, 264563
2619	87694000 (5237, 5238)	Novel Protein sim. GBank gi 2431772 (U66411) - putative type III alcohol dehydrogenase [Drosophila melanogaster]	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases	dehydrogenase	264259, 60432288, 60433438, 21908754, 264369, 60432113, 264566
2620	85314841 (5239, 5240)	Novel Protein sim. GBank gi 4322567 gb AAD16097  - (AF090436) dachshund variant 1 [Mus musculus]	Contains protein domain (PF00828) - PHD-finger	UNCLASSIFIED	52644507, 52645156, 52646842, 65274572, 22278995, 59994075, 35696288, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 35696052, 264907, 66712502, 265008, 60433356, 33657402, 52646317, 21906754, 87168474, 265010, 265017, 265018, 264448, 264369, 264288, 264687, 264768, 52644229, 264688, 264689, 21906765, 21906768, 35695917, 52644150, 264692, 33657109, 35695763, 35696423, 264556, 52644332, 18108382, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 22279002
2621	80253495 (5241, 5242)				264594, 264636
2622	81780390 (5243, 5244)	Novel Protein sim. GBank gi 4557341 ref NP_001174.1 pATP6 - ATPase, H+ transporting, lysosomal subunit 1; vacuolar proton pump, H-ATPase subunit			264488, 264908, 264907, 264908, 264512, 285007, 264758, 35695917, 264634, 264636, 264563, 264482
2623	91639306 (5245, 5246)	Novel Protein sim. GBank gi 3880355 emb CAB05299  - (Z82285) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	29331824, 35696052, 265007, 265010, 264288, 29148629

2624	81639308 (5247, 5249)	Novel Protein sim. GBank gl 388035 emb CAB05298  - (Z82285) predicted using GeneFinder [Caenorhabditis elegans]	UNCLASSIFIED	56181686, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331828, 35696052, 29146499, 68712502, 52644045, 265007, 265008, 60433356, 33108954, 21906754, 265010, 265011, 265019, 264448, 264288, 21906765, 21906766, 21906767, 29148629, 35695917, 265021, 265022, 27486265, 18108370, 60431528, 55811576, 35695855, 56182323, 18108385, 87168518, 22279002, 18108391
2625	86452068 (5249, 5250)	Novel Protein sim. GBank gl 2887429 db BAA24857  - (AB007887) KIAA0427 [Homo sapiens]	UNCLASSIFIED	264091, 264511, 263981
2626	16533797 (5251, 5252)	Novel Protein sim. GBank gl 487416 (L20302) - actin filament protein [Gallus gallus]	struct	265008
2627	87636823 (5253, 5254)	Novel Protein sim. GBank gl 88462 pir A27307 - proline-rich phosphoprotein (gene PRH1, Db allele) - human	UNCLASSIFIED	22278996, 265007, 265009, 264448, 21906787, 265021, 264558, 87168518
2628	94848254 (5255, 5256)	Novel Protein sim. GBank gl 3123552 emb CAA18609  - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0289 LIKE) [Homo sapiens]	UNCLASSIFIED	22278997, 22278999, 264259, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264907, 264909, 265008, 264591, 80433356, 60433438, 265010, 265017, 265018, 264389, 264288, 18108357, 21906765, 21906768, 265022, 65274781, 264638, 18108387, 87168518, 22279002
2629	87376490 (5257, 5258)	Novel Protein sim. GBank gl 4929595 gb AAD34058.1 AF15182 - (AF151821) CGI-63 protein [Homo sapiens]	synthase	29331825, 29331826, 264102, 265006, 264766, 35695917, 264691, 33657023, 263972, 18108374, 22279000
2630	79188364 (5259, 5260)		UNCLASSIFIED	264636, 18108385
2631	94845909 (5261, 5262)	Novel Protein sim. GBank gl 321605 pir JQ1161 - Gag protein - Visna virus (strain EV1)	Contains protein domain (PF000098) - Zinc finger, CCHC class	52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35696288, 56994075, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264905, 264509, 264907, 264908, 264511, 264512, 265007, 265008, 264910, 52646317, 33657084, 52644296, 265010, 87168559, 265017, 265018, 265019, 264760, 264762, 264448, 264288, 264369, 264768, 264769, 52644229, 21906764, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 35698423, 65274791, 35695855, 264634, 264637, 52644332, 56182323, 60432113, 264566, 264486, 264685
2632	38730414 (5263, 5264)			

2633	95011617 (5265, 5266)	Novel Protein sim. GBank gi1139548[dbj BAA10889] - (D84009) seizure-related gene product 6 type 2 precursor [Mus musculus]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	22278995, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331827, 264508, 264906, 265006, 265007, 265008, 265009, 55812038, 33657084, 55811388, 265010, 265011, 87168559, 265018, 265019, 264683, 264288, 264686, 29148629, 33657023, 264693, 33657182, 35695763, 55811576, 264639, 56182323, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264565
2634	87330921 (5267, 5268)	Novel Protein sim. GBank gi5441611[emb CAB46854.1] - (AJ388555) hypothetical protein [Canis familiaris]	UNCLASSIFIED	29331826, 263972, 264089
2635	86623144 (5269, 5270)	Novel Protein sim. GBank gi14680663[gb AAD27721.1]AF132946) CGI-12 protein [Homo sapiens]		22278997, 264259, 29331824, 68714117, 29331827, 29331828, 264907, 33657084, 265017, 265018, 264448, 264288, 21906766, 21906767, 21906768, 29148629, 18108376, 55811576, 35695855, 87168518, 22279000
2636	87260534 (5271, 5272)	Novel Protein sim. GBank gi3879146[emb CAB07646] - (Z93386) Similarly to Yeast hypothetical 52.9 KD protein (SW:P43616); cDNA EST EMBL:M89432 comes from this gene; cDNA EST EMBL:D71008 comes from this gene; cDNA EST EMBL:D73578 comes from this gene; cDNA EST EMBL:D69025 comes ...	Contains protein domain (PF01546) - Peptidase family M20/M25/M40	264569, 29331822, 29331828, 265006, 60170831, 264681, 264765, 264685, 29148627, 21908769, 29148784, 265022, 60170815, 264635, 18108385, 56526486, 22279002, 264567
2637	95011298 (5273, 5274)	Novel Protein sim. GBank gi14758208[ref NP_004081.1]pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	phosphatase Dual specificity phosphatase, catalytic domain	264488, 264489, 52644507, 264687, 52646365, 52646842, 22278994, 22278998, 22278999, 20281171, 264259, 29331822, 52645080, 68714117, 29331825, 29331826, 29331827, 35696052, 29331828, 29146488, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264591, 264592, 60432228, 264593, 264594, 33657402, 60433356, 264757, 60433438, 264596, 264758, 52646317, 21906754, 52644296, 265010, 264600, 264602, 264603, 264605, 264761, 264762, 264681, 264448, 264764, 264765, 264288, 264766, 264686, 264768, 264687, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 60170815, 264681, 33657023, 264692, 264693, 65274620, 27486284, 18108370, 264628, 264629, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264637, 264638, 52644332, 264639, 264558, 83373044, 60432113, 264564, 264565, 264566, 264488, 264567

2638	94326733 (5275, 5278)	Novel Protein sim. GBank gi 4929888 gb AAD34105.1 AF15186 - (AF151868) CGI-110 protein [Homo sapiens]	Contains protein domain (PF000076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	60424179, 52844507, 52846842, 18108398, 56182575, 22278995, 22278998, 35698288, 22278997, 22278999, 264259, 60432049, 28331822, 60424268, 26331828, 35698052, 29146498, 264905, 52844045, 56182435, 60433358, 33657402, 55812038, 55811386, 285019, 264288, 264769, 52844229, 56181562, 29148627, 29148629, 55811957, 29148784, 35695917, 265021, 52844150, 33657023, 65274620, 33657109, 35695763, 18108374, 55810784, 35698423, 55811576, 35695855, 60431850, 56182323, 60432113, 264404
2639	95381346 (5277, 5278)	Novel Protein sim. GBank gi 2190007 dbj BAA20355  - (AB004109) phosphatidylserine synthase II [Cricetulus griseus]		synthase	264488, 29331825, 35696052, 264508, 264509, 264809, 264512, 33657402, 60433438, 264758, 85658542, 264600, 265020, 265021, 33657109, 264628, 35696423, 264555, 264639, 264583, 264584, 264565, 264588, 264486
2640	87781330 (5279, 5280)	Novel Protein sim. GBank gi 3158516 (AF067617) - contains similarity to chromo (chromatin organization modifier) domains (Pfam: chromo.hmm. score: 17.76 and 27.94) and to helicases conserved C-terminal domain (Pfam: helicase_C.hmm. score: 67.00) [Caenorhabditis elegans]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	29331822, 29331826, 264906, 33109854, 265017, 265018, 21906768, 35695763, 264636, 264637, 18108387
2641	11688834 (5281, 5282)	Novel Protein sim. GBank gi 2564955 (AF030001) - unknown [Mus musculus]		UNCLASSIFIED	264828
2642	87412575 (5283, 5284)	Novel Protein sim. GBank gi 4490304 emb CAB38785.1  - (AL035878) putative protein [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	264259, 29331822, 33657402, 265019, 264369, 264691, 264634, 56526488, 22279002
2643	87643981 (5285, 5286)	Novel Protein sim. GBank gi 3789797 gb AAC67502.1  - (AF059569) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00851) - BTB/POZ domain	helicase	22278997, 264259, 29146499, 56182435, 264910, 265010, 18108351, 264682, 264683, 264369, 264684, 264685, 264686, 29148627, 264680, 33657109, 18108370, 263973, 18108374, 264634, 264557, 264558, 18108385, 264482
2644	88177671 (5287, 5288)	Novel Protein sim. GBank gi 3789797 gb AAC67502.1  - (AF059569) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00851) - BTB/POZ domain	nuc1_recpt	264107, 264687
2645	17277228 (5289, 5290)	Novel Protein sim. GBank		UNCLASSIFIED	265007
2646	94148542 (5291, 5292)	gi 1706722 sp P49749 EVX2_MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2)		UNCLASSIFIED	264909, 264687, 264632, 83373044

2647	91212878 (5293, 5294)			UNCLASSIFIED	56182575, 22278996, 35696286, 22278998, 264259, 29331822, 56182181, 29331825, 60424289, 60432289, 35696052, 68712502, 264908, 265007, 55812038, 33109954, 21906754, 33657084, 265019, 264448, 264288, 56181562, 21906766, 21906768, 21906769, 35695917, 265020, 265021, 52844150, 264693, 33657109, 33657349, 60431528, 18108374, 55810764, 35696423, 56182323, 60432113, 22279002, 264564
2648	87600587 (5295, 5296)				29146498, 56182435, 33109854, 265011, 264682, 55811957, 35695917, 264680, 263976, 18108377, 35696423, 60432113
2649	94128783 (5297, 5298)	Novel Protein sim. GBank gij3041852 (AC004539) - unknown function; similar to Y09105 (PID:g1666171) [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278998, 29331824, 29331826, 60432289, 68712502, 56182435, 60170831, 60432229, 33657402, 33108954, 21906754, 265017, 264688, 264688, 21906765, 21906768, 60170815, 264693, 263987, 18108370, 263976, 60170394, 60432113, 22279002, 264563
2650	87287533 (5299, 5300)	Novel Protein sim. GBank gij5360271 [dbj]BAA81908.1] - (AB0293335) HRPET-3 [Halicynithia torelli]			264685
2651	88088745 (5301, 5302)	Novel Protein sim. GBank gij4240225 [dbj]BAA74891.1] - (AB020675) KIAA0868 protein [Homo sapiens]	Contains protein domain (PF00054) - synthase Laminin G domain		29331824, 29331826, 29331827, 265007, 55812038, 21906754, 18108366, 18108384, 22279002, 264567
2652	10343125 (5303, 5304)	Novel Protein sim. GBank gij4493956 [embj]CAB11123.2] - (Z98551) predicted using hexExon; MAL3P6.28 (PFC08450), Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR:....		UNCLASSIFIED	264692
2653	87798735 (5305, 5306)			UNCLASSIFIED	265018, 18108370, 18108387, 264566
2654	95103240 (5307, 5308)				60424178, 65274572, 56182575, 264259, 56182181, 264908, 56182435, 55811957, 35695917, 265021, 263976, 55810764, 65274791, 56182323, 83373044, 65274727
2655	91228018 (5309, 5310)	Novel Protein sim. GBank gij3875272 [embj]CAB02861] - (Z81051) predicted using GeneFinder; similar to Zinc finger, C3HC4 type (RING finger); cDNA EST yk443h5.3 comes from this gene; cDNA EST yk443h5.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transcription factor	56182575, 56181686, 264082, 264259, 56182181, 60432289, 264907, 33657402, 55812038, 21906754, 87168559, 265017, 264448, 264369, 264288, 21906765, 21906766, 21906767, 21906768, 33657109, 18108370, 264628, 55811576, 264556, 264639, 83373044, 56526486, 264404, 60432113
2656	94562601 (5311, 5312)	Novel Protein sim. GBank gij3043718 [dbj]BAA25523] - (AB011189) KIAA0597 protein [Homo sapiens]			264693

2657	52561728 (5313, 5314)	Novel Protein sim. GBank gl 5689509 dbj BAA03038.1  - (AB029009) KIAA1088 protein [Homo sapiens]			dna_rna_bind	264693
2658	88062454 (5315, 5316)	Novel Protein sim. GBank gl 3688089 (AC005757) - R32611_1 [Homo sapiens]		Contains protein domain (PF00560) - Leucine Rich Repeat	nucleaseinhib	35696286, 264259, 29331822, 29331824, 29331826, 29331828, 265019, 264683, 21906768, 35695917, 264693, 35695855, 264637, 87168518, 264486, 264567
2659	87800755 (5317, 5318)	Novel Protein sim. GBank gl 5420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]		Contains protein domain (PF01426) - BAH domain	UNCLASSIFIED	264909, 264910, 265016, 264369, 264769, 21906769, 264693, 263972, 18108388
2660	81718472 (5319, 5320)	Novel Protein sim. GBank gl 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		Contains protein domain (PF00036) - EF hand	kinase	264488, 65274572, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 35696052, 264908, 56182435, 265008, 265009, 60433356, 264594, 265010, 265018, 55811150, 18108351, 264682, 264684, 264368, 264288, 264687, 21906765, 29148784, 35695917, 60170615, 52644150, 33657023, 33657109, 35696423, 35695855, 264556, 60170394, 18108385, 22278000, 22278002
2661	95342817 (5321, 5322)	Novel Protein sim. GBank gl 4758048 ref NP_004739.1 pCPR8 - cell cycle progression 8 protein			glycoprotein	60432049, 264259, 29331824, 29331825, 28331826, 28331827, 28331828, 264908, 264909, 264593, 33109954, 265010, 265017, 265018, 265019, 264760, 264448, 264369, 264288, 21906765, 21906768, 265022, 264691, 33657023, 27488282, 60431528, 18108374, 35695855, 18108388, 264482
2662	80228739 (5323, 5324)	Novel Protein sim. GBank gl 3874714 emb CAA91263  - (Z66494) similar to choline dehydrogenase; cDNA EST yk346d5.5 comes from this gene; cDNA EST yk346d5.3 comes from this gene [Caenorhabditis elegans]			dehydrogenase	264555, 264556, 264558, 264486
2663	87780623 (5325, 5326)	Novel Protein sim. GBank gl 1389670 (U58977) - Notch homolog Scalloped wings [Lucilia cuprina]		Contains protein domain (PF00008) - EGF-like domain	oncogene	264906, 264908, 264757, 264758, 264767, 264691, 33657023, 264638
2664	85518328 (5327, 5328)	Novel Protein sim. GBank gl 4884406 emb CAB43311.1  - (AL050190) hypothetical protein [Homo sapiens]			UNCLASSIFIED	35696286, 264508, 264595, 264288, 264685, 264686
2665	87770662 (5329, 5330)	Novel Protein sim. GBank gl 5106956 gb AAD39906.1 AF113615 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]			UNCLASSIFIED	264906, 264907, 264909, 264510, 264511, 264512, 264593, 60433438, 265019, 264681, 21906765, 21906766, 21906767, 21906768, 265020, 265022, 35696423, 35695855, 22278002, 264482, 264486
2666	87826472 (5331, 5332)	Novel Protein sim. GBank gl 5106956 gb AAD39906.1 AF113615 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]			UNCLASSIFIED	29331825, 265007, 264910, 60432229, 265019, 264288, 21906767, 264558, 22278002
2667	87422720 (5333, 5334)	Novel Protein sim. GBank gl 2500570 sp Q17533 RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0564.1		Contains protein domain (PF01138) - 3' exoribonuclease family	nuclease	264907, 29331830, 264681, 264683, 264288, 35695855, 264632, 264556, 264557, 264558, 264559, 264563, 264565, 264567

2668	91216716 (5335, 5336)	Novel Protein sim. GBank gi 5454186 ref NP_006327.1 pZYG  - ZYG homolog		UNCLASSIFIED	56181886, 35696286, 22278988, 22278989, 56182181, 29331824, 60424289, 29331825, 35698052, 29331828, 66712502, 56182435, 60433356, 264758, 21908754, 55811386, 285011, 87168559, 265017, 265019, 55811150, 264448, 264369, 264288, 21906765, 21906768, 21906768, 55811957, 35695917, 265020, 265021, 33657023, 264692, 33657109, 35695763, 60431528, 18108374, 35696423, 55811576, 264634, 60431850, 83373044, 18108385, 87168518, 22278000, 264563, 264564
2669	95415721 (5337, 5338)	Novel Protein sim. GBank gi 2147012 p JC4899 - proline rich protein - rat			264489, 264689, 21906767, 65274572, 56182575, 21908788, 29148827, 21908769, 29148629, 35696286, 35695917, 22278986, 22278988, 265021, 265022, 60170615, 52644150, 60432049, 264259, 264691, 33657023, 264692, 29331822, 29331824, 29331825, 60432289, 33657109, 29331828, 29331827, 35698052, 29331828, 29146488, 29146489, 264905, 264908, 52644045, 264909, 56182435, 35696423, 65274791, 35695855, 265006, 264910, 264635, 60432228, 264592, 264638, 56182323, 60433356, 60170394, 80433438, 264559, 264595, 55812038, 33109954, 87168558, 60432113, 265019, 264448, 264369, 264684, 264288
2670	87613234 (5339, 5340)	Novel Protein sim. GBank gi 1723523 sp Q10382 YDDB_SCHPO - HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME 1	Contains protein domain (PF00628) - PHD-finger		18108370, 263974
2671	91214836 (5341, 5342)	Novel Protein sim. GBank gi 4768277 gb AAD28444.1 AF06425 - (AF064255) very long-chain acyl-CoA synthetase homolog 2; VLCS-H2 [Homo sapiens]	transport		52646842, 56994075, 264259, 29331822, 29331824, 29331825, 29331827, 33656970, 264509, 265006, 33109954, 21908754, 264682, 264288, 265021, 33657023, 33657109, 33657182, 27486261, 27486262, 27486265, 18108376, 18108385, 264767
2672	87399123 (5343, 5344)	Novel Protein sim. GBank gi 4966346 gb AAD34677.1 AC00634 - (AC006341) Contains two PF101344 Kelch motif domains. [Arabidopsis thaliana]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	

2673	87430749 (5345, 5346)	Novel Protein sim. GBank gll5457337[emb]CAB41505.2] - (AJ238876) poly(ADP-ribose) polymerase-2 [Homo sapiens]	Contains protein domain (PF00844) - polymerase Poly(ADP-ribose) polymerase catalytic region.	22278995, 22278996, 22278997, 22278998, 29331822, 29331824, 29331828, 35696052, 60433438, 87168474, 87168559, 265017, 265018, 265019, 264448, 21906768, 21906789, 265020, 265021, 33657109, 27486262, 35695763, 60431850, 60170394, 87168518, 264563
2674	94847721 (5347, 5348)	Novel Protein sim. GBank gll4758824[ref]NP_004280.1pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	264488, 22278996, 35696286, 264091, 264259, 29331824, 29331826, 35696052, 264511, 55812038, 8569542, 264766, 21906765, 35695917, 264629, 35696423, 18108383, 87168518
2675	79563835 (5349, 5350)		UNCLASSIFIED	264691
2676	79628393 (5351, 5352)		UNCLASSIFIED	264906, 265008
2677	94328800 (5353, 5354)	Novel Protein sim. GBank gll1079042[pir]S52154 - acetyl-CoA synthetase - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00501) - synthase AMP-binding enzyme	18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 264490, 264259, 52845080, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 29146499, 29331830, 264908, 52844045, 265008, 265007, 265008, 265009, 60432229, 60433356, 60433438, 55812038, 265010, 265011, 87168559, 265017, 265019, 18108351, 264682, 264448, 264683, 264288, 21906765, 21906766, 21906767, 21908789, 21906769, 55811957, 265020, 265021, 60170615, 52644150, 264691, 33657023, 263967, 33657108, 27486264, 27486265, 33657349, 35695763, 18108370, 18108374, 18108377, 55811578, 35696423, 35695855, 83373044, 18108387, 22279000, 22279002, 264584



2678	95001694 (5355, 5356)	Novel Protein sim. GBank gi 88760 pir I40465 - alanine transaminase (EC 2.6.1.2), cytosolic - human		UNCLASSIFIED	264488, 263984, 264489, 18108394, 52846842, 35696286, 22278999, 264259, 29331825, 35698052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 264593, 264594, 264596, 264758, 33109954, 52646317, 21906754, 265010, 265011, 87188559, 264600, 264601, 264602, 264603, 265017, 265019, 264605, 264760, 264762, 18108351, 264763, 264682, 264683, 264764, 264288, 264766, 264687, 264768, 264769, 264689, 21906765, 21906767, 35695917, 265020, 265021, 52644150, 264691, 33657023, 264693, 18108384, 18108385, 33657109, 33657349, 264628, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264565, 264566, 264486, 264567
2679	95361544 (5357, 5358)	Novel Protein sim. GBank gi 1709233 sp P07514 NC5R_BOVIN - NADH-CYTOCHROME B5 REDUCTASE	Contains protein domain (PF00970) - FAD/NAD-binding Cytochrome reductase	reductase	264488, 22278995, 35696286, 264259, 29331826, 29331827, 29331828, 264809, 56182435, 264113, 264511, 265008, 60433438, 264758, 85658542, 87168474, 265011, 265017, 265019, 264288, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 264690, 33657023, 55810764, 35696423, 55811576, 264631, 18108381, 60170394, 83373044, 87168518, 264566, 264759, 264102, 264905, 264908, 265007, 265008, 33109954, 265011, 18108351, 264768, 33657023, 20281149, 263972, 264630, 264635, 264638
2680	87600356 (5359, 5360)	Novel Protein sim. GBank gi 4589604 db BAA76824.1  - (AB023187) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	264488, 22278995, 264509, 264805, 264806, 264907, 264908, 264909, 264510, 265008, 264512, 264910, 264594, 60433438, 264758, 264803, 264604, 265019, 264605, 264760, 264764, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264638, 264639, 264638
2681	90933844 (5361, 5362)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00036) - EF hand	kinase	264488, 22278995, 264509, 264805, 264806, 264907, 264908, 264909, 264510, 265008, 264512, 264910, 264594, 60433438, 264758, 264803, 264604, 265019, 264605, 264760, 264764, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264638
2682	84138934 (5363, 5364)	Novel Protein sim. GBank gi 423468 pir JQ1874 - HITF8-C protein - mouse	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264488, 22278995, 264509, 264805, 264806, 264907, 264908, 264909, 264510, 265008, 264512, 264910, 264594, 60433438, 264758, 264803, 264604, 265019, 264605, 264760, 264764, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264638
2683	87774405 (5365, 5366)	Novel Protein sim. GBank gi 5114351 gb AAD40286.1  - (AF156271) RING finger protein terf [Homo sapiens]	Contains protein domain (PF00822) - SPRY domain	interleukinrecept	264488, 22278995, 264509, 264805, 264806, 264907, 264908, 264909, 264510, 265008, 264512, 264910, 264594, 60433438, 264758, 264803, 264604, 265019, 264605, 264760, 264764, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264638

2684	85707151 (5367, 5368)	Novel Protein sim. GBank gl 4886469 emb CAB43385.1  - (AL050284) hypothetical protein [Homo sapiens]			264593
2685	88054288 (5369, 5370)	Novel Protein sim. GBank gl 3342729 (AC005331) - R31341_2 [Homo sapiens]	UNCLASSIFIED		
2686	87628690 (5371, 5372)	Novel Protein sim. GBank gl 4650844 db BAA77027.1  - (AB026190) Kelch motif containing protein [Homo sapiens]	struct	Contains protein domain (PF01344) - Kelch motif	264259, 29331822, 60432289, 29331827, 29331830, 284909, 264512, 264596, 284769, 284534, 284555, 284556, 264557, 264558, 60170394, 264559, 264486
2687	87998183 (5373, 5374)	Novel Protein sim. GBank gl 5281314 gb AAD41475.1 AF133123 - (AF133123) transcription factor IIC102 [Homo sapiens]	transcriptfactor	Contains protein domain (PF00515) - TPR Domain	18108394, 18108396, 22278996, 35696286, 22278997, 28331826, 29331828, 68712502, 21908754, 265011, 264760, 264761, 264763, 264688, 21908765, 35696423, 284559, 18108385, 264563
2688	79959584 (5375, 5376)				264908, 264780
2689	94122440 (5377, 5378)	Novel Protein sim. GBank gl 3880023 emb CAA97339  - (Z73098) Similarity to yeast hypothetical protein (Swiss Prot accession number Q06985); cDNA EST EMBL:D72982 comes from this gene; cDNA EST EMBL:D75947 comes from this gene [Caenorhabditis elegans]		Contains protein domain (PF00560) - Leucine Rich Repeat	22278997, 22278998, 22278999, 29331824, 35696052, 264908, 264908, 56182435, 264512, 264910, 265009, 60433438, 21908754, 18108351, 284682, 264683, 264767, 21906765, 21906766, 21906768, 33657023, 33657182, 27468262, 27486264, 33657349, 18108370, 18108372, 18108374, 35696423, 35695855, 18108385, 22279002
2690	88003055 (5379, 5380)	Novel Protein sim. GBank gl 2477513 (AC002398) - F25965_3 [Homo sapiens]	struct	Contains protein domain (PF00620) - RhoGAP domain	
2691	91219241 (5381, 5382)	Novel Protein sim. GBank gl 4107276 emb CAA67130  - (X98506) acetyl-CoA synthetase [Solanum tuberosum]	synthase		65274572, 56182575, 264259, 29331822, 29331824, 29331826, 29331828, 264112, 265009, 55812038, 264596, 33109954, 265017, 264448, 264288, 264369, 264684, 21906769, 60170615, 60431528, 55810764, 264634, 264636, 264556, 264637, 22279002, 264584, 264566
2692	94111914 (5383, 5384)	Novel Protein sim. GBank gl 3513303 (AC005594) - R26984_1 [Homo sapiens]	peptidase	Contains protein domain (PF00326) - Prolyl oligopeptidase family	
2693	20438807 (5385, 5386)		UNCLASSIFIED		264592
2694	94111918 (5387, 5388)	Novel Protein sim. GBank gl 3122400 sp Q35682 MUG_MOUSE - MYELOID UPREGULATED PROTEIN			264559
2695	95345513 (5389, 5390)	Novel Protein sim. GBank gl 4972740 gb AAD34765.1  - (AF132177) unknown [Drosophila melanogaster]	collagen		35686286, 56894075, 22278999, 264259, 35686052, 29331830, 265011, 264288, 56181562, 284690, 264692, 33857023, 27486282, 263976, 18108376, 35696423, 35695855, 60170394, 63373044, 56526486, 22279000, 22279002, 264566
2696	87874040 (5381, 5392)	Novel Protein sim. GBank gl 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	synthase		264594, 21906768, 18108370, 18108372

2697	91638472 (5393, 5394)	Novel Protein sim. GBank gji5689473[dbj]BAA83020.1] - (AB028991) KIAA1088 protein [Homo sapiens]		UNCLASSIFIED	35696286, 284259, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 265006, 265007, 264512, 265009, 60170831, 60433356, 264595, 264758, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 264761, 18108351, 264448, 264288, 264766, 264688, 264689, 21906765, 21906768, 265020, 265021, 60170815, 33657109, 18108376, 35696423, 35695855, 264555, 264558, 60170394, 264559, 18108387, 56526486, 87168518, 22279002, 264593, 264482
2698	94325891 (5395, 5396)	Novel Protein sim. GBank gji841318 (U22816) - mutant sterol regulatory element binding protein-2 [Cricetulus griseus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcript factor	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 33656970, 264906, 29331830, 264909, 52644045, 264910, 60433356, 33657402, 33109854, 265017, 265018, 265019, 264288, 21906765, 21906766, 21906767, 21906769, 29148829, 35695917, 265021, 265022, 52644150, 33657023, 33657182, 27486261, 35696423, 65274781, 264638, 60432113, 22279000
2699	87780650 (5397, 5398)			UNCLASSIFIED	264788, 18108357, 264690, 264691
2700	94139836 (5399, 5400)	Novel Protein sim. GBank gji5174395[ref]NP_006006.1[pB120 - Brain protein 120]		UNCLASSIFIED	60424269, 56182435, 60432229, 60433438, 55811386, 265017, 55811150, 264448, 56181582, 55811957, 264693, 33657109, 60431528, 264629, 55810764, 55811576, 65274791, 60431850, 60432113
2701	94148584 (5401, 5402)	Novel Protein sim. GBank gji1572801 (U70854) - F38A5.1 gene product [Caenorhabditis elegans]			18108394, 52645156, 35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29146499, 265006, 60433356, 33657402, 60433438, 264595, 33657084, 18108351, 264288, 264769, 18108359, 21906768, 35695917, 33657023, 27486261, 18108374, 18108379, 35696423, 18108382, 83373044, 18108384, 18108388, 60432113, 22279000
2702	57285366 (5403, 5404)	Novel Protein sim. GBank gji2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	29331828, 264512, 264555, 264556, 264557, 264558, 264559
2703	87649514 (5405, 5406)	Novel Protein sim. GBank gji5689399[dbj]BAA82883.1] - (AB028954) KIAA1031 protein [Homo sapiens]	Contains protein domain (PF00642) - Zinc finger C-x8-C-x5-C-x3-H type (and similar)		60432289, 265007, 21906765, 21906768, 265021, 264563

2704	87649515 (5407, 5408)	Novel Protein sim. GBank gij4335694[gijAAB63294] - (AF008554) Implantation-associated protein [Rattus norvegicus]			264488, 22278995, 22278998, 29331828, 29148499, 264905, 264906, 264907, 52644045, 264511, 33657402, 264600, 264602, 265017, 264605, 264761, 18108351, 264784, 264687, 264769, 265021, 264691, 264692, 18108362, 264693, 18108370, 18108374, 264634, 264635
2705	87771745 (5408, 5410)				264489, 264509, 264511, 264512, 264910, 264593, 87168474, 264604, 264288, 264687, 264769, 264838, 264566, 264486
2706	94326789 (5411, 5412)	Novel Protein sim. GBank gij3255952[emb]CAA16821.1] - (AL021728) /prediction=(method:; /match=(desc: [Drosophila melanogaster])	UNCLASSIFIED		264488, 52646842, 65274572, 22278994, 56994075, 22278997, 264259, 29331824, 29331825, 29331828, 29331828, 33658970, 264907, 264908, 264909, 52644045, 56182435, 265006, 265007, 60433438, 55812038, 21908754, 52644296, 265010, 264601, 265017, 265018, 264681, 264448, 264682, 264288, 264686, 264687, 264688, 21906786, 21906789, 55811957, 35695917, 265020, 265021, 60170815, 264690, 264691, 33557023, 264692, 264693, 65274620, 27486284, 263972, 18108374, 18108377, 264635, 264636, 264556, 60170394, 83373044, 65274727, 97169518, 22279000, 22278996, 22278998, 56182435, 21908754, 87168559, 265017, 264448, 52645129
2707	88089839 (5413, 5414)	Novel Protein sim. GBank gij3417294 (AC004381) - Unknown gene product [Homo sapiens]			65274572, 264259, 29331822, 29331825, 60432289, 29331825, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433438, 33109954, 265010, 265011, 264389, 264288, 264765, 264693, 264565
2708	91011351 (5415, 5416)	Novel Protein sim. GBank gij545790[bbs]147178 - DARPP-32=dopamine and cAMP-regulated phosphoprotein [human, brain, Peptide, 204 aa]	UNCLASSIFIED		29331822, 18108370, 18108374, 83373044
2709	94853988 (5417, 5418)	Novel Protein sim. GBank gij3169705 (AC004780) - F17127.1 [Homo sapiens]	UNCLASSIFIED		29331824, 264759, 264693, 18108362, 18108388
2710	87627979 (5419, 5420)	Novel Protein sim. GBank gij4468311[emb]CA637992] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			

2711	94111820 (5421, 5422)	Novel Protein sim. GBank gi 3122400 epiO35882 MUG_MOUSE - MYELOID UPREGULATED PROTEIN		UNCLASSIFIED	264488, 264687, 52645156, 264768, 21908764, 21908765, 21908767, 21908768, 21908769, 55811957, 56994075, 22278997, 22278998, 265020, 265021, 284690, 284259, 284691, 264692, 33657023, 29331822, 29331824, 60424269, 29331826, 33657182, 29331827, 27486262, 33857349, 264508, 284905, 284907, 60431528, 284908, 284909, 55810764, 35696423, 65274791, 35695855, 265007, 264910, 60431850, 60432229, 284557, 264558, 55812038, 33108954, 18108385, 21908754, 33657084, 87168518, 87168474, 87168559, 60432113, 265017, 22279000, 265018, 265019, 22279002, 284760, 55811150, 284681, 18108351, 264565, 284764, 264566, 264288, 264768 264488, 35696286, 22278998, 264259, 29331824, 60432289, 35696052, 264508, 284908, 66712502, 52644045, 265006, 60432229, 33857402, 60433358, 265010, 265019, 18108351, 264681, 264288, 264685, 21908765, 21908766, 21908768, 21908769, 55811857, 35695917, 265020, 265021, 60170815, 264691, 264692, 33657023, 33657109, 33657182, 33657349, 18108370, 18108374, 35696423, 35695855, 264555, 52644332, 56182323, 87168518, 60432113 66714117, 264906, 264563
2712	94312071 (5423, 5424)	Novel Protein sim. GBank gi 5081315 gb AAD39343.1 AF07660 - (AF076607) prediabetic NOD sera-reactive autoantigen [Mus musculus]	Contains protein domain (PF00515) - TPR Domain	transferrase	
2713	88003064 (5425, 5426)	Novel Protein sim. GBank F25965_3 [Homo sapiens]		UNCLASSIFIED	
2714	13528218 (5427, 5428)			UNCLASSIFIED	264636
2715	94122454 (5428, 5430)	Novel Protein sim. GBank gi 4321968 gb AAD15897  - (AF067430) Smarce1-related protein [Mus musculus]		UNCLASSIFIED	264508, 264905, 264907, 264908, 264909, 264910, 264758, 265011, 264760, 264764, 264288, 264766, 264768, 264636
2716	88003068 (5431, 5432)	Novel Protein sim. GBank gi 2477513 (AC002398) - F25965_3 [Homo sapiens]		glycoprotein	264091, 264259, 29331822, 66714117, 284908, 264369, 264693, 264556, 264563 264593, 264558
2717	80077461 (5433, 5434)	Novel Protein sim. GBank gi 3327046 db BAA31591  - (AB014516) KIAA0816 protein [Homo sapiens]			
2718	79604062 (5435, 5436)				264693
2719	88180423 (5437, 5438)	Novel Protein sim. GBank gi 746495 (U23515) - weakly similar to gastrula zinc finger protein [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 87168559, 265019, 265021, 52644150, 264691

2720	95086242 (5439, 5440)	Novel Protein sim. GBank gij1335873 (U46680) - ATP-dependent RNA helicase [Mus musculus]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	18108374, 60424179, 264489, 56182435, 21906765, 21906766, 35696423, 22278997, 265020, 265022, 265006, 265008, 264092, 264636, 60432229, 264691, 264692, 33657023, 264693, 33657402, 83373044, 29331824, 18108368, 60424269, 29331826, 18108385, 52645129, 21906754, 35696052, 29331828, 87168474, 264100, 265010, 265011, 265019, 22279002, 264905, 264482, 264563, 264906, 18108351, 264681, 18108370, 29331830, 264908, 66712502, 52644045, 264909, 264828, 18108354
2721	95345523 (5441, 5442)	Novel Protein sim. GBank gij4929663 [gb AAD34092.1 AF15185 - (AF151855) CGI-97 protein [Homo sapiens]	Contains protein domain (PF01172) - Uncharacterized protein family UPF0023	22278995, 35696286, 264259, 29331822, 29331824, 66714117, 29331826, 264908, 60433438, 265017, 18108351, 264448, 264288, 264789, 21906766, 265021, 33657109, 263969, 60431528, 264629, 55811576, 55274791, 35695855, 264631, 264637, 60170394, 56182323, 22279000
2722	91638807 (5443, 5444)	Novel Protein sim. GBank gij3212997 [gb AAC23434.1  - (AC004997) match to ESTs AA687998 (NID:g2626700), AA185465 (NID:g1741481), Z45871 (NID:g575105), and T84026 (NID:g712314); similar to various tre-like proteins including: AF040654 (P/D:g2746883), D13644 (P/D:g2104571), AL02114...	Contains protein domain (PF00566) - oncogene TBC domain	35696286, 22278999, 21906754, 265017, 264782, 264288, 21906765, 21906787, 21906788, 35695917, 18108382, 27466262, 35695855, 264558, 264559
2723	87387732 (5445, 5446)		UNCLASSIFIED	264508, 264509, 264906, 264909, 264910, 55812038, 264788, 264687, 264629, 264638, 264488
2724	87639563 (5447, 5448)	Novel Protein sim. GBank gij4680681 [gb AAD27730.1 AF13285 - (AF132855) CGI-21 protein [Homo sapiens]	ubiquitin	18108398, 22278999, 20281099, 29331824, 29331826, 60432289, 29331828, 60170831, 60432229, 60433438, 18108351, 264682, 21906766, 21906787, 21906769, 35695917, 33657023, 33657109, 18108372, 18108374, 35695855, 22279000, 22279002
2725	94853991 (5449, 5450)	Novel Protein sim. GBank gij3169705 (AC004780) - F17127_1 [Homo sapiens]	UNCLASSIFIED	264488, 52644507, 264259, 29331827, 21906754, 265011, 18108351, 264448, 264288, 264685, 264689, 35695917, 265020, 33657182, 27466261, 18108370, 18108374, 35696423, 18108385, 22279000
2726	86880589 (5451, 5452)	Novel Protein sim. GBank gij3342738 (AC005320) - R26860_1, partial CDS [Homo sapiens]	MHC	264488, 264828, 264685

2727	B1010470 (5453, 5454)	Novel Protein sim. GBank gi 731287 sp P39218 RLUA_ECOLI - RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)	Contains protein domain (PF00849) - RNA pseudouridylylate synthase	- synthase	65274572, 56182575, 22278994, 56994075, 22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 33856970, 284509, 66712502, 264910, 33657402, 60433438, 284758, 55812038, 21908754, 33657084, 55811388, 265018, 265019, 284767, 21908765, 21906767, 21906769, 55811957, 35695917, 52644150, 33657023, 33657108, 33657182, 27486281, 27486282, 27486285, 33657349, 55811576, 35696423, 35695955, 284630, 60431850, 284636, 56182323, 87168518, 60432113, 22279000, 284564, 284565
2728	94126022 (5455, 5456)	Novel Protein sim. GBank gi 3880433 emb CAA91399  (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	18108394, 56182435, 21906767, 55811957, 35695955, 265021, 264690, 284556, 264259, 264557, 29331822, 264559, 264448, 264288
2729	94126024 (5457, 5458)	Novel Protein sim. GBank gi 2408085 emb CAB16300  (Z99168) putative RNA splicing protein [Schizosaccharomyces pombe]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	65274572, 284259, 60432288, 56712502, 56182435, 284448, 264288, 264369, 55811957, 285021, 264557, 60432113
2730	94126026 (5459, 5460)	Novel Protein sim. GBank gi 3880433 emb CAA91399  (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	- transport	264887, 29331824, 29331826, 35696052, 264107, 56182435, 265008, 265009, 284592, 60431735, 285011, 264601, 265017, 18108351, 284288, 29148627, 55811957, 265021, 264690, 18108368, 18108374, 264557, 264558, 284559, 18108387, 56526486, 264566, 264486
2731	87723022 (5461, 5462)	Novel Protein sim. GBank gi 1723239 sp Q10166 YAUB_SCHPO - HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME 1	Contains protein domain (PF00795) - Carbon-nitrogen hydrolase		264259, 35696052, 265006, 264758, 284762, 264448, 284288, 29148627, 21908769, 87168518, 22279002
2732	94126028 (5463, 5464)	Novel Protein sim. GBank gi 3880433 emb CAA91399  (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	264887, 284489, 18108358, 56182435, 264689, 35696423, 55811957, 265021, 265006, 265008, 264910, 265009, 264690, 264555, 264259, 264556, 264557, 264558, 264559, 18108383, 33657109, 87168518, 265010, 284601, 60432113, 265017, 284905, 284448, 283972, 284389, 264567
2733	87363060 (5465, 5466)	Novel Protein sim. GBank gi 4519621 db BAA75670.1  (AB017614) OASIS protein [Mus musculus]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	29331825, 264509, 264909
2734	94140286 (5467, 5468)			- transcript factor	60424179, 52644507, 56182575, 264259, 29331828, 264907, 264510, 264910, 60433356, 265019, 55811150, 284681, 264763, 284687, 33657182, 18108370, 60431528, 60431850, 56182323, 83373044

2735	87712338 (5488, 5470)	Novel Protein sim. GBank gl 3850569 (AC005278) - ESTs gb T21276, gb T45403, and gb AA586113 come from this gene. [Arabidopsis thaliana]		glycoprotein	22278998, 60432289, 28331827, 28146488, 264108, 264909, 264112, 33657402, 87168474, 285017, 264762, 264448, 264764, 264684, 21808765, 264693, 33657109, 263976, 264638, 264638, 264557, 22278000, 22278002, 264567
2736	80247655 (5471, 5472)			UNCLASSIFIED	264905, 264628, 264628, 263978, 264632, 264564
2737	87604526 (5473, 5474)				264690
2738	85731808 (5475, 5476)	Novel Protein sim. GBank gl 2558501 db BAA22896] - (D63850) hepatoma-derived growth factor [Mus musculus]			264488, 265008, 264768, 264691
2739	94319834 (5477, 5478)	Novel Protein sim. GBank gl 5420387 emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264684, 83373044, 264568
2740	94148762 (5479, 5480)	Novel Protein sim. GBank gl 3417366 emb CAA75495] - (Y15197) microtubule-associated protein, MAP-115 [Mus musculus]		UNCLASSIFIED	264488, 56182575, 22278995, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 29146488, 29331830, 265006, 265007, 285008, 60432229, 33657402, 55812038, 87168474, 285010, 265011, 265017, 265018, 265019, 264605, 264681, 264288, 264369, 52844229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 264691, 264692, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 60431850, 264639, 56182323, 18108382, 18108385, 65274727, 22279002, 264584
2741	88047518 (5481, 5482)	Novel Protein sim. GBank gl 3242764 (AC005154) - similar to protein U28928 (PID:g861308) [Homo sapiens]		UNCLASSIFIED	22278998, 52644045, 52644229, 21906768, 21906769, 265020, 60170615, 264691
2742	87848644 (5483, 5484)	Novel Protein sim. GBank gl 4758412 ref NP_004472.1 pGALN - UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 2 (GAINAC-T2)	Contains protein domain (PF00852) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	264259, 264805, 264758, 55812038, 264369, 29148827
2743	87627991 (5485, 5486)	Novel Protein sim. GBank gl 4468311 emb CAB37992] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 264906, 264908, 265008, 60433438, 265017, 18108351, 264448, 264764, 264288, 21906765, 21906767, 264680, 264691, 264693, 263969, 263971, 35695855, 264637, 264558, 18108382, 60432113
2744	94126030 (5487, 5488)	Novel Protein sim. GBank gl 3880433 emb CAA91399] - (Z68521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL-C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	kinase	18108374, 264488, 56182435, 21906765, 35698423, 35695917, 35695855, 265020, 265021, 264511, 265009, 264490, 264556, 264259, 264557, 56182323, 264558, 264559, 18108383, 29331824, 18108385, 33657109, 29331826, 21906754, 29331827, 29331828, 33657349, 87168518, 265018, 264905, 264482, 264448, 264486, 264369, 264288



2745	87740125 (5489, 5490)	Novel Protein sim. GBank gij4403795jgb/AAD19826] - (AF038963) RNA helicase [Homo sapiens]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	35696286, 264509, 264905, 264907, 264908, 264909, 264510, 264512, 265008, 264759, 264801, 265017, 264604, 264763, 264288, 264886, 264769, 264693, 35696423, 35695855, 264634, 264636, 264563, 264564, 264565
2746	95418601 (5491, 5492)	Novel Protein sim. GBank gij4758738jref[NP_004680.1]pMTA1 - metastasis associated 1	Contains protein domain (PF00320) - GATA zinc finger	UNCLASSIFIED	22278998, 22278998, 22278999, 29331822, 29331828, 29331827, 35696052, 29331828, 264905, 264908, 264907, 264908, 264909, 52644045, 265006, 60170831, 264598, 55812038, 265018, 264683, 264288, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 33657023, 264693, 33657109, 18108368, 18108374, 264558, 18108385, 22279000, 264563
2747	94112677 (5493, 5494)	Novel Protein sim. GBank gij4557803jref[NP_000262.1]pNPC1 - Niemann-Pick disease, type C1		glycoprotein	264559, 52644507, 18108394, 22278995, 35696286, 22278997, 22278998, 52645080, 29331824, 56182181, 29331826, 29331827, 35696052, 264907, 264908, 264909, 265009, 33109954, 55811386, 87168474, 265010, 87168559, 264603, 265019, 264760, 264688, 264768, 21908769, 35695917, 60170815, 264692, 33657023, 52645129, 27466284, 60431528, 18108374, 35696423, 35695855, 264556, 58182323, 18108385, 264482
2748	81214983 (5495, 5496)	Novel Protein sim. GBank gij4191272jemb[CAA08984] - (AJ012295) apaG protein [Rhizobium etli]	Contains protein domain (PF00646) - F-box domain.		65274572, 29331828, 264112, 264511, 265019, 264760, 264767, 264768, 264769, 21908768, 21906769, 265020, 27466262, 58526486, 87168518, 22279000
2749	87346307 (5497, 5498)				264259, 264908, 264510, 265008, 265009, 264780, 264369, 264768, 264563
2750	87336344 (5499, 5500)	Novel Protein sim. GBank gij1872498 (U74297) - PIUS [Oryctolagus cuniculus]		UNCLASSIFIED	264488, 52644507, 18108396, 56994075, 264259, 29331825, 29331826, 29331827, 29331828, 264508, 265009, 264910, 264591, 264595, 33657084, 265011, 265019, 18108351, 264288, 264686, 264769, 264689, 55811957, 264693, 27486264, 18108370, 18108374, 264558, 18108385, 264482, 264563
2751	87057465 (5501, 5502)			UNCLASSIFIED	29331822, 29331824, 265017, 33657023
2752	88082675 (5503, 5504)	Novel Protein sim. GBank gij3041859 (AC004534) - OG-2 homeodomain protein-like; similar to U85067 (PID:g1575526) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2753	94138972 (5505, 5508)	Novel Protein sim. GBank glj3851648 (AF098301) - neural F-box protein NFB42 [Rattus norvegicus]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	56182575, 56894075, 22278988, 29331822, 29331824, 29331825, 29331826, 285007, 284593, 55812038, 33109954, 18108351, 284288, 56181562, 21906767, 21906768, 285021, 284693, 18108374, 65274791, 284632, 56182323, 22278002, 284583, 284587
2754	94115513 (5507, 5508)	Novel Protein sim. GBank glj535428 (U13736) - calmodulin-like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	struct	22278989, 66714117, 29331827, 35696052, 29331828, 284906, 284908, 284909, 285011, 285017, 285018, 285019, 284288, 21906765, 21906767, 285022, 33657023, 284693, 56182323, 18108382, 22278000
2755	86001472 (5508, 5510)	Novel Protein sim. GBank glj2986653 (AC004510) - R30385_2 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	
2756	11465908 (5511, 5512)	Novel Protein sim. GBank glj1173539 (U30473) - putative src-like adapter protein; non-catalytic src-like adapter protein containing SH3 and SH2 domains; homolog of mouse SLAP; Method: conceptual translation supplied by author [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	264594
2757	95381590 (5513, 5514)	Novel Protein sim. GBank glj3608372 (AF053768) - brain specific cortactin-binding protein CBP90 [Rattus norvegicus]		eph	85658542, 284693
2758	79637846 (5515, 5516)	Novel Protein sim. GBank glj2072200 (U94863) - p40 [Borna disease virus]		struct	284693
2759	91005312 (5517, 5518)	Novel Protein sim. GBank glj4914573 (emb) (CAB43685.1) - (AL050390) hypothetical protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	55274572, 35696286, 66714117, 29331828, 284508, 56182435, 21906754, 55811957, 264629, 264636, 56182323, 22279002
2760	79824798 (5519, 5520)	Novel Protein sim. GBank glj3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00989) - PAS domain	nuclease	264908
2761	87639597 (5521, 5522)	Novel Protein sim. GBank glj2905643 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF01352) - KRAB box	struct	22278998, 29331822, 29331830, 265010, 265019, 264288, 21906765, 21906768, 21906769, 265020, 56182323, 22279002, 264563
2762	87592699 (5523, 5524)	Novel Protein sim. GBank glj3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00989) - PAS domain	struct	18108394, 22278998, 284906, 284909, 265006, 265007, 284757, 285010, 285011, 285017, 285019, 18108351, 284448, 284683, 284686, 284768, 285020, 265021, 265022, 284691, 18108362, 284693, 18108385, 33657109, 18108368, 18108370, 18108381, 18108382, 18108384, 18108388, 87168518
2763	87539988 (5525, 5526)	Novel Protein sim. GBank glj3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264369, 35696423
2764	94305140 (5527, 5528)	Novel Protein sim. GBank glj2905643 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases		52648842, 284259, 29331822, 29331825, 29331826, 29331828, 33656970, 284905, 284907, 29331830, 265006, 265009, 21906754, 285019, 284448, 21906769, 27486282, 56182323, 56526466, 87168518, 264487

2765	94315105 (5528, 5530)	Novel Protein sim. GBank gl 468672 emb CAA17888.2  - (AL022018) /prediction=(method:; /prediction=(method:; /match=(desc: [Drosophila melanogaster])			264488, 65274572, 22278995, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264508, 264905, 264908, 264907, 264908, 264909, 264512, 264910, 265009, 264592, 264595, 264758, 55812038, 33109854, 265010, 87168559, 264600, 265018, 264760, 264761, 264762, 264763, 264448, 264764, 264288, 264766, 264767, 264788, 56181562, 21908764, 21908765, 21908768, 35695917, 265021, 264691, 264692, 33857023, 33657109, 264628, 18108370, 264829, 18108374, 55811576, 356958423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 264558, 264639, 83373044, 87168516, 22278900, 22279002, 264563, 264482
2766	94315109 (5531, 5532)	Novel Protein sim. GBank gl 544161 emb CAB46854.1  - (AJ388555) hypothetical protein [Canis familiaris]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_mta_bind	264488, 65274572, 60432289, 264907, 264909, 264511, 264512, 60433356, 264288, 264885, 264889, 35695917, 265022, 264693, 264628, 65274791, 264635, 264555, 264558, 264557, 264638, 264558, 264559, 83373044, 60432113
2767	80204297 (5533, 5534)	Novel Protein sim. GBank gl 1079451 pir AJ55463 - tropomodulin, skeletal muscle - chicken		struct	264112, 263974, 264558
2768	94322238 (5535, 5536)	Novel Protein sim. GBank gl 541322 emb CAB46721.1  - (AL031427) dJ167A19.1 (novel protein) [Homo sapiens]		UNCLASSIFIED	264488, 263994, 264489, 35696286, 22278998, 22278999, 264259, 29331822, 60432289, 29331826, 35696052, 264508, 264509, 264905, 264908, 264907, 29331830, 264908, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264757, 264596, 265011, 264604, 265019, 264760, 264681, 18108351, 264764, 264288, 264766, 264686, 264768, 18108357, 264769, 264689, 21908768, 21908769, 35695917, 265021, 265022, 33657023, 33657109, 264628, 264629, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 264639, 83373044, 264563, 264564, 264565, 264566, 264486, 264587

2769	95311088 (5537, 5538)	Novel Protein sim. GBank gij5419859jemb[CAB46375.1] - (AL086725) hypothetical protein [Homo sapiens]		tubulin	264488, 56182575, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331828, 264908, 29331830, 56182435, 264592, 33657402, 264448, 264369, 264288, 60170615, 264691, 33657023, 264682, 33657109, 18108374, 55811576, 264634, 264636, 56182323, 83373044, 60432113, 18108398, 22278995, 22278996, 22278999, 264105, 265006, 265019, 18108351, 264687, 21908765, 18108364, 264629, 18108374, 264631, 18108385, 18108388
2770	87730182 (5538, 5540)	Novel Protein sim. GBank gij5701985jemb[CAB52157.1] - (AL109736) WD repeat protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264631, 18108385, 18108388
2771	98084071 (5541, 5542)	Novel Protein sim. GBank gij3093433 (AC004125) - [Unknown gene product [Homo sapiens]]		UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 264369
2772	95357308 (5543, 5544)	Novel Protein sim. GBank gij488553jref[NP_005465.1]pNY C - histone deacetylase 5	Contains protein domain (PF00850) - Histone deacetylase family	histone	264259, 29331822, 29331824, 66714117, 60432289, 29331827, 264905, 265009, 264592, 55812038, 65274444, 264766, 21908769, 33657109, 263976, 264555, 264636, 264557, 83373044, 264563, 264564, 264486
2773	94138994 (5545, 5546)	Novel Protein sim. GBank gij3288888 (AC005253) - R26445_1 [Homo sapiens]		UNCLASSIFIED	18108374, 264686, 264687, 263976, 56182435, 264689, 55810764, 21908766, 35696423, 55811576, 65274791, 56181686, 55811957, 35695855, 264110, 265021, 264112, 265022, 265006, 265008, 264092, 264094, 60431850, 264637, 264691, 264259, 264692, 263981, 264594, 60433356, 56182323, 264693, 264757, 56182181, 55812038, 29331825, 60424289, 18108385, 29331826, 29331827, 27486261, 29331828, 35696052, 55811386, 264107, 60432113, 265017, 55811150, 18108351, 264681, 264906, 18108370, 264484, 264682, 20281069, 264448, 66712502, 264683, 264764, 264288, 264684, 264769, 263974
2774	87819808 (5547, 5548)	Novel Protein sim. GBank gij46862jplp34388jYLS3_CAEEL - HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III	Contains protein domain (PF00380) - Ribosomal protein S9/S16	ribosomalprot	22278995, 35696286, 22278996, 22278999, 264259, 29331826, 60432289, 35696052, 264112, 33657402, 21908754, 87168559, 265017, 265018, 264288, 21908766, 21908767, 21908769, 35695917, 265020, 265021, 33657023, 33657109, 18108370, 263976, 35696423, 35695855, 87168518, 22278999, 264482

2775	95307887 (5549, 5550)	Novel Protein sim. GBank gil4689132[gb]AAD27775.1[AF07704] 30S ribosomal protein S7 homolog [Homo sapiens]	Contains protein domain (PF00177) - Ribosomal protein S7p/5Ss	- ribosomal prot	264488, 22278985, 56994075, 22278986, 3598286, 22278986, 22278989, 264258, 29331822, 29331824, 29331825, 60432289, 29331827, 29331828, 35986052, 285007, 21906754, 265017, 265019, 284448, 264882, 264389, 264288, 18108354, 52844229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35985917, 265021, 265022, 60170815, 264691, 18108370, 35986423, 65274791, 35985855, 264634, 60431850, 60170394, 56182323, 264558, 18108388, 22279000, 264563, 264565, 264486, 264567
2776	87791557 (5551, 5552)				56182575, 22278988, 22278999, 264259, 29331822, 29331824, 264908, 29331830, 264510, 33657402, 21906754, 55811388, 265017, 265018, 264448, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170815, 55810764, 55811576, 264555, 56526486, 22279000
2777	79818729 (5553, 5554)			UNCLASSIFIED	264807, 264786
2778	82112411 (5555, 5556)			UNCLASSIFIED	264807, 264593, 264760, 264628
2779	87649729 (5557, 5558)	Novel Protein sim. GBank gil4680711[gb]AAD27745.1[AF13297] CGI-36 protein [Homo sapiens]		UNCLASSIFIED	22278997, 264259, 29331824, 66714117, 35686052, 265006, 264512, 264448, 264288, 29148627, 18108364, 20281149, 18108370, 264629
2780	94678397 (5559, 5560)	Novel Protein sim. GBank gil4758524[ref]NP_004825.1[pHKG] - HPK/GCK-like kinase	Contains protein domain (PF00780) - CNH domain	kinase	29146499, 65274791, 264634, 264639
2781	91220057 (5561, 5562)	Novel Protein sim. GBank gil4469352[gb]AAD21222] - (AF069502) ubiquitin specific protease UBP43 [Mus musculus]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	60424179, 29331824, 60424269, 66714117, 29331826, 56182435, 87168474, 265017, 264764, 56181562, 21906765, 21906766, 21906768, 35985917, 265020, 33657023, 35695855, 56182323, 87168518
2782	94233146 (5563, 5564)	Novel Protein sim. GBank gil4505013[ref]NP_002310.1[pLRN] - leucine-rich neuronal protein	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	65274572, 22278986, 22278988, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331828, 264905, 264907, 264908, 264909, 52844045, 265009, 265017, 265018, 264604, 265019, 264760, 264683, 264288, 264766, 264685, 264688, 264768, 52644229, 264689, 21906768, 265020, 265021, 264691, 18108362, 264692, 33657023, 264693, 33657109, 33657349, 18108370, 264628, 263978, 35695855, 264557, 56182323, 83373044, 18108385

2783	80016820 (5565, 5566)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		Im7	264909, 264628, 263876, 263981
2784	87614360 (5587, 5588)				264259, 29331822, 29331824, 29331825, 264482
2785	88071930 (5569, 5570)	Novel Protein sim. GBank gi 2134933 pr J S58860 - collapsin response mediator protein - human		UNCLASSIFIED	22278999, 264908, 264758, 265018, 264769, 21906765, 21906768, 21906768, 265020, 264564
2786	87408542 (5571, 5572)	Novel Protein sim. GBank gi 2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264905, 265017
2787	87801266 (5573, 5574)	Novel Protein sim. GBank gi 5174507 ref NP_006020.1 pMA1 - paraneoplastic neuronal antigen		UNCLASSIFIED	264768, 21906765, 21906768, 55811957, 22278999, 264093, 60170815, 264259, 29331822, 18108365, 29331824, 33857108, 29331827, 35696052, 264100, 264105, 264908, 263977, 55811576, 264635, 264637, 60433438, 60432113, 265017, 265019, 22279002, 55811150, 264369, 264288
2788	88080644 (5575, 5576)	Novel Protein sim. GBank gi 3252826 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	
2789	85491275 (5577, 5578)	Novel Protein sim. GBank gi 2495729 sp Q92556 Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA8725)		UNCLASSIFIED	264103, 21906769, 264693
2790	87602784 (5579, 5580)	Novel Protein sim. GBank gi 5101772 emb CAB45135.1  - (AJ242878) p621 [Homo sapiens]		struct	264488, 264769, 264910, 264631, 264636, 264690, 264691, 264259, 264638, 29331824, 264508, 264509, 264905, 264563, 264906, 264628, 18108370, 264907, 264764, 264908, 264288, 264909
2791	88083195 (5581, 5582)	Novel Protein sim. GBank gi 2911266 (AC002550) - Unknown gene product [Homo sapiens]			21906764, 18108368
2792	95083783 (5583, 5584)	Novel Protein sim. GBank gi 2854163 gb AAC02581.1  - (AF045642) No definition line found [Caenorhabditis elegans]			22278996, 22278997, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 35696052, 264906, 66712502, 29331830, 264909, 60432228, 60433356, 60433438, 33109954, 265010, 265011, 265017, 265018, 265019, 264682, 264448, 264288, 264369, 264768, 52844229, 21906765, 21906768, 265020, 265021, 33657023, 263974, 18108374, 65274791, 35695855, 264638, 264556, 264558, 56182323, 83373044, 18108385, 56526486, 60432113, 22278000, 264567
2793	87425476 (5585, 5586)			UNCLASSIFIED	264259, 60432289, 66712502, 265009, 264636
2794	85794830 (5587, 5588)			UNCLASSIFIED	264698, 265022, 264691, 18108388, 264667

2795	95334888 (5589, 5590)	Novel Protein sim. GBank gi 5454146 ref NP_008348.1 pUBE2 - ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5)	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	65274572, 56182575, 35696286, 22278998, 22278999, 60432049, 264259, 29331822, 29331825, 68714117, 60432289, 29331826, 29331827, 35698052, 29331828, 264907, 68712502, 56182435, 264511, 265007, 264512, 264910, 60432229, 60433356, 60433438, 33109954, 85658542, 265018, 265019, 264288, 264686, 21906764, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265021, 265022, 52844150, 33657023, 264693, 65274620, 33657109, 35696423, 55811576, 65274791, 56182323, 56526486, 60432113, 22279002, 264482, 264563, 264484, 264567
2796	94848857 (5591, 5592)	Novel Protein sim. GBank gi 4680851 gb AAD27715.1 AF13294 - (AF132940) CGI-06 protein [Homo sapiens]		UNCLASSIFIED	18108394, 65274572, 56182575, 56994075, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 264509, 264908, 264907, 264908, 66712502, 56182435, 264510, 265008, 264512, 265007, 265008, 264910, 265009, 264591, 264592, 60433356, 264594, 264595, 55812038, 264598, 21906794, 60174639, 87168474, 265010, 265011, 265017, 265018, 265019, 55811150, 264762, 18108351, 264448, 264682, 264369, 264288, 264685, 264766, 264687, 56181582, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 264692, 33657023, 18108362, 264693, 65274620, 33657109, 33657182, 27486285, 33657349, 18108374, 35696423, 65274791, 35695855, 264556, 264557, 56182323, 264558, 60170394, 83373044, 65274727, 87168518, 22278000, 264563, 264564, 264565, 264566, 264567
2797	95110780 (5593, 5594)	Novel Protein sim. GBank gi 4838557 gb AAD31040.1  - (AF143859) potassium channel modulatory factor DEBT-91 [Mus musculus]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	56182575, 22278995, 22278996, 22278997, 29331827, 29146499, 264509, 264906, 56182435, 264757, 21908754, 265010, 265017, 265018, 264681, 264682, 264683, 264686, 21906765, 21906767, 21906768, 21906769, 29148629, 265020, 52844150, 264690, 33657182, 264629, 18108376, 56182323, 22279002, 264563
2798	86198005 (5595, 5596)	Novel Protein sim. GBank gi 2852645 (AF007160) - unknown [Homo sapiens]		UNCLASSIFIED	264488, 264490, 264259, 264448, 20281149, 20281152, 264556, 264557, 264558, 264559, 264483, 264486, 264567

2789	68080651 (5597, 5598)	Novel Protein sim. GBank gi 3252825 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	22278996, 22278997, 22278998, 22278999, 60432049, 284258, 29331828, 35698052, 29331828, 264909, 60433356, 33657402, 33109954, 87168474, 264448, 52644228, 21908766, 21908767, 21908768, 35695917, 265020, 265021, 265022, 52644150, 35685855, 264634, 60432113, 22279000, 284488, 56994075, 264259, 20281089, 29331825, 29331827, 264905, 56182435, 265006, 265011, 87168559, 265017, 265019, 264448, 284288, 264766, 264686, 60170815, 264691, 264692, 27486285, 264628, 264629, 264636, 264557, 264558, 264559, 87168518, 264584, 264586, 264567, 265007, 264687
2800	88316481 (5598, 5600)	Novel Protein sim. GBank gi 4240301 dbj BAA74929.1  - (AB020713) KIAA0906 protein [Homo sapiens]		glycoprotein	284488, 56994075, 264259, 20281089, 29331825, 29331827, 264905, 56182435, 265006, 265011, 87168559, 265017, 265019, 264448, 284288, 264766, 264686, 60170815, 264691, 264692, 27486285, 264628, 264629, 264636, 264557, 264558, 264559, 87168518, 264584, 264586, 264567, 265007, 264687
2801	86088814 (5601, 5602)		Contains protein domain (PF00627) - UBA domain		
2802	88082477 (5603, 5604)	Novel Protein sim. GBank gi 2337865 (AC002464) - organic cation transporter; 50% similarity to JC4884 (P1D:g2143892) [Homo sapiens]	Contains protein domain (PF00083) - Sugar (and other) transporter	transport	264448, 35695855
2803	79577446 (5605, 5606)			UNCLASSIFIED	264639
2804	57111131 (5607, 5608)	Novel Protein sim. GBank gi 4559368 gb AAD23029.1 AC006585 - (AC006585) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF01585) - G-patch domain	peptidase	264566
2805	87398486 (5608, 5610)				264092, 264259, 29331822, 29331824, 29331827, 29331828, 264508, 265007, 265009, 21908754, 264369, 264288, 264632, 60170394, 264563, 264482
2806	87898951 (5611, 5612)	Novel Protein sim. GBank gi 1168973 sp P44403 CLPB_HAEIN - CLPB PROTEIN		UNCLASSIFIED	22278995, 22278996, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29146498, 265008, 265009, 60433438, 265017, 265018, 265019, 264448, 264288, 21906765, 21906767, 21906769, 28148629, 265022, 52644150, 56182323



2807	91720702 (5613, 5614)	Novel Protein sim. GBank gi 4466310 emb CAB37891 . (AL031432) dJ465N24.1 (PUTATIVE novel protein similar to predicted yeast and worm proteins) [Homo sapiens]		UNCLASSIFIED	52644507, 52645156, 52646842, 18108398, 56182575, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 52845080, 29331822, 29331824, 29331825, 29331826, 35696052, 29331828, 33656970, 264100, 264105, 264507, 52644045, 60433356, 264594, 60433438, 52646317, 21906754, 33109954, 33657084, 52644296, 87168474, 265011, 87188559, 265017, 265018, 265019, 18108351, 264448, 264763, 264687, 52644229, 21906765, 21906766, 21906767, 21906768, 21906789, 35695917, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 27486265, 35695763, 18108370, 18108372, 18108374, 18108376, 263977, 18108377, 35696423, 35695855, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113
2808	95359111 (5615, 5616)	Novel Protein sim. GBank gi 5541863 emb CAB51071.1 . (AL096857) hypothetical protein [Homo sapiens]		MHC	60432289, 264510, 265010, 265017, 265018, 264881, 264686, 265021, 264690, 22279000, 264566
2809	86083530 (5617, 5618)	Novel Protein sim. GBank gi 2772561 (AC004002) - similar to ciliary dynein beta heavy chain; 78% Similarity to P23098 (PID: g118965) [Homo sapiens]		ATPase_associated	18108351
2810	87259032 (5619, 5620)				
2811	91235845 (5621, 5622)			UNCLASSIFIED	264569, 22278996, 264091, 264259, 29331828, 29146499, 29146629, 29148784, 264693
2812	88093334 (5623, 5624)	Novel Protein sim. GBank gi 3264583 (AC005189) - match to ESTs H97758 (NID: g1118643) and AA085546 (NID: g1628773) [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 66712502, 264693
2813	91216765 (5625, 5626)	Novel Protein sim. GBank gi 4240273 dbj BAA74815.1 . (AB020699) KIAA0892 protein [Homo sapiens]		UNCLASSIFIED	264106
2814	90980906 (5627, 5628)	Novel Protein sim. GBank gi 3548791 (AC005620) - R33590_1 [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	transcriptionfactor	56182575, 29331828, 264906, 66712502, 55811386, 265017, 265018, 265019, 264683, 265020, 87168518, 60432113
2815	79774521 (5629, 5630)			UNCLASSIFIED	55274572
2816	95358228 (5631, 5632)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 . (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264907, 264909
				UNCLASSIFIED	264488, 35696286, 29331825, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264760, 264681, 264766, 264769, 264689, 21906765, 264693, 264628, 18108370, 264629, 264631, 264634, 264563, 264564, 264566, 264488

2817	87749542 (5633, 5634)	Novel Protein sim. GBank gij1283846 (U56966) - coded for by <i>C. elegans</i> cDNA yk30b3.5; coded for by <i>C. elegans</i> cDNA yk30b3.3 [ <i>Caenorhabditis elegans</i> ]			264259, 29331822, 29331827, 264508, 264509, 264905, 264907, 264908, 264909, 264910, 265006, 264511, 264512, 264593, 264758, 265010, 264760, 264781, 264784, 264288, 264687, 264769, 55811957, 35695917, 33657109, 263878, 264634, 264636, 264639, 264564, 264585, 264566, 264488, 264587
2818	88073579 (5635, 5636)	Novel Protein sim. GBank gij549986 (U13149) - possible apospory-associated protein [Pennisetum ciliare]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	66712502
2819	87793527 (5637, 5638)			UNCLASSIFIED	264909, 264511
2820	87765744 (5639, 5640)	Novel Protein sim. GBank gij4929773 [gbjAAD34147.1] (AF152097) CGI-05 protein [Homo sapiens]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	18108394, 52646365, 52644045, 264112, 265009, 21906754, 265017, 18108351, 264683, 264369, 264886, 264769, 21906769, 33657023, 33657109, 18108370, 18108374, 18108377, 18108385
2821	95320511 (5641, 5642)	Novel Protein sim. GBank gij399144 [spIP02747] C1QC, HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR (AB002363) KIAA0365 [Homo sapiens]	Contains protein domain (PF00386) - C1q domain	complement	264636
2822	94260221 (5643, 5644)	Novel Protein sim. GBank gij2224671 [dbjBAA20820] - (AB002363) KIAA0365 [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 60432289, 264905, 60433356, 33657402, 265011, 264760, 21906785, 60170815, 264638
2823	95320513 (5645, 5646)	Novel Protein sim. GBank gij399144 [spIP02747] C1QC, HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264766
2824	95320515 (5647, 5648)	Novel Protein sim. GBank gij399144 [spIP02747] C1QC, HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR		UNCLASSIFIED	264907
2825	19742170 (5649, 5650)				264760
2826	94311805 (5651, 5652)	Novel Protein sim. GBank gij3659683 [embjCAA22020] - (AL033503) conserved hypothetical protein [Candida albicans]			52645156, 22278994, 35696286, 22278997, 22278998, 52645080, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 33656970, 52644045, 52646317, 33657084, 52644296, 265017, 265018, 265019, 264288, 21906764, 21906765, 21906766, 21906767, 21906769, 35695917, 52644150, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 35696423, 35695855, 52644332, 18108385, 87168518, 264484

2827	95320519 (5653, 5654)	Novel Protein sim. GBank gi 399144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	284488, 263994, 284489, 85274572, 29331822, 66714117, 29331827, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 264910, 264591, 60432228, 284592, 284593, 264595, 264596, 21906754, 265011, 264600, 264601, 264602, 265017, 264604, 264605, 264288, 264766, 264767, 264689, 55811957, 264534, 284690, 284691, 284692, 264693, 263972, 264629, 35895855, 264631, 264634, 264635, 264555, 264636, 264637, 264558, 264638, 264558, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264585, 264566, 264567, 264486, 18108391
2828	91228615 (5655, 5656)	Novel Protein sim. GBank gi 3598974 (AF077000) - protein tyrosine phosphatase TD14 [Rattus norvegicus]	Contains protein domain (PF00102) - Protein-tyrosine phosphatase	phosphatase	29331822, 35898052, 264104, 264908, 265007, 264591, 265010, 265011, 265019, 264768, 264686, 55811957, 18108370, 18108374, 55810764, 35896423, 55811576, 56182323, 83373044, 87188518
2829	87651244 (5657, 5658)	Novel Protein sim. GBank gi 4680889 gb AAD27734.1 AF132955 - (AF132955) CGI-25 protein [Homo sapiens]			22278996, 22278997, 264091, 264093, 60432048, 264259, 29331822, 29331825, 29331827, 29331828, 264905, 264509, 66712502, 264510, 264511, 264593, 60433438, 21906754, 265011, 264603, 18108351, 264288, 21906765, 21906768, 21906769, 29148629, 52644150, 264693, 33657109, 18108374, 264634, 18108385, 60432113, 22279000, 264565, 264486 265008, 265019, 264639, 22279002
2830	88087108 (5659, 5660)	Novel Protein sim. GBank gi 2498667 sp Q61200 NPH1_MOUSE - NEUREXOPHILIN 1			
2831	87614717 (5661, 5662)			UNCLASSIFIED	265017
2832	87631809 (5663, 5664)			UNCLASSIFIED	22278997, 22278999, 52646317, 264288, 264688, 21906767, 80431528, 264638, 22279000
2833	87612938 (5665, 5666)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1  - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264555, 264556, 264558
2834	86974703 (5667, 5668)	Novel Protein sim. GBank gi 2224567 dbj BAA20772  - (AB002311) KIAA0313 [Homo sapiens]			263972
2835	87775712 (5669, 5670)	Novel Protein sim. GBank gi 4589532 dbj BAA76788.1  - (AB023161) KIAA0944 protein [Homo sapiens]		ATPase-associated	60432289, 29331828, 265008, 265010, 265017, 264448, 55811957, 265020, 18108370
2836	85724748 (5671, 5672)	Novel Protein sim. GBank gi 2351568 (U76618) - N-RAP [Mus musculus]	Contains protein domain (PF00412) - LM domain containing proteins	transcript factor	264259, 264112, 265010, 264762, 264764, 293974, 264555, 264558, 264559

2837	87766482 (5673, 5674)	Novel Protein sim. GBank gij5420387[emb CAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	18108394, 22278987, 22278988, 29331822, 264907, 264909, 265006, 265007, 265018, 265019, 264682, 264288, 21906766, 21906767, 55811957, 35685917, 18108374, 56182323, 22279000, 22279002
2838	87775392 (5675, 5676)	Novel Protein sim. GBank gij973378 (U31263) - core protein [Hepatitis C virus]	UNCLASSIFIED	18108394, 18108397, 264259, 29331828, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2839	85799317 (5677, 5678)	Novel Protein sim. GBank gij1575515 (U64899) - thrombospondin-related anonymous protein [Plasmodium gallinaceum]	UNCLASSIFIED	264555
2840	87774655 (5678, 5680)	Novel Protein sim. GBank gij1575515 (U64899) - thrombospondin-related anonymous protein [Plasmodium gallinaceum]		264509, 264511, 265011, 264288, 264769, 265020, 264634, 264638, 264556
2841	86982568 (5681, 5682)	Novel Protein sim. GBank gij2224605[dj BAA20790] - (AB002330) KIAA0332 [Homo sapiens]	dna_rna_bind	56182575, 35696052, 264907, 264908, 264909, 264910, 264593, 264595, 264766, 265022, 264691, 33657182, 35695763, 18108370, 35695855, 264631, 264559, 264583, 264587
2842	80080086 (5683, 5684)	Novel Protein sim. GBank gij5578957[emb CAB51350.1] - (AL050305) dJ47587.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]	UNCLASSIFIED	264600
2843	91012494 (5685, 5686)	Novel Protein sim. GBank gij5578957[emb CAB51350.1] - (AL050305) dJ47587.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]		264906, 264907, 264908, 264909, 264910, 264764, 35695855, 83373044, 18108385
2844	58731154 (5687, 5688)	Novel Protein sim. GBank gij585123[sp Q08878 FBLC_MOUSE - FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)]	Contains protein domain (PF00008) - EGF-like domain	264685
2845	94321719 (5689, 5690)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	homeobox	29146498, 87168474, 264686, 35696423, 83373044, 264564
2846	88318613 (5691, 5692)	Novel Protein sim. GBank gij5306263[gb AAD41995.1 AC006233] unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	29331830, 264909, 265008, 265011, 87168559, 264629, 264556
2847	81811757 (5693, 5694)	Novel Protein sim. GBank gij3399676 (AC005390) - R31180.1 [Homo sapiens]	UNCLASSIFIED	264908, 264766, 264769, 264629, 264637, 264566
2848	87612943 (5695, 5696)	Novel Protein sim. GBank gij5262615[emb CAB45747.1] - (AL080156) hypothetical protein [Homo sapiens]	UNCLASSIFIED	264490, 264259, 264508, 264905, 264907, 264510, 265007, 265008, 264591, 264592, 264593, 264594, 264595, 55812038, 265010, 265011, 264604, 264763, 264764, 264765, 264766, 264686, 264628, 264629, 264555, 264638, 264556, 264557, 264638, 264558, 264559, 264563, 264566, 264567
2849	88084283 (5697, 5698)	Novel Protein sim. GBank gij3342218 (AC004131) - Unknown gene product [Homo sapiens]		29331822, 35696052, 264509, 264906, 265007, 264594, 265018, 264288, 263972, 35696423, 18108384, 56526486, 18108390
2850	87623636 (5699, 5700)		UNCLASSIFIED	35696286, 265008, 265009, 265018, 264288, 35695917, 264693, 18108374, 35695855, 22279000

2851	87820548 (5701, 5702)	Novel Protein sim. GBank gij4321619[gb]AAD15788.1] - (AF051088) seven transmembrane domain orphan receptor [Mus musculus]		UNCLASSIFIED	264906, 264907, 56182435, 264758, 55811386, 265010, 18108351, 264448, 264369, 21908785, 264691, 264692, 264693, 35695855, 264556, 18108385, 264567, 264591
2852	86987023 (5703, 5704)	Novel Protein sim. GBank gij1825728 (U88308) - similar to drosophila membrane protein PATCHED SP:P18502 (PID:g129645) [Caenorhabditis elegans]		UNCLASSIFIED	
2853	87784630 (5705, 5706)	Novel Protein sim. GBank gij2702347 (AF027503) - putative membrane-associated guanylate kinase 1 [Mus musculus]	Contains protein domain (PF00397) - kinase WW domain		56182575, 55811150, 264690, 27486282, 27488285, 264632, 56182323, 56528486, 2279002
2854	88083557 (5707, 5708)	Novel Protein sim. GBank gij2795825 (AC004021) - kelch protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to A45773 (PID:g1079086) [Homo sapiens]	Contains protein domain (PF01344) - dna_ma_bind Kelch motif		35696286, 29331824, 29331826, 29331828, 264908, 264768, 264693, 22279002, 264482
2855	94723856 (5709, 5710)	Novel Protein sim. GBank gij1504040[gb]BAA13219] - (D66863) similar to D.melanogaster peroxidase(U11052) [Homo sapiens]	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat		22278994, 29331822, 29331824, 29331825, 264906, 264908, 265009, 33109954, 265018, 265019, 284448, 21906765, 265020, 264690, 27486285, 83373044, 22279000, 22279002, 264482
2856	88093359 (5711, 5712)	Novel Protein sim. GBank gij3284583 (AC005189) - match to ESTs H97758 (NID:g118643) and AA085546 (NID:g1628773) [Homo sapiens]			21906766, 22278997, 265022, 29331822, 29331826, 27486282, 265007, 265009, 285017, 264482, 264563, 18108351
2857	85348288 (5713, 5714)	Novel Protein sim. GBank gij3041855 (AC004537) - similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	Contains protein domain (PF00628) - struct PHD-finger		22278995, 35696286, 29331824, 29331825, 35696052, 264103, 264108, 56182435, 21906765, 21906769, 265020, 18108368, 35695763, 22279002, 264563
2858	8743748 (5715, 5716)	Novel Protein sim. GBank gij462585[sp]P35227[ME18_HUMAN - DNA-BINDING PROTEIN MEL-18 (ZINC FINGER PROTEIN 144)]	Contains protein domain (PF00097) - dna_ma_bind Zinc finger, C3HC4 type (RING finger)		264569, 264887, 22278995, 22278996, 22278997, 22278999, 264259, 29331826, 29331827, 29331828, 264509, 264905, 264906, 29331830, 264908, 52644045, 264909, 264511, 264512, 265007, 265008, 264910, 265009, 264593, 60433356, 264595, 264758, 21908754, 265010, 265011, 264604, 265018, 264760, 18108351, 264763, 264682, 264764, 264765, 264288, 264369, 264685, 264766, 264768, 18108357, 264769, 21908766, 21908767, 265021, 264534, 60170615, 264691, 264692, 18108370, 264629, 18108374, 264631, 264636, 263981, 18108381, 264558, 18108385, 22279002, 264564, 264566, 264488, 264567, 60424179, 65274572, 29331828, 264905, 264511, 264758, 265011, 21908767, 21908769, 55811957, 265021, 56182323
2859	90937675 (5717, 5718)	Novel Protein sim. GBank gij4325320[gb]AAD17331.1] - (AF124427) claudin-15 [Mus musculus]	UNCLASSIFIED		

2860	87532599 (5719, 5720)	Novel Protein sim. GBank gll4469186[emb CAB38414.1] - (AL031588) dJ1163J1.2.1 (novel protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridyate)-Methyltransferases) (isoform 1) [Homo sapiens]	UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264510, 264511, 33109954, 18108351, 264683, 264765, 264389, 264686, 21908765, 264691, 264692, 264683, 18108388, 22278002, 284482
2861	86898507 (5721, 5722)	Novel Protein sim. GBank gll3941730 (AF108083) - BS4 [Homo sapiens]		264369, 264682
2862	87568585 (5723, 5724)	Novel Protein sim. GBank gll4505013[ref NP_002310.1p LRN] - leucine-rich neuronal protein	UNCLASSIFIED	264691, 264638
2863	91220421 (5725, 5726)	Novel Protein sim. GBank gll3249088 (AC004473) - Contains similarity to goliath protein gb M87204 from D. melanogaster. [Arabidopsis thaliana]	struct Contains protein domain (PF00096) - struct Zinc finger, C2H2 type	56994075, 35686286, 22278998, 29331822, 29331824, 35696052, 29331828, 264106, 264511, 55812038, 33657084, 55811386, 265018, 265019, 21906765, 21906766, 21906769, 35685917, 265020, 265022, 33657023, 33657108, 33657349, 264629, 18108376, 60431850, 56182323, 18108385, 18108387, 87168518, 22279002, 284259, 264910
2864	87420030 (5727, 5728)	Novel Protein sim. GBank gll1079451[pir A55463 - Iropomodulin, skeletal muscle - chicken	struct	
2865	95312191 (5728, 5730)	Novel Protein sim. GBank gll438840 (L19046) - MSA-2 [Plasmodium falciparum]		22278995, 21906764, 264482
2866	95105480 (5731, 5732)	Novel Protein sim. GBank gll585703[sp Q07066 PMP2_RAT - 22 KD PEROXISOMAL MEMBRANE PROTEIN	glycoprotein	65274572, 22278996, 22278998, 22278999, 264259, 29331824, 29331827, 29331828, 60433438, 21906754, 265018, 264448, 264764, 52844150, 83373044
2867	86908001 (5733, 5734)	Novel Protein sim. GBank gll4580997[gb A024571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]	UNCLASSIFIED	284488, 264768, 21908768, 22278998, 265022, 264259, 264508, 264805, 264907, 264511, 264910, 264635, 264636, 264637, 265011, 265017, 265018, 265019, 264583, 264088, 264566, 264764, 264369, 264567, 264486, 264288, 264766

2868	95303283 (5735, 5736)	Novel Protein sim. GBank gij1282868[embjCAA63923] - (X94232) t-Cell activation protein [Homo sapiens]		18108392, 264488, 22278994, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 264508, 52644045, 264828, 265006, 265007, 265008, 265009, 264591, 60432228, 264593, 60433356, 264595, 21906754, 265017, 265019, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 264691, 33657182, 18108368, 27486261, 27486262, 27486264, 27486265, 18108370, 18108374, 35696423, 35695855, 264632, 58182323, 87188518, 264404, 22279000, 22279002, 264482, 264563, 264564, 264567, 264487
2869	88094412 (5737, 5738)		UNCLASSIFIED	264369
2870	84404574 (5739, 5740)		UNCLASSIFIED	264369, 264908, 264764, 21906769, 264634
2871	88318621 (5741, 5742)	Novel Protein sim. GBank gij5306263[gbjAAD41995.1]AC00623 - (AC00623) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264907, 265008, 265017, 265018, 264682, 264764, 18108354, 265021, 27486265, 264629, 18108387, 264567
2872	95312197 (5743, 5744)	Novel Protein sim. GBank gij112205[pirjB39066 - proline-rich protein 15 - rat]	kinase	263981
2873	88094252 (5745, 5746)		UNCLASSIFIED	264488, 18108374, 264768, 264687, 264688, 264689, 35696423, 35696286, 35695917, 264510, 264511, 265007, 264512, 265008, 264910, 264534, 264634, 264635, 264555, 264592, 264259, 264556, 60433438, 60432289, 35696052, 265011, 264600, 264601, 60432113, 264508, 264563, 264482, 264509, 264905, 264906, 264564, 18108351, 264763, 18108370, 264907, 264566, 264908, 264764, 264288, 264567, 264909, 264488, 264766, 18108391

2874	94313549 (5747, 5748)	Novel Protein sim. GBank gij3212854 (AC004005) - unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	52644507, 52645156, 52646365, 56182575, 22278994, 22278995, 56994075, 35696286, 60432049, 264259, 52645080, 29331822, 56182181, 29331824, 60424269, 29331825, 66714117, 29331826, 29331827, 35696052, 29331828, 33656970, 66712502, 52644045, 265007, 265009, 60433356, 264758, 55812038, 18108348, 52646317, 33109954, 33657084, 265017, 264604, 265018, 265019, 264682, 264369, 264288, 264688, 52644229, 21906766, 21906767, 21906768, 55811857, 265020, 265021, 265022, 52644150, 33657023, 52645128, 18108374, 18108376, 35696423, 56182323, 18108387, 87168518, 60432113, 22279000, 22279002, 264563, 264565
2875	88083726 (5749, 5750)	Novel Protein sim. GBank gij2781386 (AC004010) - similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	glycoprotein	22278996, 22278997, 22278999, 29331826, 29331828, 29146499, 66712502, 265008, 265017, 18108351, 264683, 264689, 21906767, 18108376, 18108377, 55811576, 60170394, 22279000, 264487
2876	88090854 (5751, 5752)	Novel Protein sim. GBank gij2979530 (AC004449) - R33683_2 [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	
2877	94747029 (5753, 5754)	Novel Protein sim. GBank gij4704208 [emb]CABA1646.1] - (AL035419) dJ1100H13.1 (putative novel protein) [Homo sapiens]	Contains protein domain (PF00167) - Fibroblast growth factor	52646365, 65274572, 56182575, 22278997, 22278998, 22278999, 60432049, 52645080, 60424269, 60432289, 29331827, 35696052, 29331828, 66712502, 52644045, 56182435, 60433356, 33657402, 33657084, 265019, 55811150, 264448, 264369, 21906766, 21906768, 21906769, 265020, 33657023, 33657109, 33657182, 27486262, 264629, 60431528, 55811576, 52644332, 56182323, 264558, 83373044, 18108385, 56528486, 60432113, 22279000, 22279002, 264563
2878	88085309 (5755, 5756)	Novel Protein sim. GBank gij3876775 [emb]CAB03067] - (Z81077) predicted using GeneFinder; Similarity to Yeast protein 8248 (TR:G587531) [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264259, 29331822, 29331826, 264905, 264508, 264907, 264909, 264510, 265006, 264511, 264512, 33657402, 264758, 21906754, 18108351, 264681, 264682, 264288, 264684, 264685, 264768, 264689, 21906769, 264690, 33657023, 264693, 18108364, 33657109, 264629, 18108374, 264630, 264632, 264556, 264637, 264639, 264558, 18108385, 18108387, 264563, 264564, 264565, 264566, 264486, 264567



2878	87860122 (5757, 5768)	Novel Protein sim. GBank gi 4895145 gb AAD32752.1  - (AF127374) unknown [Streptomyces lavendulae]	Contains protein domain (PF00315) - Uracil-DNA glycosylase	UNCLASSIFIED	18108359, 264259, 264905, 18108370, 264629, 264908, 264909, 18108374, 18108377, 265006, 264910, 264637, 60170394, 264559, 265017, 264564, 264565, 264567, 264684, 264369
2880	94851439 (5759, 5760)	Novel Protein sim. GBank gi 4680703 gb AAD27741.1  (AF132966) CGI-32 protein [Homo sapiens]			264488, 52646365, 52646842, 22278994, 35698286, 22278998, 22278999, 264258, 29331822, 29331824, 29331825, 29331826, 29331827, 35698052, 29331828, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 52644045, 264510, 265006, 264511, 285007, 264512, 265009, 264910, 264594, 21806754, 52646317, 52644296, 87168559, 264600, 264604, 264605, 264760, 264764, 264288, 264766, 264768, 264687, 264769, 21806766, 21806769, 35695917, 265021, 264690, 264692, 33657023, 52645129, 33657109, 33657182, 27486262, 33657349, 264629, 18108374, 35695855, 264634, 264635, 264636, 264637, 264638, 264557, 52644332, 264558, 264559, 83373044, 264404, 22279000, 264563, 264483, 264567, 264486
2881	87650539 (5761, 5762)	Novel Protein sim. GBank gi 733571 (U23452) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	22278998, 29331822, 52644045, 21806765, 264639, 60432113
2882	87714367 (5763, 5764)	Novel Protein sim. GBank gi 118112 (U41559) - No definition line found [Caenorhabditis elegans]			264488, 22278998, 22278999, 29331822, 29331826, 264908, 60170831, 60433356, 55812038, 264681, 264682, 264686, 264687, 264688, 21806768, 21806769, 264693, 263967, 18108374, 55811576, 56182323, 22279002, 264566
2883	95362875 (5765, 5766)	Novel Protein sim. GBank gi 4868008 gb AAD31087.1  (AF106934) vitamin D receptor-interacting protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264112, 264682
2884	87784643 (5767, 5768)	Novel Protein sim. GBank gi 2224697 dbj BAA20832  - (AB002376) KIAA0378 [Homo sapiens]			265018, 264634
2885	83006308 (5769, 5770)	Novel Protein sim. GBank gi 1255889 (U53344) - T07H6.5 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264686, 264693
2886	91237823 (5771, 5772)	Novel Protein sim. GBank gi 1255889 (U53344) - T07H6.5 gene product [Caenorhabditis elegans]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complement/recept	60432049, 264259, 29331828, 264808, 264511, 264595, 60433438, 264598, 265017, 264605, 283989, 283972, 264555, 83373044, 87168518, 264566
2887	91227860 (5773, 5774)	Novel Protein sim. GBank gi 3882323 dbj BAA34521.1  - (AB018344) KIAA0801 protein [Homo sapiens]		UNCLASSIFIED	18108351, 264686, 264629, 264631, 264639, 83373044, 264482
2888	95105816 (5775, 5776)	Novel Protein sim. GBank gi 4508015 ref NP_003447.1  pZNF2 - zinc finger protein 205 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript/factor	264488, 264259, 29331828, 264508, 264906, 264593, 264758, 264766, 264769, 18108374, 83373044, 264486

2889	87606562 (5777, 5778)				UNCLASSIFIED	58994075, 29331824, 265009, 264760, 18108354, 264288
2890	78703853 (5779, 5780)	Novel Protein sim. GBank gl 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	264591, 264786
2891	88094428 (5781, 5782)	Novel Protein sim. GBank gl 3877750 emb CAB01508  - (Z78064) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D65865 comes from this gene; cDNA EST EMBL:D68451 comes from this gene; cDNA EST EMBL:D66026 comes from this gene; cDNA EST EMBL:D69658 comes from this gene...			UNCLASSIFIED	264591, 264595, 264369, 264685, 264693, 264628, 264563, 264568
2892	95419745 (5783, 5784)	Novel Protein sim. GBank gl 4929759 gb AAD34140.1 AF15190 - (AF151903) CGI-145 protein [Homo sapiens]			UNCLASSIFIED	65274572, 35688286, 29331828, 264110, 265009, 60433438, 265018, 265019, 18108351, 264288, 21906765, 21906766, 21906769, 55811957, 264690, 65274620, 263987, 35695855
2893	87798014 (5785, 5786)				UNCLASSIFIED	264259, 265010, 264682, 18108370, 264555, 264556
2894	87755985 (5787, 5788)	Novel Protein sim. GBank gl 5669015 gb AAD46135.1  - (AF080171) zinc finger protein ZNF232 [Homo sapiens]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	transcript factor		264259, 265006, 60433438, 52644286, 265011, 264369, 35695917, 18108381, 18108392, 18108388
2895	86938778 (5789, 5790)	Novel Protein sim. GBank gl 3924709 emb CAA84646  - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blast score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB...	Contains protein domain (PF01437) - Plexin repeat			29331824, 265007, 264762, 264636, 264563
2896	87752122 (5791, 5792)	Novel Protein sim. GBank gl 4885549 ref NP_005456.1 pPKBG - protein kinase B gamma	Contains protein domain (PF000089) - Eukaryotic protein kinase domain	kinase		18108392, 18108394, 18108398, 22278998, 264259, 29331822, 29331824, 29146499, 264906, 284908, 265007, 265009, 265018, 265019, 264369, 264685, 264689, 21906766, 265021, 264693, 33657182, 264639, 18108384, 18108388, 264567
2897	95413057 (5793, 5794)	Novel Protein sim. GBank gl 4502877 ref NP_001298.1 pCLDN - Clostridium perfringens enterotoxin receptor 1			UNCLASSIFIED	60424179, 56182575, 22278996, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331825, 60424269, 60432289, 29331826, 29331828, 35696052, 264908, 56182435, 265009, 264910, 60170831, 60431735, 60433356, 60433438, 65274444, 55811386, 265018, 18108351, 264448, 264288, 264687, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 264534, 33657023, 33657109, 35695783, 264628, 264629, 60431528, 18108374, 55810764, 55811576, 35696423, 35695855, 264555, 56182323, 18108385, 264404, 22279000, 22279002, 264556
2898	87750340 (5795, 5796)				UNCLASSIFIED	22278995, 264604, 18108385, 264566

2899	80357670 (5797, 5798)	Novel Protein sim. GBank gi 4581470 emb CAB40137.1  - (Y18483) SLC7A8 protein [Homo sapiens]	UNCLASSIFIED	284764, 21906764, 264692
2900	84233538 (5799, 5800)		glycoprotein	65274572, 56182575, 35696286, 60432049, 264259, 29331824, 66714117, 29331826, 35696052, 29331828, 66712502, 56182435, 285008, 265007, 265008, 265009, 60433356, 264758, 265018, 264764, 264765, 264288, 264768, 21906764, 21906766, 21906769, 265020, 264692, 264693, 32833988, 264631, 83373044, 60432113
2901	87444731 (5801, 5802)	Novel Protein sim. GBank gi 4759272 ref NP_004614.1 pTTC4 - tetrairicopeptide repeat domain 4	phosphatase	22278995, 22278997, 22278999, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 33656870, 264910, 265009, 21908754, 33657084, 87168474, 265010, 265018, 21906764, 21906765, 21906766, 21906767, 21906769, 33657023, 264693, 33657109, 33657349, 35696423, 35695855, 263981, 56182323, 22279002
2902	85745271 (5803, 5804)	Novel Protein sim. GBank gi 2414615 emb CAB16364  - (Z99259) hypothetical protein [Schizosaccharomyces pombe]		264683, 264681
2903	87606733 (5805, 5806)	Novel Protein sim. GBank gi 1079318 pir S52241 - XLCL2 protein - African clawed frog		264887, 22278994, 264259, 29331826, 29331828, 264905, 52644045, 56182435, 264511, 265017, 265018, 18108351, 264448, 264683, 264769, 264689, 35695917, 52644150, 87168518, 60432113, 22279002
2904	86458072 (5807, 5808)	Novel Protein sim. GBank gi 5639823 gb AAD45885.1 AF14367 - (AF143676) multispinning nuclear envelope membrane protein nurim [Homo sapiens]	UNCLASSIFIED	52646365, 22278999, 264259, 35696052, 265011, 265017, 264683, 264768, 35695917, 265020, 263967, 18108374, 35695855, 264637, 264952, 18108385, 18108387, 265009, 264681, 284682
2905	84449926 (5809, 5810)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7 - HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	oncogene	
2906	95341051 (5811, 5812)	Novel Protein sim. GBank gi 4889256 gb AAD27831.1 AF12185 - (AF121858) sorting nexin 8 [Homo sapiens]	UNCLASSIFIED	22278996, 35696286, 22278998, 264259, 60432289, 29331828, 29331830, 66712502, 285009, 60170831, 33109954, 264448, 264683, 264288, 264689, 21906766, 21906767, 21906768, 55811857, 35695917, 265022, 52644150, 264691, 33657023, 264692, 264693, 35695855, 60432113, 284566

2807	91211383 (5813, 5814)	Novel Protein sim. GBank gll1707079 (U80451) - contains strong similarity to a DNAJ-like domain (P.S:PS00636) [Caenorhabditis elegans]	Contains protein domain (PF00226) - DnaJ domain	eph	52644507, 56182575, 56181686, 22278995, 56994075, 35696286, 60432049, 56182181, 35696052, 80431735, 284595, 55812038, 21908754, 55811386, 265019, 284682, 264369, 56181562, 21908766, 55811957, 35695917, 265020, 265021, 33657023, 33657109, 60431528, 55811576, 35696423, 35695855, 264638, 22279000
2808	80414246 (5815, 5816)	Novel Protein sim. GBank gll2673917 (AC002561) - putative ATP-dependent RNA helicase [Arabidopsis thaliana]		helicase	265009, 33109954, 18108351, 264766, 265021, 284691, 264892, 18108374, 264556, 284638, 264557, 284558
2809	87420225 (5817, 5818)			eph	284259, 87168474, 265018, 18108365, 264628
2810	86601075 (5819, 5820)	Novel Protein sim. GBank gll4539335[emb]CAB37483.1] - (AL035539) putative protein [Arabidopsis thaliana]			22278995, 264509, 264512, 265007, 33657402, 265017, 264369, 265022, 18108365, 264628
2811	94216615 (5821, 5822)	Novel Protein sim. GBank gll4469187[emb]CAB38415.1] - (AL031588) dJ1163J1.3 (novel protein similar to mouse B99) [Homo sapiens]		glucoamylase	52646365, 18108387, 22278995, 22278997, 22278998, 22278999, 28331824, 28331825, 52644045, 265006, 265018, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 18108370, 18108372, 18108374, 22279000
2812	87731803 (5823, 5824)	Novel Protein sim. GBank gll4929637[gb]AAD34079.1]AF15184 - (AF151842) CGI-84 protein [Homo sapiens]	Contains protein domain (PF00904) - Involucrin repeat		52644516, 264092, 60432049, 264259, 52645080, 28331824, 28331825, 66712502, 33109954, 264760, 264683, 264288, 264686, 265021, 264693, 18108368, 263976, 264404
2813	87713823 (5825, 5826)	Novel Protein sim. GBank gll854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	52644507, 52645156, 52646942, 58182575, 35696286, 22278997, 264259, 52645080, 28331827, 35696052, 28331828, 264828, 52644045, 56182435, 55812038, 52646317, 21908754, 52644286, 87168474, 265017, 265018, 265019, 18108351, 264682, 264686, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 27486261, 27486262, 27486265, 35695763, 55811576, 35695855, 52644332, 22279000, 22279002, 264563
2814	87797300 (5827, 5828)				264557

2915	88081072 (5828, 5830)	Novel Protein sim. GBank gi 5174485 ref NP_006030.1 pKIAA - endocytic receptor (macrophage mannose receptor family)	Contains protein domain (PF00059) - eph Lectin C-type domain	264569, 264488, 264687, 264768, 21908768, 52646842, 21906767, 21908768, 56182575, 29148829, 35695917, 22278998, 22278997, 22278998, 285021, 22278999, 52644150, 264691, 284259, 60432049, 264692, 52645129, 33657109, 33657182, 29331827, 27486261, 35696052, 29331828, 27486262, 27486264, 27486265, 33657349, 29146498, 29146498, 264908, 264908, 264907, 18108370, 264908, 18108372, 52644045, 18108374, 56182435, 35695855, 264112, 264510, 265008, 60432229, 264593, 60433356, 56182323, 18108382, 55812038, 18108385, 33109954, 21908754, 33657084, 87168518, 265010, 265011, 60432113, 265017, 265018, 22279000, 265018, 55811150, 264681, 18108351, 264763, 264448, 264683, 264566, 18108354, 264389, 264288, 264766, 52645156, 65274572, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278998, 264259, 29331822, 29331824, 29331825, 66714117, 60432288, 29331826, 29331827, 29331828, 33656970, 264509, 264908, 29331830, 52644045, 264909, 56182435, 60170831, 264592, 264593, 33657402, 60433356, 52646317, 21906754, 33109954, 33657084, 52644296, 85658542, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21908769, 55811957, 35695917, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486264, 35695763, 18108376, 55811578, 35696423, 65274791, 35695855, 52644332, 264557, 264638, 56182323, 18108387, 87168518, 22279002, 264482
2916	95337780 (5831, 5832)	Novel Protein sim. GBank gi 5104851 dbj BAA80165.1  - (AP000081) 305aa long hypothetical dTDP-4- dehydrohamose reductase [Aeropyrum pernix]	dehydrogenase	60433438, 264602, 264682, 87168518, 60432113
2917	87454546 (5833, 5834)	Novel Protein sim. GBank gi 3169065 emb CAA19260.1  - (AL023704) putative translocation elongation factor-Tu fa mily [Schizosaccharomyces pombe]	UNCLASSIFIED	264638
2918	85690529 (5835, 5836)	Novel Protein sim. GBank gi 539218 pir S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		
2919	87641497 (5837, 5838)	Novel Protein sim. GBank gi 2564955 (AF030001) - unknown [Mus musculus]		66714117, 66712502, 263981

2820	87769523 (5839, 5840)				35696286, 22278997, 264259, 52645080, 29331824, 28331826, 29331827, 264828, 264909, 58182435, 264511, 264758, 33109954, 21908754, 52644298, 265010, 285011, 264601, 265017, 265019, 264681, 264687, 21908767, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486282, 27486284, 27486285, 35696423, 35695855, 264632, 264636, 264637, 264638, 58182323, 60170394, 18108385, 87168518, 60432113
2821	91639982 (5841, 5842)	Novel Protein sim. GBank gij4580013jgb/AAD24202: jU83194_ - (U83194) TRAF4-associated factor 2 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		35696286, 22278997, 264091, 264092, 264094, 264259, 28331822, 29331824, 29331826, 29331827, 35696052, 29146498, 264104, 264105, 264107, 264509, 264110, 264112, 264512, 60433358, 21906754, 87168474, 265017, 18108351, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 263974, 18108374, 263976, 263977, 18108376, 264555, 263981, 58526488, 87168518, 22279000, 22279002, 264908, 264909, 264511, 285006, 285008, 264593, 33657402, 60174639, 18108351, 264763, 21906765, 29146627, 35695917, 264692, 264629, 263978, 58811576, 35695855, 264555, 264558, 58182323, 60170394, 22279000, 264486
2822	87749762 (5843, 5844)	Novel Protein sim. GBank gij4589514jdbjBAA76779.1  - (AB023152) KIAA0935 protein [Homo sapiens]	Contains protein domain (PF01074) - Glycosyl hydrolases family 38	kinase	264908, 264909, 264511, 285006, 285008, 264593, 33657402, 60174639, 18108351, 264763, 21906765, 29146627, 35695917, 264692, 264629, 263978, 58811576, 35695855, 264555, 264558, 58182323, 60170394, 22279000, 264486
2823	95337799 (5845, 5846)	Novel Protein sim. GBank gij483526jemb[CAB42898.2] - (Z83844) dJ37E16.4 (similar to mouse p116Rip protein) [Homo sapiens]	Contains protein domain (PF00169) - PH domain	struct	264488, 18108397, 22278995, 22278996, 22278997, 22278998, 22278999, 29331825, 29331826, 29331827, 29331830, 264511, 265008, 33657402, 265011, 265017, 265018, 264683, 18108354, 21906765, 21906767, 21906768, 21906769, 52644150, 264691, 264692, 33657109, 263974, 18108376, 264631, 264636, 18108385, 18108387, 22279000, 264563, 264568
2824	87791967 (5847, 5848)	Novel Protein sim. GBank gij2133095jprj S72254 - ribosomal protein L36, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00444) - Ribosomal protein L36	ribosomalprot	265017, 264628, 20281152, 264556
2825	95090120 (5849, 5850)	Novel Protein sim. GBank gij2388986jemb[CAB11718] - (Z8980) actin associated protein [Schizosaccharomyces pombe]	UNCLASSIFIED		58182575, 35696288, 264259, 60432289, 29331827, 264508, 52644045, 264910, 264591, 60432229, 58812038, 21906754, 264681, 264448, 264683, 264288, 264685, 52644229, 264689, 21906765, 21906766, 21906768, 21906769, 265021, 265022, 60170615, 264692, 33657023, 264693, 33657109, 35696423, 65274791, 58182323

2928	95343003 (5851, 5852)	Novel Protein sim. GBank gij283032[pilj]S22456 - hydroxyproline-rich glycoprotein - perennial teasinte			29331828, 265011, 264768, 264689, 264764, 264288, 264630, 264637
2928	20452179 (5855, 5856)			UNCLASSIFIED	264559
2929	91622920 (5857, 5858)	Novel Protein sim. GBank gij3413320[emb]CAA06915] - (AJ008215) CMP-N-acetylneuraminic acid synthetase [Mus musculus]		UNCLASSIFIED	284569, 264489, 22278994, 35696286, 22278996, 22278998, 22278999, 264094, 264259, 52645080, 29331822, 29331824, 6671417, 29331825, 29331826, 29331827, 35696052, 33696970, 264109, 29331830, 52644045, 265009, 33109954, 52644296, 87168559, 264760, 264762, 264448, 264764, 264288, 264766, 264768, 21908765, 21908768, 21908769, 35695917, 264691, 33657023, 264693, 33657109, 18108374, 263976, 35698423, 35695855, 263981, 22279000, 22279002, 264567, 264486
2930	95302755 (5859, 5860)			UNCLASSIFIED	56182575, 56181886, 35696286, 22278996, 22278998, 22278999, 264259, 29331825, 60432289, 29331828, 264905, 52644045, 56182435, 265009, 60170831, 264592, 60432229, 60433356, 87168474, 265010, 265011, 265017, 265018, 265019, 264762, 264448, 264683, 264288, 264766, 21908765, 21908769, 35695917, 60170615, 33657023, 33657109, 264628, 18108370, 18108372, 35696423, 35695855, 264556, 56182323, 60432113, 264567
2931	94312693 (5861, 5862)	Novel Protein sim. GBank gij3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]	Contains protein domain (PF00471) - Ribosomal protein L33	UNCLASSIFIED	52645156, 22278997, 22278998, 29331822, 52645080, 29331824, 60432289, 33656970, 60433356, 60433438, 33109954, 21908765, 21908768, 21908767, 21908768, 265020, 52644150, 33657023, 33657109, 33657182, 27486265, 35698423, 35695855, 264555, 87168518, 60432113, 264566, 264906, 264907
2932	79632623 (5863, 5864)				
2933	91720770 (5865, 5866)	Novel Protein sim. GBank gij3378056 (AF017777) - helicase [Drosophila melanogaster]	helicase		264488, 18108392, 56182575, 22278999, 264091, 264259, 29331825, 60432289, 29331827, 264508, 52644045, 56182435, 265007, 265009, 264592, 60433356, 60433438, 21908754, 265017, 264682, 264288, 52644229, 21908765, 21908768, 21908769, 265022, 52644150, 33657023, 33657109, 27486265, 264635, 264636, 60170394, 56182323, 18108385, 60432113, 264565, 264566, 264567

2834	86576025 (5867, 5868)				22278997, 22278999, 29331824, 33657402, 264691, 27486262, 264628, 87168518, 22279000
2835	86410578 (5868, 5870)			UNCLASSIFIED	56182575, 22278995, 60433356, 33657402, 264758, 33109854, 21806754, 265018, 265019, 264448, 264769, 21906764, 21906765, 265021, 264892, 33657023, 33657109, 33657349, 55810764, 22279000
2836	87605863 (5871, 5872)	Novel Protein sim. GBank gj14153662 (AC005065) - determined by GENSCAN prediction and spliced EST; match to EST R84329 (NID:942735) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	nuclease	22278997, 29331827, 29331828, 265009, 265017, 264605, 265020, 55811576, 18108387, 60432113, 264563
2837	84853086 (5873, 5874)	Novel Protein sim. GBank gj15174409 [ref NP_006101.1 pCD2B - CD2 antigen (cytoplasmic tail)-binding protein 2]		UNCLASSIFIED	56994075, 22278999, 264259, 60432049, 29331822, 56182181, 29331827, 29331828, 264906, 264908, 264909, 56182435, 265008, 264512, 264910, 60170831, 60433356, 265011, 265018, 18108351, 264448, 264288, 264766, 52644229, 21906765, 29148784, 65274791, 264556, 56182323, 60170394, 264558, 60432113, 264565, 264488, 264567
2838	95419773 (5875, 5876)	Novel Protein sim. GBank gj13319990 [emb CAA76720] - (Y17267) ubiquitin-conjugating enzyme [Mus musculus]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	264488, 56182575, 22278998, 35896286, 22278997, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264107, 264905, 66712502, 52644045, 56182435, 264511, 265008, 265009, 60432229, 33657402, 60433438, 55812038, 21808754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264681, 264288, 264689, 21908765, 21906767, 21906768, 55811957, 35695917, 265020, 60170815, 264690, 264691, 264692, 33657023, 264693, 65274620, 33657109, 18108370, 18108374, 263976, 35696423, 35695855, 264555, 264556, 18108381, 56182323, 60170394, 83373044, 18108385, 56526488, 60432113, 22279002
2839	87786622 (5877, 5878)	Novel Protein sim. GBank gj13979900 [emb CAA99909] - (Z75547) similar to WD domain, G-beta repeat; cDNA EST yk371b7.5 comes from this gene; cDNA EST yk312h1.5 comes from this gene; cDNA EST yk465d5.5 comes from this gene; cDNA EST yk472c4.5 comes from this gene; cDNA EST yk292f8.....	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase-associated	264907, 265018, 264681, 264685, 264686



2940	95011103 (5879, 5880)			UNCLASSIFIED	2227898, 29331822, 29331824, 66714117, 29331826, 29331828, 284905, 284908, 66712502, 29331830, 265011, 265017, 284784, 284369, 21906768, 21906767, 33657023, 33657108, 3283386, 18108374, 18108377, 264634, 83373044, 18108385, 18108387, 264566
2941	21423370 (5881, 5882)	Novel Protein sim. GBank gi 3413872 dh BAA32300  - (AB007924) KIAA0455 protein [Homo sapiens]		UNCLASSIFIED	284557
2942	87430203 (5883, 5884)	Novel Protein sim. GBank gi 1172845 sp P46829 RB25_RABIT - RAS-RELATED PROTEIN RAB-25		glycoprotein	264910, 265010, 264768
2943	95314504 (5885, 5886)	Novel Protein sim. GBank gi 4929653 gb AAD34087.1 AF15185 - (AF151850) CGI-92 protein [Homo sapiens]		collagen	60432049, 264258, 60432289, 29331827, 29146498, 265008, 284593, 60433356, 60433438, 285010, 285011, 265017, 265018, 284683, 264768, 18108381, 65274727, 60432113, 264567
2944	95081083 (5887, 5888)	Novel Protein sim. GBank gi 4678282 emb CAB41190.1  - (AL049660) 1-acylglycerol-3-phosphate acyltransferase-like protein [Arabidopsis thaliana]	Contains protein domain (PF00415) - Regulator of chromosome condensaiton (RCC1)	ATPase_associated	56984075, 22278988, 60432049, 264259, 29331822, 29331824, 60424269, 60432289, 29331826, 29331828, 284905, 264907, 52644045, 284909, 284511, 265008, 265009, 284594, 21906754, 87168559, 284603, 265017, 265018, 18108351, 264682, 264766, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170815, 52644150, 284690, 264691, 33657023, 264692, 264693, 33657109, 33657182, 33657349, 18108370, 18108374, 18108377, 55811576, 35698423, 35698555, 264635, 264555, 264556, 56182323, 60170394, 264558, 284559, 83373044, 56526486, 87168518, 60432113, 22279002, 284482, 264563, 264484, 264567
2945	94233560 (5889, 5890)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	60424179, 22278995, 22278996, 22278998, 22278999, 264259, 56182181, 29331824, 60424269, 60432289, 35696052, 264808, 265006, 60433356, 55812038, 264759, 55811386, 265018, 264681, 18108351, 264448, 264683, 264369, 264288, 284687, 56181562, 21906787, 21906788, 21906769, 35695917, 265020, 265021, 264693, 60431528, 55810764, 35696423, 35695855, 264630, 60170394, 83373044, 22279000, 264566, 264567

2846	84317315 (5891, 5892)	Novel Protein sim. GBank gil5441952 gb AAD43195.1 AF07286 - (AF072864) peroxisomal membrane protein PMP 24 [Homo sapiens]		UNCLASSIFIED	284488, 284259, 284508, 284509, 284808, 284907, 284809, 284510, 284511, 285007, 284512, 284910, 284591, 284593, 18108351, 284764, 284288, 284684, 284769, 285021, 284682, 33857109, 284628, 284628, 18108374, 284631, 284634, 284636, 284637, 18108380, 284638, 284639, 83373044, 284585, 284586, 284486, 284567
2847	87382852 (5893, 5894)	Novel Protein sim. GBank gil3540281 gb AAC34383.1  - (AF058116) All-1 related protein [Fugu rubripes]		UNCLASSIFIED	22278995, 22278998, 22278997, 22278999, 29148498, 284508, 29331830, 285007, 285008, 285009, 60432228, 21906754, 285010, 285017, 285019, 284766, 284685, 21906765, 21906766, 21906767, 21906768, 21906769, 285020, 284628, 18108370, 284629, 284630, 18108387, 60432113
2848	87626527 (5895, 5896)	Novel Protein sim. GBank gil5566614 gb AAB65654.2  - (AF001533) mitogen-induced [Mus musculus]			52646842, 22278995, 284259, 29331824, 29331825, 29331827, 29331830, 284809, 285007, 285009, 285019, 284763, 284684, 284288, 284685, 284686, 21906767, 284691, 284692, 284693, 18108374, 55811576, 18108385, 22279002, 284563, 284567
2849	88175545 (5897, 5898)	Novel Protein sim. GBank gil2132923 pir  S67133 - probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	22278998, 22278997, 60432289, 29331826, 29331827, 29331828, 35868052, 28146499, 284104, 284107, 284905, 68712502, 284908, 60433356, 60433438, 87168559, 284764, 52644229, 58181562, 21906767, 21906768, 21906769, 285022, 60170615, 33857023, 35868423, 263981, 284558, 60432113, 22279002
2850	95088870 (5899, 5900)	Novel Protein sim. GBank gil466102 sp P34629 YQJ6_CAEEL - PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III	Contains protein domain (PF00883) - peptidase Cytosol aminopeptidase family		284488, 35868286, 284259, 35868052, 284907, 285007, 284910, 285017, 285018, 284288, 284768, 35869517, 285020, 18108362, 18108370, 18108379, 358696423, 65274791, 358695855, 284556, 56526486, 284486
2851	87392357 (5901, 5902)	Novel Protein sim. GBank gil4688902 emb CAB41450.1  - (AJ238248) centaurin beta2 [Homo sapiens]			284693

2952	95329952 (5903, 5904)	Novel Protein sim. GBank gij596693jembjCAB51405.1] - (AL098881) hypothetical protein [Homo sapiens]	Contains protein domain (PF00850) - CRAL/TRIO domain.	Transcript factor	264687, 52645156, 21806786, 21906769, 22278998, 265020, 264690, 60432049, 264259, 264693, 29331822, 18108365, 29331825, 60432289, 33657109, 18108368, 29331827, 35696052, 27486282, 264508, 264905, 20281149, 264908, 264907, 29331830, 264908, 264909, 35695855, 264511, 265008, 265009, 264910, 264635, 264636, 60432229, 264638, 60433358, 264639, 264758, 87168518, 265017, 22279000, 22279002, 264760, 264563, 264482, 18108351, 264448, 264288
2953	88093575 (5905, 5906)	Novel Protein sim. GBank gij119522spjP10658jSERC_RABIT - PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP)	Contains protein domain (PF00286) - Aminotransferases class-V	UNCLASSIFIED	18108398, 56984075, 22278886, 29331822, 29331824, 28331825, 29331827, 35696052, 264508, 264905, 264908, 264907, 264510, 264591, 264594, 33857402, 264595, 264596, 264758, 52646317, 21806754, 33657084, 52644296, 87168559, 264600, 264760, 264681, 18108351, 264764, 264369, 264288, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33857023, 18108384, 52645129, 33857109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565
2954	88086288 (5907, 5908)	Novel Protein sim. GBank gij4885281refjNP_005251.1pGDF9 - growth differentiation factor 9	Contains protein domain (PF00019) - Tgf domain	tgf	29331822
2955	87698426 (5909, 5910)	Novel Protein sim. GBank gij3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331825, 29331826, 35696052, 264908, 52644045, 264512, 60432229, 265018, 265019, 55811150, 264769, 21906767, 21906768, 21906769, 285021, 60170615, 55810764, 264567
2956	85780745 (5911, 5912)	Novel Protein sim. GBank gij4889254jgbjAAD27830.1AF12185 - (AF121857) sorting nexin 7 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		22278996, 264259, 29331827, 264908, 21908788
2957	90933301 (5913, 5914)	Novel Protein sim. GBank gij4503023refjNP_000088.1pCPT2 - carnitine palmitoyltransferase II precursor		cadherin	22278999, 264259, 29331824, 29331827, 265008, 264595, 264758, 265010, 265011, 264448, 264763, 264683, 264288, 264685, 18108357, 29148629, 264690, 18108362, 264693, 18108370, 60431528, 18108374, 264634, 18108381, 56182323, 18108382, 18108385, 18108388, 56526486, 87168518, 264482, 264487
2958	87440014 (5915, 5916)	Novel Protein sim. GBank gij4240257jdbjBAA74907.1] - (AB020691) KIAA0884 protein [Homo sapiens]			264595, 264596, 264681, 264369, 264629, 264631, 264567

2859	95109420 (5917, 5918)	Novel Protein sim. GBank gij988221 (U33005) - Tbc1 [Mus musculus]	Contains protein domain (PF00566) - oncogene TBC domain	263994, 22278997, 264259, 60432049, 29331826, 29331828, 35696052, 29331830, 66712502, 56182435, 265006, 264512, 265008, 265009, 60433356, 60433438, 264596, 265017, 265018, 264683, 264288, 264766, 264769, 21906766, 21906767, 21906769, 265020, 60170615, 264692, 27486285, 18108374, 65274781, 35695855, 83373044, 56528486, 60432113
2860	87420091 (5918, 5920)		UNCLASSIFIED	35696286, 56182435, 87168474, 265010, 60170615, 35696423, 56182323, 18108383, 87168518, 264483
2861	95413416 (5921, 5922)	Novel Protein sim. GBank gij599646(emb CAB05177.2) - (Z82266) predicted using GeneFinder: similar to WD domain, G-beta repeats [Caenorhabditis elegans]	transcriptfactor Contains protein domain (PF00400) - WD domain, G-beta repeat	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 264907, 264908, 52644045, 265006, 33657402, 21906754, 87168474, 265011, 87168559, 265017, 21906769, 265020, 60170815, 264692, 33657023, 35695763, 18108370, 18108374, 35696423, 264632, 264636, 18108385, 87168518, 22278002, 264564, 264587
2862	87912700 (5923, 5924)		UNCLASSIFIED	35696286, 22278997, 264092, 264094, 264259, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264508, 264907, 264908, 264909, 264510, 264512, 264593, 264594, 60433438, 264758, 52646317, 264602, 264603, 264605, 264760, 264762, 264764, 264288, 264766, 264688, 264768, 264636, 264637, 264638, 264639, 18108385, 264769, 35695917, 265020, 264691, 264634, 264583, 264585, 264586, 264587, 264486
2863	95313464 (5925, 5926)	Novel Protein sim. GBank gij4240223(dbj BAA74890.1) - (AB020674) KIAA0867 protein [Homo sapiens]	transcriptfactor Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	18108392, 56994075, 22278998, 22278999, 29331822, 29331825, 29331826, 29331827, 29331828, 265007, 265008, 264592, 264594, 21906754, 265018, 264760, 264687, 29148627, 29148784, 265020, 33657023, 264693, 65274820, 33657182, 27486261, 264629, 55810784, 35696423, 264555, 264636, 264637, 264557, 264558, 264563
2864	94324617 (5927, 5928)		UNCLASSIFIED	264259, 29331828, 33657402, 265017, 265018, 264692, 18108368, 35696423, 83373044, 18108388

2865	80384762 (5929, 5930)	Novel Protein sim. GBank gi 4885447 ref NP_005452.1 pKRML - Kreisler (mouse) maf- related leucine zipper homolog			transcriptfactor	264259, 29331826, 264508, 264509, 264805, 264907, 264908, 264909, 264511, 265008, 264910, 264591, 264593, 264594, 33657402, 265011, 264760, 264762, 264764, 264288, 264685, 264766, 264692, 33657109, 264628, 264829, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264583, 264587, 18108391, 60432289, 264682, 264448
2866	91725248 (5931, 5932)	Novel Protein sim. GBank gi 5262751 emb CAB45690.1  - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]				
2867	94658303 (5933, 5934)	Novel Protein sim. GBank gi 624225 (U19181) - Rabin3 [Rattus norvegicus]			UNCLASSIFIED	264488, 264508, 264509, 264908, 264909, 264511, 264910, 264594, 264758, 85658542, 264762, 264764, 265021, 264556, 18108381, 264564, 264486
2868	85302776 (5935, 5936)	Novel Protein sim. GBank gi 4929715 gb AAD34118.1 AF15188 - (AF151881) CGI-123 protein [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)			264887, 52645156, 21906765, 52646365, 21908767, 18108398, 35696423, 22278998, 35696286, 22278997, 265020, 22278999, 265021, 265022, 264093, 264636, 264690, 52644150, 264259, 33657023, 52645080, 264693, 29331822, 56182181, 29331824, 66714117, 29331825, 33108954, 52645129, 29331826, 21906754, 33657182, 29331827, 29331828, 35698052, 27485262, 87168518, 87168474, 265010, 87168559, 265018, 22278000, 265018, 22279002, 264583, 18108351, 264906, 264907, 264448, 86712502, 264586, 264369, 264288
2869	95310957 (5937, 5938)	Novel Protein sim. GBank gi 3024743 sp O24734 THSA_SULS7 - THERMOSOME, ALPHA SUBUNIT (CHAPERONIN ALPHA SUBUNIT)		eph		52646842, 22278996, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331828, 264509, 264909, 52644045, 56182435, 265009, 60433438, 55812038, 21906754, 265011, 87168559, 265018, 265019, 264448, 264288, 264369, 52644229, 21906766, 21906768, 21906769, 29148784, 265020, 265021, 52644150, 264691, 33657109, 18108374, 56182323, 60170394, 87168518, 60432113, 22279000
2870	88088071 (5939, 5940)	Novel Protein sim. GBank gi 3165407 (AC004755) - fos37502.1 [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox		

2971	94186930 (5941, 5942)	Novel Protein sim. GBank gil728637[sp]P39194[ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		Im7	264488, 56182575, 35696286, 56994075, 29331824, 29331826, 29146499, 264508, 264905, 264907, 264112, 264910, 21908754, 87168559, 265018, 265019, 18108351, 264889, 21908765, 21906767, 21908768, 265020, 265021, 60170615, 18108364, 264628, 264629, 18108374, 264636, 264556, 264558, 83373044, 18108384, 18108385, 87168518, 264584, 264587 265017, 35695917, 265021, 33657109, 22278002, 264563
2972	86625943 (5943, 5944)	Novel Protein sim. GBank gil728636[sp]P39193[ALU6_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	29331822, 264692, 33657349, 55811576, 264583
2973	91215301 (5945, 5946)	Novel Protein sim. GBank gil2746789 (AF040642) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	18108392, 52644507, 56182575, 56181686, 22278985, 22278986, 35696286, 22278987, 22278988, 22278989, 264259, 52845080,
2974	91673002 (5947, 5948)	Novel Protein sim. GBank gil786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	29331824, 29331825, 66714117, 60424269, 29331826, 29331827, 29331828, 35696052, 66712502, 264908, 52644045, 265007, 264910, 265009, 80433438, 33109954, 21906754, 55811386, 52644286, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264448, 264369, 264288, 52644229, 18108359, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 52644150, 264691, 264692, 33857023, 27486262, 27486264, 35695763, 18108370, 18108376, 55810764, 55811576, 35696423, 35695855, 264630, 264635, 264557, 52644332, 264558, 83373044, 18108387, 87168518, 60432113, 22278000, 264482, 264487
2975	95325213 (5949, 5950)	Novel Protein sim. GBank gil3880812[emb]CAA19508] - (AL023839) similar to HECT-domain (ubiquitin-transferase); cDNA EST yk480d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00632) - HECT-domain (ubiquitin- transferase).	ubiquitin	29331824, 29331827, 29331828, 264910, 85658542, 265011, 265018, 264448, 264288, 264769, 21906767, 265020, 264691, 264559, 83373044
2976	87771202 (5951, 5952)	Novel Protein sim. GBank gil5679138[gb]AAD46874.1[AF16093] - (AF160934) BcDNA LD14189 [Drosophila melanogaster]		transport	22278986, 264908, 265007, 265010, 265011, 265017, 265019, 18108351, 264685, 264689, 18108370, 264639, 18108385 264509, 264288
2977	81725254 (5953, 5954)	Novel Protein sim. GBank gil5262751[emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		UNCLASSIFIED	

2978	87332059 (5955, 5956)	Novel Protein sim. GBank gij746549 (U23522) - No definition line found [Caenorhabditis elegans]	Contains protein domain (PF00480) - ROK family	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432289, 29331827, 29146499, 58182435, 265006, 265007, 265009, 60433356, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 264288, 264685, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 35696423, 264639, 60432113, 22279000, 22279002
2979	91725256 (5957, 5958)	Novel Protein sim. GBank gij5262751 [emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]	complement		264488, 65274572, 56994075, 22278999, 264093, 29331822, 29331824, 264286, 55811957, 33657023, 33657109, 18108370, 55811576, 56182323, 60432113, 264482
2980	86296600 (5959, 5960)			UNCLASSIFIED	265009, 21906767, 263981, 22279000
2981	87376330 (5961, 5962)				264629, 264584
2982	95303675 (5963, 5964)	Novel Protein sim. GBank gij4929787 [gb]AAD34144.1 [AF15190] - (AF151907) CGI-149 protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264092, 29331824, 29331827, 29331828, 264905, 264591, 264592, 264594, 264595, 264596, 33657084, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 18108365, 33657182, 33657349, 35696423, 83373044, 22279000, 22279002
2983	91725258 (5965, 5966)	Novel Protein sim. GBank gij5262751 [emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]			60424178, 52646842, 18108398, 22278997, 264093, 60432049, 264259, 29331822, 60432289, 33656970, 264905, 52644045, 265006, 60431735, 87188474, 265018, 265019, 18108351, 264448, 21906765, 21906768, 35695917, 33657023, 52645129, 18108370, 35696423, 83373044, 56528486, 60432113, 264404, 22279002
2984	94136467 (5967, 5968)	Novel Protein sim. GBank gij2393734 (AC002542) - similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619) [Homo sapiens]	ATPase associated		
2985	87099072 (5969, 5970)	Novel Protein sim. GBank gij103160 [pir]S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)	UNCLASSIFIED		264910, 55812038, 56181562, 55811957, 264628, 55810764, 264632, 264635, 60432113
2986	86284861 (5971, 5972)				55811957, 264566
2987	88455934 (5973, 5974)		UNCLASSIFIED		264369

2988	96357753 (5975, 5976)	Novel Protein sim. GBank gij4679028[gjb AAD27002.1] - (AF077207) HSPC021 [Homo sapiens]		UNCLASSIFIED	264488, 65274572, 22278995, 22278996, 22278997, 22278999, 264092, 264094, 264259, 60432048, 29331824, 29331826, 60432289, 35696052, 29331828, 264107, 264905, 264907, 264908, 66712502, 264828, 264909, 56182435, 265008, 265007, 265008, 60170831, 60432229, 264593, 60433356, 264757, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264682, 264448, 264369, 264288, 264685, 52644229, 21908765, 21908767, 21906769, 35695917, 265021, 265022, 52644150, 264690, 33657023, 65274620, 263967, 33657109, 27486262, 18108370, 18108372, 18108374, 55810764, 65274791, 35695955, 264635, 264636, 264637, 263981, 264638, 56182323, 83373044, 60432113, 22279000, 264563, 264564, 264565, 264566, 264567
2989	91225118 (5977, 5978)	Novel Protein sim. GBank gij113671[sp P23964 ALUF_HUMAN - IIII ALU CLASS F WARNING ENTRY IIII		kinase	22278996, 22278997, 264905, 264511, 60170831, 264593, 265019, 21906765, 21906767, 21906768, 18108374
2990	87330444 (5979, 5980)	Novel Protein sim. GBank gij2829838[sp P97348 RHOD_MOUSE - RHO-RELATED GTP-BINDING PROTEIN RHOD	Contains protein domain (PF00071) - Ras family	oncogene	265007, 264512, 18108351, 264288, 264689, 265020, 264691, 33657023, 33657109
2991	94325361 (5981, 5982)			UNCLASSIFIED	264563
2992	85425164 (5983, 5984)			UNCLASSIFIED	264259, 265019, 264689, 18108385
2993	94325363 (5985, 5986)			UNCLASSIFIED	264488, 29331822, 265017, 264761, 21906769, 65274791, 263981, 264565
2994	94136634 (5987, 5988)	Novel Protein sim. GBank gij2496548[sp Q50658 YU02_MYCTU - HYPOTHETICAL 29.7 KD PROTEIN CY339.02		transport	22278994, 22278995, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 265006, 265009, 264910, 33109954, 87168474, 87168559, 265018, 265019, 264448, 264288, 21906766, 21906767, 21908768, 21906768, 265021, 265022, 33657023, 264693, 35695855, 83373044, 18108385, 22279000, 264565, 264568, 264905, 264907, 265019, 18108351, 264683
2995	87591070 (5989, 5990)	Novel Protein sim. GBank gij2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]			
2996	91013798 (5991, 5992)	Novel Protein sim. GBank gij2829812 (AC002291) - Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	65274572, 35696286, 264259, 29331824, 35696052, 29146499, 264508, 264907, 265007, 265008, 60433438, 18108348, 265017, 264681, 264683, 264288, 264766, 264769, 264689, 35695917, 60170815, 33657023, 264692, 264634, 264555, 18108381, 18108382, 18108388, 264484



2997	87627440 (5993, 5994)	Novel Protein sim. GBank gi 4589652 dbj BAA76948.1  - (AB023221) KIAA1004 protein [Homo sapiens]		homeobox	264488, 56182575, 264259, 66714117, 29331826, 35698052, 264508, 264509, 264907, 264908, 265006, 87168474, 265019, 264448, 264882, 264885, 264786, 21908764, 21908766, 21908768, 21908769, 27486261, 18108374, 35698423, 264634, 264635, 264636, 264557, 18108385, 87168518
2998	88095381 (5995, 5996)	Novel Protein sim. GBank gi 3947599 emb CAA22252  - (AL034364) cDNA EST yk255b9.3 comes from this gene; cDNA EST yk255b9.5 comes from this gene; cDNA EST EMBL:M75923 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	52646365, 22278997, 264508, 264908, 18108351, 21908765, 21908767, 18108370, 18108374, 35698423, 264636, 264639
2999	94847055 (5997, 5998)	Novel Protein sim. GBank gi 15408 sp P18835 CC19_CAEEL - CUTICLE COLLAGEN 19		UNCLASSIFIED	56182575, 22278996, 29147620, 29331825, 29146498, 29146499, 264905, 66712502, 265008, 265009, 21906754, 85658542, 18108351, 29148627, 29148629, 60170615, 33657109, 27486262, 18108370, 18108374, 264556, 264557, 264558, 60170394, 18108385, 264563
3000	95099370 (5999, 6000)	Novel Protein sim. GBank gi 1163174 (U32575) - similar to yeast Sec8p. Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author [Rattus norvegicus]		UNCLASSIFIED	264887, 22278997, 22278999, 264259, 29331822, 29331824, 35698052, 29146498, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 265008, 265009, 264910, 33657402, 284757, 264595, 264596, 264758, 21906754, 285011, 264600, 265017, 265018, 264605, 265019, 264760, 264761, 264762, 264681, 264682, 264764, 264288, 264685, 264766, 264686, 264768, 264769, 21906765, 21906768, 35695917, 265020, 264691, 264692, 33657023, 264693, 33657109, 33657182, 27486281, 264628, 264629, 18108374, 18108376, 35698423, 35695855, 264830, 264631, 264632, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 60170394, 83373044, 20798451, 22279002, 264563, 264486, 264567
3001	88078454 (6001, 6002)	Novel Protein sim. GBank gi 2078470 (AC002073) - Putative gene. Genscan predictions confirmed by EST splicing.; coded for by human cDNAs AA122029 (NID:g1678048), D31562 (NID:g844442), AA158721 (NID:g1733515), R59640 (NID:g830335) and F13082 (NID:g709111) [Homo sapiens]		calhepsin	18108394, 52646842, 56182575, 29331824, 29331825, 29331827, 264910, 33109954, 52644296, 265017, 265019, 264288, 265020, 265021, 52644150, 264692, 35695763, 55810764, 35696423, 56182323, 18108387, 264563, 264584
3002	87718167 (6003, 6004)	Novel Protein sim. GBank gi 3599478 (AF085185) - Myosin-1A [Acanthamoeba castellanii]		UNCLASSIFIED	264488, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 264510, 265009, 21906754, 264682, 264688, 33657023, 264565

3003	86848078 (6005, 6006)	Novel Protein sim. GBank gll1754869 (U30292) - collagen type XIII alpha-1 chain [Mus musculus]	Contains protein domain (PF01391) - collagen triple helix repeat (20 copies)	264512, 264593, 264584, 264567, 264486
3004	86066876 (6007, 6008)	Novel Protein sim. GBank gll2224629[dbj]BAA208021 - (AB002342) KIAA0344 [Homo sapiens]		29331830, 21906769, 264691, 33657109, 263972, 18108385
3005	87794843 (6008, 6010)	Novel Protein sim. GBank gll4680659[gb]AAD27719.1[AF132944] CGL-10 protein [Homo sapiens]	Contains protein domain (PF01360) - oxygenase Monooxygenase	29331822, 29331824, 29331827, 60433438, 265011, 265019, 21908766, 21908767, 21908768, 265020, 33657023, 33657349, 60170394, 22278002, 264567
3006	87422224 (6011, 6012)	Novel Protein sim. GBank gll3930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - MHC Ank repeat	264259, 29331822, 264512, 21906754, 265018, 264687, 21908765, 264691, 264555, 264556, 264558, 18108385
3007	90936005 (6013, 6014)	Novel Protein sim. GBank gll2565052 (U80738) - CAGH1a [Homo sapiens]	Contains protein domain (PF00096) - transcript factor Zinc finger, C2H2 type	52644507, 52645156, 65274572, 264909, 264512, 265018, 264760, 264448, 264765, 264688, 60170615, 18108374, 20281152, 264636, 52644332
3008	80416248 (6015, 6016)			264905, 264593, 264766, 264636
3008	81213387 (6017, 6018)	Novel Protein sim. GBank gll3127193 (AF062389) - kidney-specific protein [Rattus norvegicus]	Contains protein domain (PF05051) - synthase AMP-binding enzyme	52646942, 58182575, 22278995, 22278996, 264259, 29331825, 29331828, 29331827, 29331828, 35696052, 264508, 264509, 264907, 56182435, 264511, 265007, 264512, 265008, 264757, 264758, 55812038, 264759, 33109954, 21906754, 265010, 265011, 264600, 265017, 265018, 265019, 264760, 18108351, 264288, 264369, 21908764, 21906765, 21908767, 55811957, 265020, 265021, 264691, 18108368, 27486262, 20281149, 18108370, 55811576, 264637, 264556, 264557, 18108381, 264558, 56182323, 264559, 18108385, 18108388, 22278002, 264486
3010	95317217 (6019, 6020)	Novel Protein sim. GBank gll4927370[gb]AAD33084.1[AF067972] DNA cytosine methyltransferase 3 alpha [Homo sapiens]	Contains protein domain (PF01923) - UNCLASSIFIED Protein of unknown function	264686, 264687, 21906767, 21906769, 55811957, 22278995, 35695917, 22278996, 22278997, 265020, 265021, 60170615, 264692, 33657023, 29331822, 264693, 18108364, 29331824, 33657109, 60432289, 29331827, 27486261, 29331828, 264508, 264909, 55811576, 35695855, 265008, 264556, 60433438, 83373044, 18108387, 65274727, 60432113, 265017, 22279000, 265019, 264564, 264682, 264764
3011	94323597 (6021, 6022)	Novel Protein sim. GBank gll5052319[gb]AAD38501.1[AF118838] c1inn; adult-onset type II cirrulinemia protein [Homo sapiens]	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	35696052, 58182435, 264758, 21908754, 265018, 264760, 264762, 18108351, 264682, 264448, 21906766, 65274620, 18108374, 264482, 264564
3012	87753087 (6023, 6024)		UNCLASSIFIED	263972

3013	91238789 (6025, 6026)	Novel Protein sim. GBank gij3702286 (AC005787) - R33374_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor	264488, 263894, 35696286, 22278997, 264259, 29331824, 60424289, 66714117, 35696052, 264905, 264908, 264907, 264908, 264909, 56182435, 264511, 264512, 264910, 264591, 264592, 264593, 264594, 33657402, 60433438, 264595, 264596, 55812038, 264758, 33109954, 21908754, 265010, 265018, 264604, 264760, 264682, 264683, 264764, 264369, 264288, 264765, 264768, 264686, 264768, 264687, 21908787, 35695917, 265020, 33657023, 264692, 264693, 33657109, 264628, 264629, 55811578, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 264553, 264555, 264556, 264557, 264760
3014	79877263 (6027, 6028)	Novel Protein sim. GBank gij3878374[emb]CAA93081] - (Z68879) Similarity to Yeast Chl12p protein (PIR Acc. No. S54453); cDNA EST EMBL:D27950 comes from this gene; cDNA EST EMBL:D27949 comes from this gene; cDNA EST EMBL:D33447 comes from this gene; cDNA EST EMBL:D33316 comes from...		ATPase_associated	
3015	86995465 (6029, 6030)				22278995, 22278996, 22278997, 264259, 29331824, 29331828, 264908, 265007, 265008, 264910, 265011, 265017, 265019, 264691, 33657109, 18108370, 35695855, 264556, 264554
3016	87759945 (6031, 6032)	Novel Protein sim. GBank gij1168819[sp]P41733[CC91_YEAST - CELL DIVISION CONTROL PROTEIN 91		UNCLASSIFIED	52644507, 52646842, 56994075, 52645080, 29331822, 29331824, 35696052, 33656970, 52644045, 264598, 33657084, 265017, 265019, 52644229, 21906767, 35695917, 52644150, 33657023, 33657109, 27486261, 27486262, 27486284, 33657349, 27486265, 35695763, 35695855, 87168518
3017	95011154 (6033, 6034)	Novel Protein sim. GBank gij4586658[dbj]BAA76851.1] - (AB023224) KIAA1007 protein [Homo sapiens]			264488, 18108397, 22278996, 35696286, 22278998, 264259, 29331822, 60432289, 264908, 29331830, 264909, 56182435, 265006, 265007, 265008, 265009, 264591, 60433356, 60433438, 52646317, 21908754, 55811386, 265010, 265011, 87168559, 265017, 265018, 265019, 264288, 264687, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 65274620, 52645129, 33657109, 33657182, 18108370, 263972, 18108374, 264631, 52644332, 83373044, 18108385, 18108388, 56526486, 87168518, 264404, 60432113, 22279000, 264567

3018	11073891 (6035, 6036)				264558	
3019	94148231 (6037, 6038)	Novel Protein sim. GBank glj3219332 (AC004020) - Unknown gene product [Homo sapiens]			264569, 52644507, 18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 264808, 56182435, 265007, 265008, 60432229, 264593, 60433356, 55812038, 21906754, 87188474, 265011, 87188559, 265017, 265018, 265019, 264681, 18108351, 264448, 264682, 264683, 18108354, 264685, 264687, 264689, 21908766, 21906768, 21906769, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 52645129, 33657349, 264629, 65274791, 264634, 52644332, 56182323, 18108385, 87188518, 22279000, 22279002, 264563	oncogene
3020	94318251 (6039, 6040)	Novel Protein sim. GBank glj3414809 (AF061529) - /js [Mus musculus]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)		264488, 263994, 35696286, 264259, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 80174839, 264600, 264603, 264760, 264762, 264882, 264783, 264764, 264288, 264369, 264766, 264687, 264688, 264769, 55811957, 35695917, 33657023, 264628, 35696423, 35695855, 264630, 264632, 264634, 264635, 264636, 264637, 264556, 264557, 264638, 264639, 83373044, 18108385, 264584, 264587, 264486	ATPase-associated
3021	80478512 (6041, 6042)	Novel Protein sim. GBank glj3880889[emb]CAB090051 - (Z9559) cDNA EST yk236d4.5 comes from this gene; cDNA EST EMBL-C13455 comes from this gene; cDNA EST yk329g6.5 comes from this gene; cDNA EST CEMSH45R comes from this gene [Caenorhabditis elegans]			264769, 264629, 264482	
3022	87718500 (6043, 6044)				264259, 28331826, 28331828, 264288, 264566	UNCLASSIFIED
3023	95305484 (6045, 6046)	Novel Protein sim. GBank glj416592[sp]P32323JAGAI_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR	Contains protein domain (PF00614) - Phospholipase D. Active site motif		264488, 22278995, 35696286, 22278997, 29331828, 35696052, 264907, 29331830, 52644045, 56182435, 60432229, 264592, 60433356, 60433438, 264689, 21908767, 55811957, 35695917, 265021, 18108376, 263978, 264635, 264558, 22279000, 60432049, 264760, 21906769, 55811957, 35695917, 264690, 264555, 264559, 264593, 55811576	UNCLASSIFIED
3024	86675305 (6047, 6048)					UNCLASSIFIED
3025	65706629 (6049, 6050)	Novel Protein sim. GBank glj295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]				

3026	87643662 (6051, 6052)	Novel Protein sim. GBank gij3024052[sp P97924 KARI_RAT - KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)]		UNCLASSIFIED	22278986, 22278987, 264490, 29331825, 264111, 265007, 60170831, 265010, 87168559, 265019, 21908765, 28148627, 263987, 20281149, 20281069, 263975, 293977, 20281071, 58528486, 22279000, 18108394, 22278996, 22278998, 35696286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264907, 29331830, 264908, 264909, 264510, 265007, 265008, 265009, 264910, 33657402, 264596, 21906754, 265010, 265011, 87168559, 264600, 265018, 18108351, 264682, 264683, 264764, 264288, 264685, 264687, 264769, 264689, 21908765, 21908766, 21908767, 21908768, 21908769, 29148629, 35695917, 265020, 265021, 265022, 52844150, 264692, 33657023, 264693, 52645129, 33657109, 27486281, 18108374, 55811576, 35696423, 65274791, 264636, 264556, 264557, 264638, 60170394, 264639, 264558, 83373044, 18108385, 56526486, 22279000, 22279002, 22278985, 22278986, 22278987, 22278989, 284259, 29331824, 29331827, 35696052, 264908, 265007, 265008, 265009, 60170831, 21908754, 265011, 87168559, 265018, 264762, 264683, 264765, 264689, 21908765, 21908768, 21908769, 29148629, 35695917, 265021, 265022, 33657109, 27486265, 264628, 264629, 18108374, 35696423, 35695855, 264638, 60170394, 22279000, 22279002, 264482, 264584
3027	94844563 (6053, 6054)	Novel Protein sim. GBank gij4929847[gb AAD34084.1 AF15184 - (AF151847) CGI-89 protein (Homo sapiens)]	Contains protein domain (PF01528) - DHHC zinc finger domain	UNCLASSIFIED	22278986, 22278987, 22278989, 29331827, 264905, 264509, 264908, 264510, 264511, 264512, 87168474, 265019, 18108351, 21908768, 264534, 264690, 264893, 263989, 18108370, 284558, 22279000, 22279002, 264482
3028	94231997 (6055, 6056)	Novel Protein sim. GBank gij3080521[emb CAA18650] - (AL022599) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278986, 22278987, 22278989, 29331827, 264905, 264509, 264908, 264510, 264511, 264512, 87168474, 265019, 18108351, 21908768, 264534, 264690, 264893, 263989, 18108370, 284558, 22279000, 22279002, 264482
3029	87618284 (6057, 6058)			UNCLASSIFIED	22278986, 22278987, 22278989, 29331827, 264905, 264509, 264908, 264510, 264511, 264512, 87168474, 265019, 18108351, 21908768, 264534, 264690, 264893, 263989, 18108370, 284558, 22279000, 22279002, 264482
3030	87544928 (6059, 6060)	Novel Protein sim. GBank gij3757726[emb CAA18782] - (AL022727) dJ8019.1 (olfactory receptor-like protein [hs6M1-1]) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	Im7	22278986, 22278987, 22278989, 29331827, 264905, 264509, 264908, 264510, 264511, 264512, 87168474, 265019, 18108351, 21908768, 264534, 264690, 264893, 263989, 18108370, 284558, 22279000, 22279002, 264482
3031	91677853 (6081, 6062)	Novel Protein sim. GBank gij4530587[gb AAD22105.1] - (AF132000) TADA1 protein [Homo sapiens]		UNCLASSIFIED	22278986, 22278987, 22278989, 29331827, 264905, 264509, 264908, 264510, 264511, 264512, 87168474, 265019, 18108351, 21908768, 264534, 264690, 264893, 263989, 18108370, 284558, 22279000, 22279002, 264482

3032	94130124 (6063, 6064)	Novel Protein sim. GBank gij1019951 (U37429) - similar to M. musculus MERS and other AHPC/TSA proteins [Caenorhabditis elegans]	Contains protein domain (PF00534) - synthase Glycosyl transferases group 1	22278996, 35696286, 264259, 29331824, 29331828, 264907, 29331830, 264756, 33109954, 87168474, 87168559, 265019, 264288, 21906769, 265021, 264693, 35696423, 35695855, 264636, 56182323, 83373044, 87168518
3033	95308321 (6065, 6066)	Novel Protein sim. GBank gij5031573 [ref] NP_005712.1 pACTR - ARP3 (actin-related protein 3, yeast) homolog	Contains protein domain (PF00022) - struct Actin	35696286, 264259, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265008, 264591, 21908754, 265010, 265019, 264681, 264369, 264768, 21906764, 21906768, 35695917, 33657023, 264628, 35695855, 264632, 264635, 264639, 264482, 264563
3034	80415373 (6067, 6068)		UNCLASSIFIED	264906, 264907, 264510, 264592, 265010, 264762, 264766, 264637, 264638, 264486
3035	91220682 (6069, 6070)	Novel Protein sim. GBank gij3738207 [emb] [CAA21262] - (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe]	UNCLASSIFIED	264636
3036	91718323 (6071, 6072)	Novel Protein sim. GBank gij728837 [sp] P39194 [ALU7_HUMAN - III] ALU SUBFAMILY SQ WARNING ENTRY IIII	kinase	264807, 33657402, 265021
3037	95307434 (6073, 6074)	Novel Protein sim. GBank gij4406590 [gb] AAD20040] - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]		265017
3038	95421807 (6075, 6076)	Novel Protein sim. GBank gij5360093 [gb] AAD42865.1 [AF155099] NY-REN 18 antigen [Homo sapiens]	Contains protein domain (PF00627) - UNCLASSIFIED UBA domain	22278996, 22278997, 264259, 264905, 265007, 265009, 60433356, 21906754, 265018, 265019, 18108351, 264687, 21906765, 265020, 265021, 65274620, 27486262, 264636, 56182323, 18108385, 22279000
3039	87332257 (6077, 6078)	Novel Protein sim. GBank gij4757128 [emb] [CAB42094.1] - (AJ238717) ZRP protein [Rattus norvegicus]	UNCLASSIFIED	35696286, 29331828, 264109, 264110, 264511, 265007, 21906754, 265011, 264681, 264683, 264687, 21906768, 264691, 18108370, 263972, 264629, 18108374, 263977, 35696423, 264584, 18108391, 264692, 264558, 18108382, 18108385, 264587
3040	80833517 (6079, 6080)	Novel Protein sim. GBank gij4884278 [emb] [CAB43247.1] - (AL050037) hypothetical protein [Homo sapiens]		
3041	88312357 (6081, 6082)	Novel Protein sim. GBank gij3876073 [emb] [CAB04122.1] - (ZB1505) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene; cDNA EST EMBL:D28024 comes from this gene; cDNA EST EMBL:D33210 comes from this gene; cDNA EST EMBL:D33441 comes from this ...	UNCLASSIFIED	56994075, 22278997, 22278998, 29331827, 33656970, 33109854, 21906754, 87168559, 264600, 264683, 21906765, 21906768, 22279002
3042	85749402 (6083, 6084)	Novel Protein sim. GBank gij790236 (U21156) - sarcolemmal associated protein-2 [Oryctolagus cuniculus]	glycoprotein	264636

3043	87773026 (6085, 6086)	Novel Protein sim. GBank gi 540656 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	35696286, 60424269, 35696052, 264508, 264905, 68712502, 56182435, 55811386, 52644296, 55811150, 35695917, 60170615, 33657109, 18108374, 264634, 60431850
3044	87646182 (6087, 6088)	Novel Protein sim. GBank gi 4104922 (AF042276) - 0251 homolog [Pseudomonas putida]	Contains protein domain (PF01209) - ubiE/COQ3 methyltransferase family	glycoprotein	22278996, 22278998, 22278999, 29331824, 56182435, 264511, 265007, 60170831, 60432229, 60433358, 33109954, 18108351, 264288, 35695917, 18108388, 18108370, 60170394
3045	94127598 (6089, 6090)	Novel Protein sim. GBank gi 4589680 dbj BAA76859.1  - (AB023232) KIAA1015 protein [Homo sapiens]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	dna_ma_bind	264488, 264259, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264511, 265006, 264591, 264593, 33109954, 264604, 264784, 264683, 264288, 264766, 264768, 21908765, 21908768, 55811957, 35695917, 27486262, 18108370, 264628, 18108374, 35695955, 264630, 264632, 264635, 264563, 264564, 264566
3046	88098247 (6091, 6092)			UNCLASSIFIED	22278999, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264906, 52646317, 55811957, 60432113, 22278000, 22279002, 264482, 264564
3047	95089924 (6093, 6094)			UNCLASSIFIED	264488, 22278996, 22278997, 22278999, 29331824, 29331825, 56182435, 264511, 265008, 265009, 265011, 265017, 264768, 21908768, 21908769, 35695917, 52644150, 33657349, 65274791, 35695855, 264555, 60432113, 22279000, 264566
3048	87629419 (6095, 6096)	Novel Protein sim. GBank gi 4588034 gb AAD25962.1 AF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	264102, 28148784
3049	88229955 (6097, 6098)	Novel Protein sim. GBank gi 5454158 ref NP_006286.1 pVARS - valyl-IRNA synthetase 1	Contains protein domain (PF01406) - (RNA synthetases class I (C))	UNCLASSIFIED	22278997, 29331826, 264907, 284758, 87168559, 265018, 264448, 21908766, 265020, 33657109, 35695855, 60432113, 22279000
3050	87643679 (6099, 6100)	Novel Protein sim. GBank gi 4589642 dbj BAA76843.1  - (AB023216) KIAA0999 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331825, 264909, 265007, 264512, 265019, 264288, 21908766, 265020, 264893, 18108385, 56526466, 87168518, 22279002, 264566
3051	87750599 (6101, 6102)				22278997, 264595, 265019, 264288, 264693, 87168518
3052	57108030 (6103, 6104)	Novel Protein sim. GBank gi 117528 sp P14755 CRYL_RABIT - LAMBDA-CRYSTALLIN		dehydrogenase	264534

3053	95350373 (6105, 6106)	Novel Protein sim. GBank gij3947613jemb CAA19465.1  - (AL023828) cDNA EST EMBL:M89008 comes from this gene; cDNA EST yk282d3.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56181686, 22278995, 35696286, 22278998, 264259, 60432289, 265008, 265009, 60433438, 21908754, 265010, 87168559, 284603, 265018, 265019, 264763, 264764, 264288, 21906765, 21906766, 21908768, 21908769, 35695917, 18108374, 35696423, 264638, 56182323, 22279000, 264563
3054	86843510 (6107, 6108)	Novel Protein sim. GBank gij1076211 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	35696286, 35696052, 29331830, 264908, 264909, 264512, 284910, 265017, 264604, 264766, 265020, 33657109, 264628, 35695855, 264638, 264564, 264566, 264486
3055	95350537 (6109, 6110)	Novel Protein sim. GBank gij4680655 gb AAD27717.1 AF13294 - (AF132942) CGI-08 protein [Homo sapiens]		transport	60424178, 65274572, 56182575, 35696286, 22278998, 22278999, 60432049, 264259, 60424289, 60432289, 35696052, 58182435, 265006, 265008, 60170831, 60432229, 60431735, 60433356, 264594, 60433438, 21906754, 55811386, 265011, 87168559, 265019, 18108351, 264683, 264288, 264369, 264689, 21906768, 55811957, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 60431528, 18108374, 55810764, 55811576, 35696423, 65274791, 264636, 60431850, 18108381, 56182323, 60170394, 18108385, 60432113, 264564, 264565, 264566
3056	91661636 (6111, 6112)	Novel Protein sim. GBank gij728837 sp P39194 ALU7_SQ WARNING ENTRY IIII		glycoprotein	264488, 264569, 18108394, 52646842, 22278997, 22278998, 22278999, 264259, 66714117, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264808, 264909, 265006, 264512, 265007, 265008, 265009, 264910, 33657402, 55812038, 264596, 264758, 285010, 265011, 265017, 265019, 264760, 18108351, 264762, 264763, 264764, 284288, 264766, 264687, 18108357, 264768, 264769, 264689, 21908765, 21908766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264691, 264693, 33657109, 18108370, 264628, 264629, 18108374, 55811578, 35696423, 35695855, 284630, 284631, 264632, 264634, 264635, 264636, 264637, 264638, 18108381, 83373044, 18108385, 22279000, 22279002, 264563, 264564, 264565, 264566, 264488, 264567



3057	95412746 (6113, 6114)	Novel Protein sim. GBank gij3878119[embjCAA88860] - (Z49068) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...		struct	264508, 264905, 264907, 264908, 264909, 264510, 264512, 264910, 264592, 264594, 264767, 18108374, 264635, 264555, 264637, 264639, 264563, 264564, 264565, 264486
3058	79646226 (6115, 6116)	Novel Protein sim. GBank		UNCLASSIFIED	264593
3059	87629425 (6117, 6118)	gij4588034[gbjAAD25962.1] (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HCA type (RING finger)	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264490, 264259, 29331824, 29331825, 29331827, 35696052, 29331828, 265007, 60433438, 265017, 265018, 265019, 264681, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906769, 29148629, 29148784, 265022, 52644150, 18108370, 264636, 18108385, 264563, 264567
3060	79346691 (6119, 6120)			UNCLASSIFIED	264567
3061	87740984 (6121, 6122)			UNCLASSIFIED	264112, 52644296, 21906768, 33657023, 263974, 18108385
3062	87618465 (6123, 6124)	Novel Protein sim. GBank gij4454690[gbjAAD20963] - (AF070857) glutathione S-transferase subunit 13 homolog [Homo sapiens]		transferase	264908, 265008, 18108351, 264566
3063	80078023 (6125, 6126)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	18108359, 264558
3064	91241526 (6127, 6128)	Novel Protein sim. GBank gij4240315[dbjBAA74936.1] - (AB020720) KIAA0913 protein [Homo sapiens]	Contains protein domain (PF00403) - Heavy-metal-associated domain	UNCLASSIFIED	52646355, 52646842, 65274572, 56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 264259, 60432049, 29331824, 66714117, 264508, 264907, 264908, 56182435, 265009, 60432229, 60433438, 55812038, 52644296, 265018, 264682, 264288, 264686, 264768, 264687, 52644229, 264689, 21906768, 264691, 264692, 264693, 18108370, 18108377, 55811576, 264638, 56182323, 264558, 264639, 18108385, 22279000, 22279002
3065	91639201 (6129, 6130)	Novel Protein sim. GBank gij5656743[gbjAAD45960.1] (AC005067) Supported by Human EST H08032.1 (NID:g872854), mouse EST AAB70042.1 (NID:g2985487), and gencan [Homo sapiens]		UNCLASSIFIED	22278996, 22278998, 264093, 264094, 264095, 29331824, 60424269, 66714117, 264100, 264907, 265007, 264591, 60432229, 264593, 265011, 265019, 18108351, 264768, 264767, 21906765, 21906766, 264693, 20281069, 22279000, 22279002, 264482, 264566, 264567

3066	91224437 (6131, 6132)	Novel Protein sim. GBank gi 4884268 emb CAB43245.1  - (AL050028) hypothetical protein [Homo sapiens]	UNCLASSIFIED	18108397, 22278995, 56994075, 22278996, 264905, 66712502, 265006, 264512, 284910, 264758, 60174639, 284760, 18108351, 264764, 264683, 18108359, 264692, 18108364, 18108368, 18108370, 18108377, 18108379, 60170394, 264567
3067	95422551 (6133, 6134)	Novel Protein sim. GBank gi 4689258 gb AAD27832.1 AF12185 - (AF12185) sorting nexin 9 [Homo sapiens]	Contains protein domain (PF00787) - struct PX domain	264488, 264489, 35696286, 22278996, 56994075, 264259, 28331822, 28331825, 35696052, 28331828, 284508, 284905, 264508, 264906, 264907, 264908, 264909, 264112, 264510, 264511, 264512, 265008, 265009, 284910, 264591, 264592, 264583, 264594, 264757, 264585, 264586, 264758, 265010, 265011, 87168559, 284601, 284602, 264603, 264604, 264605, 265019, 264780, 264762, 284448, 264763, 284764, 284288, 264369, 284766, 264768, 264687, 264769, 264689, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 264534, 52644150, 264691, 33657023, 264693, 264628, 60431528, 283977, 35695855, 264630, 284631, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 56526486, 87168518, 22279000, 22279002, 264563, 264483, 264564, 264565, 264566, 264567, 264486
3068	85360651 (6135, 6136)	Novel Protein sim. GBank gi 3878119 emb CAA88860  - (Z49066) similar to GTP-binding protein; cDNA EST	Contains protein domain (PF01926) - struct GTPase of unknown function	22278996, 56994075, 22278998, 22278999, 264259, 264107, 264905, 28331830, 52644045, 264110, 60170831, 264592, 264594, 33657402, 21906754, 33109954, 87168474, 87168559, 265017, 284448, 264764, 264683, 264766, 52644229, 21906765, 21906766, 21906768, 21906769, 60170815, 33657023, 18108370, 18108376, 264634, 264557, 60170394, 56162323, 18108385, 87168518, 22279000, 284482
3069	95412753 (6137, 6138)	EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...		

3070	94319173 (6139, 6140)	Novel Protein sim. GBank gll3877788[emb](CAB05527) - (Z83110) cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST yk472b5.5 comes from this gene; cDNA EST yk468c10.3 comes from this gene; cDNA EST yk468c10.5 comes from this gene; cDNA EST EM...		synthase	264488, 22278994, 22278995, 22278996, 56894075, 22278997, 22278999, 264259, 29331822, 29147620, 29331824, 66714117, 29331826, 29146498, 29146499, 66712502, 29331830, 52644045, 58182435, 264511, 265007, 264512, 264910, 60170831, 264592, 264758, 33108954, 21906754, 87168474, 265019, 18108351, 264448, 264683, 264288, 52644229, 264689, 21906765, 21906766, 21906787, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 264691, 33657023, 27486261, 27486264, 264628, 18108370, 18108377, 55811578, 35695855, 264634, 264635, 18108381, 60170394, 56182323, 264556, 83373044, 18108385, 18108387, 56526486, 264404, 264563, 264566
3071	94325573 (6141, 6142)	Novel Protein sim. GBank gll4502425[ref](NP_001709.1)pBMP6 - bone morphogenetic protein 6 precursor	Contains protein domain (PF00085) - Igf Thioedoxin		264488, 65274572, 18108398, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 66714117, 29331826, 35698052, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 52644045, 58182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432228, 264592, 60433356, 33657402, 60433438, 33108954, 52644296, 87168474, 265010, 265017, 264681, 264288, 264685, 264766, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 263971, 18108374, 18108377, 35696423, 55811576, 65274791, 35695855, 264630, 264635, 264636, 264557, 60170394, 83373044, 60432113, 22278900, 22278902, 264563, 264564, 264565, 264566, 264567, 56182575, 29331822, 29331824, 29331825, 29146498, 264908, 52644045, 56182435, 265009, 60433438, 55812038, 18108351, 264683, 264369, 52644229, 52644150, 33657023, 264693, 33657109, 18108374, 55811576, 65274791, 264555, 56182323, 60432113, 264564
3072	95115892 (6143, 6144)	Novel Protein sim. GBank gll1263289 (U47856) - fibroin-4 [Araneus diadematus]		transcriptfactor	

3073	86147248 (6145, 6146)	Novel Protein sim. GBank gij134840 sp P22528 CORB_HUMAN - CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN)		UNCLASSIFIED	264769
3074	88089351 (6147, 6148)	Novel Protein sim. GBank gij3419847 (AC004982) - similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens]		UNCLASSIFIED	264488, 265019, 264448, 264288, 21906767, 264693, 18108368, 18108370, 18108374, 264597
3075	88095752 (6149, 6150)	Novel Protein sim. GBank gij4557349 ref NP_000456.1 pBARD - BRCA1 associated RING domain 1	Contains protein domain (PF00023) - Ark repeat	homeobox	264509, 264907, 264689, 264693, 56526486
3076	87819219 (6151, 6152)			UNCLASSIFIED	18108398, 29331822, 29331827, 60432229, 265017, 264691, 264693
3077	88734277 (6153, 6154)	Novel Protein sim. GBank gij3023956 sp Q00808 HET1_PODAN - VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	65274572, 35696052, 264511, 60170831, 87168474, 264369, 35695917, 33657182, 27488264, 33657349, 35695763, 35695855, 264639
3078	88089355 (6155, 6156)	Novel Protein sim. GBank gij3900850 (AC004994) - similar to KIAA0600; similar to d1026456 (PID:g3043724) [Homo sapiens]			22279002
3079	87821893 (6157, 6158)	Novel Protein sim. GBank gij3875410 emb CAB02876  - (Z81052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene [Caenorhabditis elegans]		transport	29331824, 29331826, 264758, 55811386, 265017, 55811150, 52644229, 21906768, 265020, 265021, 264693, 18108370, 264631, 52644332, 22279002
3080	95288274 (6159, 6160)	Novel Protein sim. GBank gij5257221 gb AAD41265.1  - (AF117887) protein arginine methyltransferase [Mus musculus]		interferon	264488, 52644507, 22278998, 22278998, 264490, 264259, 29331824, 68714117, 29331825, 29331826, 29331827, 29331828, 29148499, 264508, 264905, 264828, 52644045, 56182435, 285006, 264591, 264596, 21908754, 60174639, 265010, 264682, 264448, 264763, 264683, 264764, 264288, 264685, 264769, 264688, 264689, 21906765, 21906767, 21906769, 55811957, 35695917, 265020, 60170615, 52644150, 264682, 33657023, 264693, 65274620, 33657109, 27486261, 35695763, 264628, 18108370, 65274791, 264558, 56182323, 60170394, 264482, 264565, 264484
3081	88084864 (6161, 6162)	Novel Protein sim. GBank gij728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	18108388, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264810, 264595, 264758, 265011, 265018, 264760, 264761, 264763, 264764, 18108354, 264685, 264766, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264555, 264638, 18108382, 18108385, 264563, 264565, 264566
3082	80310121 (6163, 6164)				264764, 55811957, 264555, 264564

3083	88095756 (6165, 6166)	Novel Protein sim. GBank gij868241 (U29488) - C56C10.3 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264259, 29331824, 264106, 265008, 264591, 264592, 21906754, 264288, 264767, 21906768, 21906769, 29148784, 264691, 264632, 22279000
3084	87448568 (6167, 6168)	Novel Protein sim. GBank gij476774 (prijA37475 - probable structural component p38 - borna disease virus)			22278995, 60432289, 35696052, 264905, 264906, 264907, 284908, 264909, 265006, 265007, 264910, 264593, 264595, 264758, 264369, 264288, 264766, 35695917, 265020, 18108374, 35696423, 264631, 264556, 264555, 264566, 264567, 264486
3085	87795781 (6169, 6170)	Novel Protein sim. GBank gij2565057 (U80741) - CAGH44 [Homo sapiens]		UNCLASSIFIED	265011, 264681
3086	87769942 (6171, 6172)	Novel Protein sim. GBank gij3894189 (AC005662) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	22278998, 264092, 264259, 29331822, 29331825, 264108, 264112, 18108351, 264687, 263967, 263974, 55810764, 263981, 18108385, 264487
3087	87462988 (6173, 6174)				52846385, 56994075, 22278997, 22278998, 29331824, 29331825, 35696052, 60433438, 33109954, 21906754, 52646317, 265017, 264682, 264369, 264684, 21906767, 21906768, 265020, 264691, 33657023, 33657109, 52645129, 33657182, 27488262, 35695855, 87168518
3088	91224441 (6175, 6176)	Novel Protein sim. GBank gij3355304 (AF001549) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264591
3089	95361242 (6177, 6178)	Novel Protein sim. GBank gij4689146 (gb/AAD27782.1) (AF07704) lambda-crystallin [Homo sapiens]	Contains protein domain (PF00725) - dehydrogenase 3-hydroxyacyl-CoA dehydrogenase		18108397, 65274572, 56182575, 56181686, 56994075, 35696286, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 29331828, 264907, 29331830, 264909, 56182435, 264510, 265007, 60170831, 60432229, 21906754, 55811386, 265017, 265018, 265019, 264760, 55811150, 264288, 264766, 56181562, 21906765, 21906766, 21906767, 21906768, 265021, 60170615, 27486262, 18108370, 60431528, 35696423, 264558, 264559, 60432113, 264486

3080	95342371 (6178, 6180)	Novel Protein sim. GBank gi 1354050 (U47024) - MEM3 [Mus musculus]		UNCLASSIFIED	60424179, 52845156, 65274572, 56182575, 56181686, 22278995, 35698286, 56994075, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 29331828, 35698052, 33656970, 264908, 264908, 52644045, 264828, 265008, 265007, 265008, 60170831, 60432229, 60433358, 33657402, 55812038, 264758, 21906754, 33109954, 52846317, 55811386, 52844296, 87168474, 265011, 87168559, 265017, 265018, 265019, 55811150, 18108351, 264681, 264448, 264288, 264369, 18108357, 264768, 52644229, 56181562, 21906764, 21908765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265022, 60170615, 264690, 52844150, 284691, 33657023, 18108365, 65274820, 33657109, 18108368, 33657182, 27486281, 27486285, 35695763, 18108374, 18108376, 55810764, 35698423, 55811576, 65274781, 35695855, 264557, 56182323, 83373044, 18108387, 18108388, 87168518, 22278000, 22278002, 264563, 264482
3091	95317424 (6181, 6182)	Novel Protein sim. GBank gi 3873932 emb CAB01859  - (Z79598) Similarity to Bovine aspartyl beta hydroxylase (TR:G162694); cDNA EST EMBL:D27916 comes from this gene; cDNA EST EMBL:D27915 comes from this gene; cDNA EST EMBL:D64681 comes from this gene; cDNA EST EMBL:D68138 comes f...		UNCLASSIFIED	35696286, 29331822, 35696052, 264508, 264509, 264905, 264906, 264908, 264909, 264510, 264758, 265010, 265011, 264683, 264685, 264768, 264768, 264769, 264683, 264628, 35696423, 35695855, 264632, 264635, 264639, 264482, 264563, 264486

3092	95314592 (6183, 6184)	Novel Protein sim. GBank gi 1710756 sp P15880 RS2_HUMAN - 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)	Contains protein domain (PF00333) - Ribosomal protein S5	- ribosomal prot	264488, 60424179, 18108386, 22278995, 56994075, 22278998, 35698288, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 29146488, 29146499, 264508, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264113, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264591, 264592, 60431735, 264593, 264594, 60433438, 264595, 264758, 21906754, 265010, 265011, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 265019, 264760, 264762, 264681, 18108351, 264763, 264682, 264448, 264764, 264683, 264288, 264369, 264765, 264766, 264686, 264767, 264687, 264768, 264769, 264688, 21906764, 264689, 21906765, 21908766, 21906767, 21906768, 21906769, 29148629, 29148784, 35695917, 265020, 265021, 264534, 60170815, 264690, 264691, 264682, 65274620, 33657109, 27486262, 264628, 264629, 18108374, 263978, 18108377, 35696423, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264557, 264558, 264639, 60170394, 18108385, 264259, 29331824, 35696052, 264905, 265006, 60432229, 60431735, 264684, 264369, 264288, 264766, 21906767, 35698423, 83373044, 18108385
3093	94318457 (6185, 6186)	Novel Protein sim. GBank gi 5002587 emb CAB44347.1  - (Y17454) LSFR1 protein [Homo sapiens]		UNCLASSIFIED	
3094	94316675 (6187, 6188)	Novel Protein sim. GBank gi 400734 sp P31044 PBP_RAT - PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (23 KD MORPHINE-BINDING PROTEIN) (P23K)	Contains protein domain (PF01161) - Phosphatidylethanolamine-binding protein	collagen	18108398, 264259, 60432289, 29331827, 264511, 264763, 264288, 264767, 265022, 264691, 264693, 65274791, 56182323, 264564, 264565

3095	8484162 (6189, 6190)	Novel Protein sim. GBank g 4877759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]	Contains protein domain (PF01454) - MAGE family	UNCLASSIFIED	18108397, 56182575, 22278995, 35696286, 56994075, 22278997, 22278999, 264259, 60432049, 66714117, 29331825, 60432289, 35696052, 33856970, 29146499, 264508, 264905, 264509, 29331830, 264909, 264510, 264511, 264512, 265007, 265008, 265009, 60170831, 264758, 21906754, 85658542, 265010, 265011, 87188559, 265017, 265018, 265019, 264760, 264681, 264682, 264683, 264764, 264369, 264288, 264686, 264768, 264769, 264688, 21906765, 21906766, 21906767, 55811957, 35695917, 265020, 265021, 265022, 52644150, 264691, 264692, 33657023, 264683, 263872, 18108376, 55811576, 35696423, 264952, 60170394, 264639, 83373044, 18108385, 18108387, 65274727, 87188518, 60432113, 264482, 264563, 264564, 264566, 264487, 18108391 22278995, 22278996, 22278997, 22278998, 29331824, 29331825, 29331826, 29331827, 33656970, 264905, 264908, 265008, 264910, 33657402, 265011, 265017, 265018, 264369, 21906766, 21906767, 21906768, 35695917, 265020, 60170615, 264691, 264692, 264693, 27486261, 27486262, 18108370, 60431528, 264634, 264636, 264639, 22279000, 264566 264488, 29331822, 29331825, 60432289, 29331826, 35696052, 29331828, 29331830, 264594, 55812038, 33109954, 33657084, 87168474, 87168559, 52644229, 21906765, 21906767, 18108376, 35696423, 52644332, 264638, 60432113, 22279002
3096	87756128 (6191, 6192)	Novel Protein sim. GBank g 3882221 dbj BAA34470.1  - (AB018293) KIAA0750 protein [Homo sapiens]	Contains protein domain (PF00307) - struct Calponin homology (CH) domain		
3097	88264895 (6193, 6194)	Novel Protein sim. GBank g 4468288 emb CAB37981  - (AL022395) dJ273N12.1 (PUTATIVE protein based on EST matches) [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	
3098	80258024 (6195, 6196)				264634, 264637, 264565
3099	91243325 (6197, 6198)	Novel Protein sim. GBank g 303603 dbj BAA02145.1  - (D12621) cytochrome P-450L TBV [Homo sapiens]		cyto450	264488, 35696286, 29331822, 29331824, 29331825, 29331827, 265007, 265008, 265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 56182323, 22279002, 264563
3100	87602421 (6199, 6200)	Novel Protein sim. GBank g 1083764 pir B48013 - proline- rich proteoglycan 2 precursor, parolid - rat		UNCLASSIFIED	29331825, 60432289, 35696052, 264910, 60432229, 264592, 264286, 264693, 263967, 264635
3101	79602134 (6201, 6202)			UNCLASSIFIED	264908, 264693, 264628, 264630, 264632



3102	91220892 (6203, 6204)	Novel Protein sim. GBank gi 5305708 gb AAD41781.1 AF12853 - (AF128536) cytoplasmic phosphoprotein PACSIN2 [Homo sapiens]	Contains protein domain (PF00018) - struct SH3 domain	35696286, 22278996, 22278999, 29331827, 35698052, 264909, 264512, 265008, 60170831, 60433356, 33109954, 18108351, 264684, 264689, 21908767, 60170615, 264692, 33657023, 264638, 22279000, 264482, 264564 35695917, 264565
3103	90838004 (6205, 6206)	Novel Protein sim. GBank gi 464564 sp P35292 RB17_MOUSE - RAS-RELATED PROTEIN RAB-17	UNCLASSIFIED	
3104	87340633 (6207, 6208)	Novel Protein sim. GBank gi 5032207 ref NP_005696.1 ptSSC - tumor-suppressing STF cDNA 6	UNCLASSIFIED	264259, 264684, 264632, 33657182, 264558
3105	94148603 (6209, 6210)			22278987, 264259, 29331824, 35686052, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264511, 264910, 264591, 264594, 264758, 264760, 264681, 264762, 264764, 264288, 264768, 264768, 264687, 264769, 21906766, 21906768, 35695917, 33657023, 264692, 264693, 264628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 83373044, 264404, 22278002, 264563, 264565, 264566, 264486, 264567
3106	95361416 (6211, 6212)	Novel Protein sim. GBank gi 1938574 (U97190) - B0025.2 gene product [Caenorhabditis elegans]		22278996, 22278997, 22278998, 22278999, 264092, 264093, 264094, 26331822, 264906, 264907, 264908, 52644045, 56182435, 264112, 265008, 265009, 55812038, 265017, 265018, 264683, 264686, 264687, 264768, 52844229, 21906765, 21906768, 21906769, 55811957, 265020, 265022, 264690, 52644150, 264692, 264693, 18108370, 18108377, 55811576, 56182323, 18108385, 18108388, 22279000, 264563
3107	95343272 (6213, 6214)	Novel Protein sim. GBank gi 3341441 emb CAA768511 - (Y17794) winged-helix transcription factor [Gallus gallus]		22278995, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 264259, 29331822, 29331825, 29331826, 60432289, 29331827, 29331828, 33659970, 264105, 264512, 265009, 60433356, 60433438, 265011, 265017, 265018, 21906765, 21906768, 21906767, 21906769, 265021, 264691, 33657109, 27486261, 27486265, 18108370, 263972, 18108374, 55811576, 18108385, 56526488, 264482, 264487, 56182435, 264288, 264690, 264564
3108	87340635 (6215, 6216)	Novel Protein sim. GBank gi 5032207 ref NP_005696.1 ptSSC - tumor-suppressing STF cDNA 6	UNCLASSIFIED	

3109	94318461 (6217, 6218)	Novel Protein sim. GBank gjl5002587[emb]CAB44347.1] - (Y17454) LSR1 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	struct	264480, 264908, 265007, 264910, 264593, 264683, 264684, 264687, 21906767, 21906768, 264693, 18108370, 264629, 18108374, 264632, 264638, 22279000
3110	95090716 (6218, 6220)	Novel Protein sim. GBank gjl1076211[pir]S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	264488, 65274572, 22278995, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264908, 264510, 265006, 265007, 265008, 265009, 60432229, 33657402, 60433356, 265011, 87168559, 264600, 265017, 285018, 265019, 18108351, 264288, 264369, 21906768, 21906767, 21906768, 265020, 60170515, 264693, 65274620, 18108370, 264639, 18108384, 22279000, 264563, 18108390
3111	87754512 (6221, 6222)	Novel Protein sim. GBank gjl3282231 (U75454) - C2H2 type zinc finger protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264488, 18108388, 66712502, 265017, 265018, 265019, 264448, 21906767, 265020, 33657023, 18108365, 18108388, 35698423, 52644332, 18108385, 18108388
3112	88043639 (6223, 6224)	Novel Protein sim. GBank gjl3900848 (AC005023) - match to EST AA361117 (NID:2013436) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	
3113	88207098 (6225, 6226)	Novel Protein sim. GBank gjl245910 (AF005856) - anon2A5 [Drosophila yakuba]	Homeobox domain	lm7	18108397, 22278999, 264259, 29331824, 35698052, 264907, 264757, 60433438, 87168559, 264763, 264448, 18108354, 264288, 21906767, 21906769, 35695917, 264690, 264691, 264692, 264693, 18108365, 18108381, 18108384, 18108385, 18108388, 87168518, 22279000, 22279002
3114	79843167 (6227, 6228)	Novel Protein sim. GBank gjl4968270[gbl]AAB52261.2] - (U87002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E-value=1e-13, N=1 [C...	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	hydrolase	
3115	94117986 (6229, 6230)	Novel Protein sim. GBank gjl5032225[ref]NP_005676.1pWBSC - Williams-Beuren syndrome chromosome region 11		transcriptfactor	60424179, 56182575, 264259, 29331824, 60424269, 29331826, 68712502, 264510, 265007, 60431735, 60433356, 55812038, 55811386, 265019, 264288, 264689, 21906769, 264691, 33657023, 264693, 60431528, 263974, 60431850, 56182323, 264559, 22279000, 22279002
3116	79642855 (6231, 6232)			UNCLASSIFIED	264905, 264758, 21906784, 264690
3117	87771288 (6233, 6234)			UNCLASSIFIED	264510, 265011, 18108351, 264288, 264689, 264681, 18108368, 18108372, 263981, 264558, 264564

3118	94665848 (6235, 6236)	Novel Protein sim. GBank gij3880563jembjCAB01444.1] - (Z78018) predicted using GeneFinder; similar to serine/threonine kinase; cDNA EST yk353d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF000008) - tgf EGF-like domain	52645156, 52646842, 65274572, 56182575, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 264905, 264908, 29331830, 52644045, 56182435, 264510, 264511, 265007, 265008, 265009, 264757, 52646317, 21906754, 33657084, 52644286, 87168474, 87168559, 265017, 265018, 264605, 265019, 264762, 264448, 264882, 264684, 264288, 264766, 56181562, 21906765, 21906766, 21906768, 21906769, 265020, 265022, 264690, 52644150, 264691, 33657023, 264693, 33657109, 33657349, 264628, 18108370, 60431528, 18108374, 35696423, 65274791, 60170394, 83373044, 87168518, 22279000, 22279002, 264488, 265006, 264288
3119	85728786 (6237, 6238)		Contains protein domain (PF00328) - Histidine acid phosphatase	
3120	87344040 (6239, 6240)	Novel Protein sim. GBank gij5019819gbjAAD37863.1jAF14315 - (AF143152) putative NADH oxidoreductase complex I subunit [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264509, 264510, 264511, 264512, 264288, 264486
3121	94110735 (6241, 6242)	Novel Protein sim. GBank gij4501877jrelNP_001088.1lpACRj - acrosin		52844507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278996, 22278999, 264259, 29331824, 29331827, 35696052, 52644045, 265008, 52646317, 87168474, 87168559, 21906765, 52644150, 33657023, 18108374, 264637
3122	11814528 (6243, 6244)		UNCLASSIFIED	264638
3123	88083003 (6245, 6246)	Novel Protein sim. GBank gij2439517 (AC002563) - putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860) [Homo sapiens]	Contains protein domain (PF00780) - CNH domain	18108392, 29331822, 29331824, 29331825, 264905, 265007, 55812038, 265019, 18108351, 264682, 264288, 264766, 21906764, 21906765, 21906768, 21906769, 55811957, 18108365, 18108366, 27486265, 18108374, 18108381, 18108384, 22279000, 22279002, 264482
3124	87766898 (6247, 6248)		UNCLASSIFIED	264905
3125	91216607 (6249, 6250)	Novel Protein sim. GBank gij4980826jbiAAD35412.1jAE00171 - (AE001714) oxidoreductase, short chain dehydrogenase/reductase family [Thermotoga maritima]	Contains protein domain (PF00106) - short chain dehydrogenase	56181866, 264259, 66714117, 60432289, 29331826, 29331827, 264907, 264908, 264828, 265009, 60433356, 33657402, 60433438, 264758, 18108351, 264288, 29148827, 29148628, 33657023, 33657109, 18108382, 56526486

3126	95337205 (6251, 6252)			UNCLASSIFIED	22278999, 264490, 264259, 60432049, 29331822, 60432289, 29146498, 52644045, 56182435, 265009, 60433438, 265010, 87168559, 265017, 265018, 55811150, 264763, 264683, 264369, 264685, 29148629, 33657023, 264693, 33657109, 18108374, 55811576, 18108385, 60432113, 22279002, 35696286, 22278996, 22278999, 26331826, 264908, 60433438, 87168559, 264604, 21908765, 21906769, 33657023, 33657349, 264629, 18108374, 18108377, 22279000, 22279002
3127	91639233 (6253, 6254)	Novel Protein sim. GBank gj 2828280 emb CAA16694.1  - (AL021687) putative protein [Arabidopsis thaliana]			
3128	87674330 (6255, 6256)	Novel Protein sim. GBank gj 3885828 (AF090133) - lin-7-A [Rattus norvegicus]		misc_channel	22278996, 264259, 52644045, 265008, 21908754, 265017, 265018, 21906768, 18108376, 18108397, 22279000, 22279002
3129	87755412 (6257, 6258)	Novel Protein sim. GBank gj 3135273 (AC003058) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - kinase WD domain, G-beta repeat		56182575, 264259, 29331825, 29331828, 52644045, 56182435, 60433356, 264600, 264682, 264763, 264784, 264369, 264288, 264686, 55811957, 264692, 33657023, 33657109, 60432113, 264564, 264566, 264636
3130	14993960 (6259, 6260)	Novel Protein sim. GBank gj 3329465 (AF064553) - NSD1 protein [Mus musculus]			
3131	95351469 (6261, 6262)	Novel Protein sim. GBank gj 1848277 (U86136) - telomerase-associated protein TP-1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	56182575, 264259, 29331824, 264807, 56182435, 264594, 60433438, 55812038, 33109954, 21906754, 33657084, 87168474, 264448, 264766, 21906769, 55811957, 265020, 265021, 265022, 60170615, 33657023, 33657109, 33657182, 27486261, 33657349, 65274791, 60170394, 56182323, 83373044, 87168518, 264564

3132	95415459 (6263, 6264)	Novel Protein sim. GBank gi 4680647 gb AAD27713.1 AF13293 - (AF132938) CGI-03 protein [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	ubiquitin	52644507, 52646842, 52646365, 65274572, 56182575, 22278994, 22278995, 35698288, 5894075, 22278996, 22278997, 22278998, 22278999, 80432049, 52645080, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 28331828, 35696052, 264508, 52644045, 56182435, 264910, 60170831, 60432228, 80433356, 33657402, 55812038, 52646317, 21908754, 52644296, 85658542, 87168559, 285017, 265018, 265019, 264448, 264288, 264369, 52644229, 21906765, 21908766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 264682, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 18108374, 18108376, 55811576, 35695855, 18108385, 18108387, 56526486, 87168518, 60432113, 22278002
3133	87379414 (6265, 6266)	Novel Protein sim. GBank gi 4507613 ref NP_003738.1 pTNKS - TANKYRASE		polymerase	22278994, 22278998, 264905, 265008, 285007, 87168559, 264760, 21906767, 18108374, 22279000, 22278002, 264563 264595, 264369, 264685, 264628, 264566
3134	94649816 (6267, 6268)	Novel Protein sim. GBank gi 1729827 sp P54633 TALA_DICDI - FILOPODIN (TALIN HOMOLOG)			
3135	86389356 (6269, 6270)	Novel Protein sim. GBank gi 3093478 (AF012927) - fibrinogen-binding protein [Streptococcus equi]		struct	22278996, 264095, 29331826, 33657402, 18108348, 263974
3136	94845839 (6271, 6272)	Novel Protein sim. GBank gi 827101 pir S44092 - probable carrier protein c2 - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	22278998, 264259, 264828, 265006, 265008, 60433438, 265019, 264764, 264288, 264768, 264688, 265020, 27486262, 263972, 65274791, 264557, 264558
3137	88257847 (6273, 6274)	Novel Protein sim. GBank gi 3342730 (AC005331) - R31341_1 [Homo sapiens]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264510, 265008, 21908754, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264682, 264768, 21906765, 21906766, 21906767, 21906769, 55811857, 35695917, 265020, 265021, 52644150, 18108370, 18108374, 22279000, 22279002, 264482, 264486

3138	94130186 (8275, 8276)	Novel Protein sim. GBank gij4406759igb[AAD20070] - (AC006836) hypothetical protein [Arabidopsis thaliana]			264569, 264488, 264907, 264511, 264593, 33109854, 87188559, 264881, 264884, 264685, 264688, 264687, 264768, 264688, 264689, 264691, 264692, 264693, 33657109, 264631, 264634, 264635, 264636, 264637, 60170394, 83373044, 18108385, 18108388, 60432113, 22279000, 22278002
3139	87325503 (8277, 8278)	Novel Protein sim. GBank gij228938iprf[1814452C - Hyp-rich glycoprotein [Zea mays diploperennis]	UNCLASSIFIED		22278997, 22278998, 22278999, 264905, 265018, 265019, 21908765, 265020, 264636, 264557
3140	91222692 (8278, 8280)	Novel Protein sim. GBank gij932[emb]CAA37773] - (X53744) 68kDa subunit of signal recognition particle [Canis familiaris]	struct		22278995, 56994075, 35696286, 264808, 264909, 60433356, 21908754, 52644296, 87188474, 87188559, 264683, 264288, 264685, 264686, 265022, 264693, 27486282, 35695955, 264630, 264555, 264566
3141	87323564 (8281, 8282)	Novel Protein sim. GBank gij3213227 (AF035209) - putative v-SNARE VIIa [Mus musculus]	UNCLASSIFIED		56182575, 35696286, 29331828, 264909, 265009, 265018, 18108351, 264389, 21908766, 29148627, 265020, 264628, 264629, 264631, 18108385
3142	95419028 (8283, 8284)	Novel Protein sim. GBank gij2498197[sp]Q95245[C561_PIG - CYTOCHROME B561 (CYTOCHROME B-561)]	cytochrome		52645158, 52646365, 22278995, 35696286, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331827, 29148499, 56182435, 265007, 60170831, 60432229, 33637402, 264595, 60433438, 264758, 21908754, 264288, 264768, 264687, 52644228, 21908765, 21908767, 21908768, 60170615, 52644150, 65274620, 33657109, 35695763, 18108370, 18108376, 65274791, 35695855, 264631, 264557, 87168518, 60432113, 22279000
3143	95351475 (8285, 8286)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED		264488, 56182575, 22278996, 22278998, 22278999, 29331822, 29331824, 60432289, 35696052, 29331828, 264508, 264905, 264906, 264907, 264908, 264909, 52644045, 56182435, 264511, 264512, 265008, 264910, 60432229, 33657402, 60433356, 60433438, 55612038, 265011, 265019, 264760, 264763, 264448, 264764, 264684, 264288, 264685, 264686, 264768, 264689, 21908765, 21908766, 21908767, 21908769, 35695917, 264690, 33657023, 264693, 263987, 33657108, 264628, 264629, 18108374, 263976, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 87168518, 60432113, 22279000, 22278002, 264563, 264566, 264486

3144	95336329 (6287, 6288)	Novel Protein sim. GBank gil488446[emb]CAB43322.1] - (AL050225) hypothetical protein [Homo sapiens]			264488, 18108396, 22278996, 35696286, 22278997, 22278999, 29331826, 29331827, 35696052, 29331828, 264106, 265008, 265007, 265009, 33657402, 85658542, 265011, 18108351, 264448, 264369, 21906765, 21906766, 21906767, 265020, 265021, 52644150, 27486261, 18108370, 18108374, 35696423, 56182323, 83373044, 22279000, 22279002, 264567
3145	86611657 (6288, 6290)	Novel Protein sim. GBank gil3879709[emb]CAB03330] - (Z81118) Similarly to Human endosomal protein P162 (TR:Q15075); cDNA EST EMBL:Z14487 comes from this gene; cDNA EST EMBL:Z14556 comes from this gene; cDNA EST EMBL:D27011 comes from this gene; cDNA EST EMBL:D27015 comes from t...	UNCLASSIFIED		265008, 55812038, 265010, 21906766, 29148627, 21906768, 29148784, 264692, 33657023, 33657109, 35695763, 263981, 56182323, 87168518
3146	87756314 (6291, 6292)	Novel Protein sim. GBank gil2135746[pir]S69890 - mitogen inducible gene mlg-2 - human	Contains protein domain (PF00169) - PH domain.	- struct	264259, 29331826, 29331828, 29331830, 264510, 264511, 265007, 265009, 264600, 265017, 18108351, 264448, 264369, 21908766, 265021, 264692, 33657109, 18108374, 35696423, 35695855, 60432113, 264564
3147	94848512 (6293, 6294)	Novel Protein sim. GBank gil3874279[emb]CAB07315.1] - (Z92825) predicted using GeneFinder; cDNA EST yk315e12.3 comes from this gene; cDNA EST yk315e12.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	UNCLASSIFIED	56181886, 35696286, 60432048, 264259, 56182181, 29331825, 60432289, 35696052, 56182435, 265008, 264910, 60431735, 60433356, 60433438, 265010, 264448, 264288, 265022, 33657023, 33657109, 60431528, 65274791, 264631, 56182323, 264404, 22279002
3148	95352169 (6295, 6296)	Novel Protein sim. GBank gil5225322[gb]AA040851.1[AF08310] - (AF083108) sirtuin type 3 [Homo sapiens]	UNCLASSIFIED		35696286, 35696052, 264511, 85658542, 87168474, 264764, 35696423, 264555, 264556, 264557, 264558, 83373044, 56526486, 60432113
3149	95308548 (6297, 6298)	Novel Protein sim. GBank gil4200446 (AF102777) - FYVE finger-containing phosphoinositide kinase [Mus musculus]	Contains protein domain (PF01363) - FYVE zinc finger	- eph	29331822, 35696052, 264109, 29148628, 18108381
3150	87655472 (6299, 6300)	Novel Protein sim. GBank gil3378454[emb]CAA76893] - (Y17850) ganglioside-induced differentiation associated protein 1 [Mus musculus]	Contains protein domain (PF00043) - Glutathione S-transferases.	transferase	264259, 29331822, 29331824, 29331825, 29331827, 52646317, 264686, 35695855, 56182323, 264639
3151	87772355 (6301, 6302)	Novel Protein sim. GBank gil172591 (M63577) - SFP1 [Saccharomyces cerevisiae]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	- oncogene	29331822, 265008
3152	85698108 (6303, 6304)		UNCLASSIFIED		21906754, 87168559, 264605, 21908768, 52644150, 27486264, 35696423, 22279000

3153	95317299 (6305, 6306)	Novel Protein sim. GBank gi 4895041 gb AAD27705.1 AF14395 - (AF143957) coronin-3 [Mus musculus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	struct	264488, 52646365, 35698286, 22278996, 22278997, 22278998, 60432049, 264259, 29331826, 60432289, 33656970, 264508, 264908, 33657402, 264595, 60433438, 87168474, 87168559, 264601, 265019, 264448, 264682, 264764, 264288, 264389, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 29148784, 265021, 265022, 60170615, 52644150, 264690, 264691, 33657023, 65274820, 33657109, 18108370, 35695855, 264638, 60170394, 87168518, 60432113, 22279000, 22279002, 22278998, 264259, 29331824, 68712502, 265008, 265010, 265017, 18108354, 264691, 33657023, 264693, 20281149, 18108374
3154	87718573 (6307, 6308)	Novel Protein sim. GBank gi 4680601 gb AAD27720.1 AF13294 - (AF132945) CGI-11 protein [Homo sapiens]		ATPase associated	22278998, 264259, 29331824, 68712502, 265008, 265010, 265017, 18108354, 264691, 33657023, 264693, 20281149, 18108374
3155	87762394 (6309, 6310)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		UNCLASSIFIED	29331828, 264509, 264905, 264908, 264510, 264511, 264512, 33657402, 264681, 264683, 33657023, 18108370, 264634, 264639, 18108355, 264563, 264488
3156	87737449 (6311, 6312)	Novel Protein sim. GBank gi 5630078 gb AAD45821.1 AC00601 - (AC006017) N-acetylgalactosaminyltransferase; similar to Q10473 (PID:g1709559) [Homo sapiens]	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 29331828, 29331827, 35696052, 52644045, 265007, 265009, 60170831, 60432229, 60433358, 21906754, 33109954, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 264288, 264689, 21906766, 21906768, 21906769, 35695917, 285020, 265022, 264692, 18108370, 35696423, 56182323, 22279002
3157	88259577 (6313, 6314)				18108396, 264259, 29331826, 35696052, 29146498, 87168559, 265017, 264448, 264288, 264691, 18108366, 52645129, 35696423, 52644332
3158	80034118 (6315, 6316)	Novel Protein sim. GBank gi 5308084 gb AAD41895.1 AF15677 - (AF156778) ASB-3 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	264488, 263974
3159	94124114 (6317, 6318)	Novel Protein sim. GBank gi 5531272 emb CAB50897.1  - (AJ243800) WSC4 homologue [Kluyveromyces fragilis]		UNCLASSIFIED	56182575, 22278998, 29331824, 264106, 60433356, 264758, 265011, 87168559, 264448, 18108354, 264768, 21908769, 265020, 264691, 264692, 33657109, 18108374, 35696423, 264555, 60170394, 22279000
3160	80221068 (6319, 6320)	Novel Protein sim. GBank gi 3330525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - Ank repeat	struct	18108351, 264555, 264556, 264557, 264558, 264559



3161	88074111 (6321, 6322)				264488, 22278995, 22278997, 22278998, 264259, 29331822, 60432289, 26331828, 5264045, 265017, 265018, 264448, 264288, 21908764, 21908767, 265020, 18108374, 264638, 264568
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Table 2

Tissue ID	Tissue Name	Tissue Information	Disease Association
20281069	192xN	Protein-protein Interactions	Any
20281071	192xN	Protein-protein Interactions	Any
20281149	192xN	Protein-protein Interactions	Any
20281152	192xN	Protein-protein Interactions	Any
264111	276xN	Protein-protein Interactions	Any
264112	276xN	Protein-protein Interactions	Any
263966	384xN	Protein-protein Interactions	Any
263967	384xN	Protein-protein Interactions	Any
264110	552xN	Protein-protein Interactions	Any
18108379	SPH 52.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia.
18108381	SPH 52.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108383	SPH 52.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108368	SPH 52.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108384	SPH 52.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108394	SPH 53.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia.
18108355	SPH 53.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108359	SPH 53.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108361	SPH 53.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108362	SPH 53.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108366	SPH 53.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108354	SPH 54.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia.
18108392	SPH 54.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108348	SPH 54.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108382	SPH 54.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108395	SPH 54.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108365	SPH 54.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108397	SPH 55.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia.
18108398	SPH 55.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108364	SPH 55.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	
18108388	SPH 55.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108358	SPH 55.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
20281099	SPH 56.2 (MG63)		
20281100	SPH 56.3 (U1SMC)		
264404	SPH.1 (Brain)	Whole Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264510	SPH.10 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264511	SPH.11 (Placenta)	Placenta	Infertility, birth defects
264512	SPH.12 (Thyroid)	Thyroid	Hyperparathyroidism, Hypoparathyroidism
264555	SPH.13 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264556	SPH.14 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264557	SPH.15 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264558	SPH.16 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264559	SPH.17 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264569	SPH.19 (One Fetal tissue and two cell lines)	Mixed	
264687	SPH.19.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264688	SPH.19.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264689	SPH.19.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264690	SPH.19.4 (Fetal Liver)	Fetal liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264691	SPH.19.5 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264692	SPH.19.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264693	SPH.19.7 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264482	SPH.2 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264600	SPH.21 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264601	SPH.22 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264602	SPH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264603	SPH.24 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264604	SPH.25 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264605	SPH.26 (Placenta)	Placenta	Infertility, birth defects
264634	SPH.28 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis ,Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264635	SPH.29 (Fetal Kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264483	SPH.3 (Bone Marrow)	Bone marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264636	SPH.30 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264637	SPH.31 (P)ancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264638	SPH.32 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264639	SPH.33 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264484	SPH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264758	SPH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264760	SPH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation

264762	SPH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264764	SPH.44.4 (Prostate)	Prostate	Prostate Cancer
264766	SPH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264768	SPH.44.6 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264769	SPH.44.7 (Uterus)	Uterus	Infertility, birth defects
264905	SPH.48.1 (Burkitt's Lymphoma- Raji)	Burkitt's Lymphoma	Lymphoma, blood cancers
264906	SPH.48.2 (Thalamus- Brain)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264907	SPH.48.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
264908	SPH.48.4 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
264909	SPH.48.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
264910	SPH.48.6 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
265006	SPH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
265007	SPH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
265008	SPH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
265009	SPH.50.4 (fetal lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
265010	SPH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
265011	SPH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
18108385	SPH.51.1 (MCF-7)	Breast Cancer	Breast Cancer
18108370	SPH.51.2 (CCRF-CEM)	Cancer Cell line	Cancer
18108374	SPH.51.3 (K-562)	Cancer Cell line	Cancer
18108351	SPH.51.4 (OVCAR-3)	Ovarian cancer	Ovarian cancer
18108372	SPH.51.5 (HL-60)	Cancer Cell line	Cancer
264486	SPH.6 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264508	SPH.8 (Fetal Brain)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264509	SPH.9 (Lymph Node)	Lymph Node	Lymphedema , Allergies
20798451	SRH 56.3 (Uterine SMC)		
264487	SRH.1 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264534	SRH.11 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264535	SRH.12 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264563	SRH.19 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264488	SRH.2 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264564	SRH.20 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264565	SRH.21 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264566	SRH.22 (Placenta)	Placenta	Infertility, birth defects
264567	SRH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264591	SRH.25 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264592	SRH.26 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264593	SRH.27 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264594	SRH.28 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264595	SRH.29 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264489	SRH.3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264596	SRH.30 (Placenta)	Placenta	Infertility, birth defects
264628	SRH.33 (Fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264629	SRH.34 (Lymph Node)	Lymph Node	Lymphedema, Allergies
264630	SRH.35 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264631	SRH.36 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264632	SRH.37 (Fetal Brain)	Fetal Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264490	SRH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264681	SRH.43.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264682	SRH.43.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264683	SRH.43.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264684	SRH.43.4 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264685	SRH.43.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264686	SRH.43.7 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264757	SRH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264759	SRH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264761	SRH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264763	SRH.44.4 (Prostate)	Prostate	Prostate Cancer
264765	SRH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host

264767	SRH.44.6 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264828	SRH.46.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264887	SRH.47.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
18108377	SRH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
18108380	SRH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
18108396	SRH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108391	SRH.50.4 (fetal lung)	Fetal Lung	Airway diseases, infection
18108357	SRH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
18108390	SRH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
264532	SRH.9 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
263974	736xN		
263976	736xN		
263981	736xN		
20281166	96xN		
20281169	96xN		
20281171	96xN		
263994	cDNA-ORF Selection		
264080	Mx96		
21906754	NQH 6.1 (HH729)		
22278996	NQH 6.10 (PrEC)	Endothelial cells	heart disease, cancer
22278997	NQH 6.11 (CAEC)	Endothelial cells	heart disease, cancer
22278998	NQH 6.12 (CSC)	Cancer Cell line	Cancer
22278999	NQH 6.13 (NHNPC)	Cancer Cell line	Cancer
22279000	NQH 6.14 (NHMC-RM)	Cancer Cell line	Cancer
22279002	NQH 6.15 (Hypothalamus)	Hypothalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
21906764	NQH 6.2 (In Dated Platelets)	Platelets	Clotting diseases, stroke
21906765	NQH 6.3 (HuVec)	Endothelial cells	heart disease, cancer
87168474	NQH 6.3 (Sized-HUVEC)	Endothelial cells	heart disease, cancer
21906766	NQH 6.4 (UIMVEC- myo)	Cancer Cell line	Cancer
21906767	NQH 6.5 (NHEM-neo)	Cancer Cell line	Cancer
21906768	NQH 6.6 (NHEK)	Cancer Cell line	Cancer
21906769	NQH 6.7 (ByCAEC)	Endothelial cells	heart disease, cancer
22278994	NQH 6.8 (NHA)	Cancer Cell line	Cancer



22278995	NQH 6.9 (PrSC)	Cancer Cell line	Cancer
27486261	NQH 7.1 (Jurkat E6-untreated)	Cancer Cell line	Cancer
27486262	NQH 7.2 (TF1-untreated)	Cancer Cell line	Cancer
27486264	NQH 7.3 (U87-untreated)	Cancer Cell line	Cancer
27486265	NQH 7.4 (THP1-untreated)	Cancer Cell line	Cancer
29331822	NQH 8.1 (Brain- amygdala)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331824	NQH 8.2 (Brain-hippocampus)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331825	NQH 8.3 (Brain- substantia nigra)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331826	NQH 8.4 (small intestine)	Small intestine	digestive diseases, obesity, diabetes
29331827	NQH 8.5 (Spinal cord)	Spinal chord	paralysis, neurodegenerative disorders
29331828	NQH 8.6 (stomach)	Stomach	Stomach cancer
29331830	NQH 8.7 (Trachea)	Trachea	Airway diseases, infection
87168518	NQH 9.1 (Sized-MG-63_treatment pool)		
87168559	NQH 9.2 (Sized-HEPG2 untreated)		
35695763	NQH.10.1 (MCF-7untreated)	Cancer Cell line	Cancer
35695855	NQH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
35695917	NQH.10.3 (JAR)	Cancer Cell line	Cancer
35696052	NQH.10.4 (PA-1)	Cancer Cell line	Cancer
35696286	NQH.10.5 (CADMEC)	Endothelial cells	heart disease, cancer
35696423	NQH.10.6 (CADMEC_LA)	Endothelial cells	heart disease, cancer
52644045	NQH.11.1 (SK-PN-DW)	Cancer Cell line	Cancer
52644150	NQH.11.2 (Chorionic Villus Cells)	Chorionic villus	fertility, birth defects
52644229	NQH.11.3 (A549)	Cancer Cell line	Cancer
52644296	NQH.11.4 (U266B1)	Cancer Cell line	Cancer
52644332	NQH.11.5 (Daoy)	Cancer Cell line	Cancer
52644507	NQH.11.6 (SW1783)	Cancer Cell line	Cancer
52645080	NQH.12.1 (U-118MG)	Cancer Cell line	Cancer
52645129	NQH.12.2 (A204)	Cancer Cell line	Cancer
52645156	NQH.12.3 (T24)	Cancer Cell line	Cancer
52646317	NQH.12.4 (G-401)	Cancer Cell line	Cancer
52646365	NQH.12.5 (CaSki)	Cancer Cell line	Cancer
52646842	NQH.12.6 (SHP-77)	Cancer Cell line	Cancer

60424179	NQH.14.1 (Yale75_breast carcinoma)	Breast carcinoma	Breast Cancer
60424269	NQH.14.2 (Yale78B_ovarytumor)	Ovary tumor	Ovarian cancer
60431528	NQH.14.3 (Yale79_prostateBPH)	Prostate	Prostate Cancer
60431602	NQH.14.4 (Yale80_ProstateAdenocarcinoma)	Prostate	Prostate Cancer
60431735	NQH.14.5 (Yale86_UterineMyoma)	Uterine Myoma	Uterine Cancer
60431850	NQH.14.6 (Yale207_Myometrium)	Myometrium	Fertility
60432049	NQH.15.1 (Yale99_cervix)	Cervix	Osteoporosis, cervical cancer
60432113	NQH.15.2 (Yale45_spleen[TP])		Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
60432229	NQH.15.3 (Yale16_Skin)	Skin	wound healing, melanoma
60432289	NQH.15.4 (Yale137_Parotid)		
60433356	NQH.15.5 (Yale38_SmallIntestine)	Small intestine	digestive diseases, obesity, diabetes
60433438	NQH.15.6 (Yale28_ColonAscending)	Colon	Colon cancer
65274444	NQH.17.1 (Larynx)	Larynx	Cancer
65274572	NQH.17.2 (Duodenum)	Duodenum	
65274620	NQH.17.3 (Kidney, Primary tumors)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
65274727	NQH.17.4 (Lung Pleura, normal)	Lung	Airway diseases, infection
65274791	NQH.17.5 (Lung, Normal Adult)	Lung	Airway diseases, infection
83373044	NQH.18.230 (Pooled adrenal gland, placenta)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
85658542	NQH.18.560 (Pooled uterus, BeWo pool)	Uterus	Infertility, birth defects
33656970	NQH.9.1 (MG-63_treatment pool)	Cancer Cell line	Cancer
33657023	NQH.9.2 (HEPG2 untreated)		Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
33657084	NQH.9.3 (PC3_untreated)	Cancer Cell line	Cancer
33657109	NQH.9.4 (TF-1_TPA)	Cancer Cell line	Cancer
33657182	NQH.9.5 (TF-1_TPO)	Cancer Cell line	Cancer
33657349	NQH.9.6 (TF-1_Hermin)	Cancer Cell line	Cancer
33657402	NQH.9.7 (HFDPC)	Cancer Cell line	Cancer
264259	NQH1 (Mixture of eight adult & two fetal tissues)		
264288	NQH2 (Ten tissues plus lymphocyte control)		
264448	NQH3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
265017	NQH4.1 (lymph node)	Lymph Node	Lymphedema, Allergies

265018	NQH4.2 (fetal kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
66712502	NQH4.2 (Sized)		
265019	NQH4.3 (pituitary gland)		Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
66714117	NQH4.3 (Sized)		
265020	NQH4.4 (testis)	testis	Infertility, birth defects
265021	NQH4.5 (fetal liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
265022	NQH4.6 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
18108376	NQH5.1 (MCF-7)	Breast cancer	Breast Cancer
18108387	NQH5.2 (CCRF-CEM)	Cancer Cell line	Cancer
264952	NRL1: HPLC FRACTIONATION OF RELIG		
263971	Old BB3 Baits		
263969	Old BB5 Baits		
263975	ORFSEL		
263972	OTHER Baits		
263978	pGALORF		
264106	PPBAITS		
264088	QC-YA7		
264089	QC-YA8		
264102	Resequenced Interactors		
264369	RRH.1		
60170394	RRH.10.1 (MCF-7untreated)	Breast cancer	Breast Cancer
60170615	RRH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
60170831	RRH.10.3 (JAR)	Cancer Cell line	Cancer
60174639	RRH.11.8 (HeLa)	Cancer Cell line	Cancer
264113	rrQEA Baits		
263973	RRQEA_B5 baits		
29146498	SRD 3.1 (SKMC)	Cancer Cell line	Cancer
29146499	SRD 3.2 (SKMC)	Cancer Cell line	Cancer
29147620	SRD 3.3 (RPTEC)	Cancer Cell line	Cancer
29148627	SRD 3.4 (HRCE)	Cancer Cell line	Cancer
29148629	SRD 3.6 (HRE)	Cancer Cell line	Cancer
29148784	SRD 3.7 (HRE)	Cancer Cell line	Cancer
55810764	SRD.7.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
55811150	SRD.7.2 (pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
55811386	SRD.7.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,

55811576	SRD.7.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
55811957	SRD.7.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
55812038	SRD.7.6 (Fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
56181562	SRD.8.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
56181686	SRD.8.2 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
56182181	SRD.8.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
56182323	SRD.8.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
56182435	SRD.8.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
56182575	SRD.8.6 (Fetal Kidney)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
32833986	SRD4: HL adapter		
56526486	SRD5: I:rr fragments		
33109954	SRD5: long-RXRJ		
56994075	SRD9.1 (CS/SC)	Cancer Cell line	Cancer
263977	TSC Screen 1		

# Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences

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 ctcggtatgg acatcaaggg tcacaccgtt cacaaggtga tggtcgctga aggtgctgac  
 180  
 attgccgagg aatactactt ctcgatcttg ctcgaccgtg gagagcgtcg ctaccttgcg  
 240  
 atgtgctcgc gtgaggggtgg catggacatc gagacccttg ctaaggagcg ccccgagggt  
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 ctcgccaaagg tgccggtcga cccgattgac ggcgttgacg atgctaaagc ccgcgaaatc  
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 cttagcgagg cagggttccc cgactctgag caggacgcta tcgtcccggc tgttctcaag  
 420  
 ctgtgggaga cctaccgtga cgaggatgcc accctcgtcg aggtcaacc gatgatcaag  
 480  
 accggcgatg gacgcaccc ggctatcgac ggcaagatga ctgttgacaa caacgcatcc  
 540  
 ttccgccagc ctgaccgcgc cggcttggtg gatcgcgcga ccaccgaccc gctcgagttg  
 600  
 cgtgccggcg agctcgggtc caactacgtc aagcttgacg gcaacgtcgg cgtcatcgga  
 660  
 aacggtgctg gtctggatc gagcaccctt gactcgggtg cgtacgccgg tgagaacttc  
 720  
 ccgggatctc cagctccccg taacttcctc gacatcgggt gcggcgccct gcccgagatc  
 780  
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 840  
 gtctttggcg gtatcaccgc ctgtgaccag gtggcgcttg gtatcaaggg cgctctcgag  
 900  
 aagttgggcg acaaggccgt gaagccgctc gtcgtccgtc tggacggcaa cgctgtggcc  
 960  
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 987

<210> 4  
 <211> 329  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
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 Ala Ala Glu Arg Ala Glu Ala Ile Leu Gly Met Asp Ile Lys Gly His  
 35 40 45

Thr Val His Lys Val Met Val Ala Glu Gly Ala Asp Ile Ala Glu Glu  
 50 55 60  
 Tyr Tyr Phe Ser Ile Leu Leu Asp Arg Gly Glu Arg Arg Tyr Leu Ala  
 65 70 75 80  
 Met Cys Ser Arg Glu Gly Gly Met Asp Ile Glu Thr Leu Ala Lys Glu  
 85 90 95  
 Arg Pro Glu Ala Leu Ala Lys Val Pro Val Asp Pro Ile Asp Gly Val  
 100 105 110  
 Asp Asp Ala Lys Ala Arg Glu Ile Leu Ser Glu Ala Gly Phe Pro Asp  
 115 120 125  
 Ser Glu Gln Asp Ala Ile Val Pro Ala Val Leu Lys Leu Trp Glu Thr  
 130 135 140  
 Tyr Arg Asp Glu Asp Ala Thr Leu Val Glu Val Asn Pro Met Ile Lys  
 145 150 155 160  
 Thr Gly Asp Gly Arg Ile Leu Ala Ile Asp Gly Lys Met Thr Val Asp  
 165 170 175  
 Asn Asn Ala Ser Phe Arg Gln Pro Asp Arg Ala Gly Leu Val Asp Arg  
 180 185 190  
 Ala Thr Thr Asp Pro Leu Glu Leu Arg Ala Gly Glu Leu Gly Leu Asn  
 195 200 205  
 Tyr Val Lys Leu Asp Gly Asn Val Gly Val Ile Gly Asn Gly Ala Gly  
 210 215 220  
 Leu Val Met Ser Thr Leu Asp Cys Val Ala Tyr Ala Gly Glu Asn Phe  
 225 230 235 240  
 Pro Gly Ser Pro Ala Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala  
 245 250 255  
 Ser Ala Glu Ile Met Ala Asn Gly Leu Asp Leu Ile Met Ser Asp Glu  
 260 265 270  
 Gln Val Arg Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys  
 275 280 285  
 Asp Gln Val Ala Leu Gly Ile Lys Gly Ala Leu Glu Lys Leu Gly Asp  
 290 295 300  
 Lys Ala Val Lys Pro Leu Val Val Arg Leu Asp Gly Asn Ala Val Ala  
 305 310 315 320  
 Glu Gly Arg Lys Ile Leu Glu Glu Phe  
 325

&lt;210&gt; 5

&lt;211&gt; 622

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

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 120  
 gaacatagct tgtcataaca tctctgcagg gttctcccaa acccctttct gcctggcaac  
 180  
 agctgacatc acacctagct gtaagtcctt gtagatcgca aattactttt tggagactgg  
 240  
 gggtagcagg ggcattgggg taatagcctt ctagcccttt ttgagggaaa cacatgggtg  
 300

aggctatttt ggggctggga agtggggggcc tgggtgtcccc tggatggctg tgctggcctc  
 360  
 tggctgcaag ggagaggggc acaggcaagg acatgacccc cgtcaaccct gagccccctc  
 420  
 cagaaattta accagagcct gtccctcctt tcttgctgc cccaacatc tcacaatccc  
 480  
 tcctgtgatg gcagatgtct ccattctactc tacagacacc tgcaactatc attcccttga  
 540  
 tccgtggtaa ttaggagggga actcctctgt gaagaaccgc ttctaccatc ctcttttaga  
 600  
 aactctttct ccactgggat cc  
 622

<210> 6

<211> 121

<212> PRT

<213> Homo sapiens

<400> 6

Met	Ser	Leu	Pro	Val	Pro	Leu	Ser	Leu	Ala	Ala	Arg	Gly	Gln	His	Ser
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His	Pro	Gly	Asp	Thr	Arg	Pro	Pro	Leu	Pro	Ser	Pro	Lys	Ile	Ala	Ser
		20						25					30		
Pro	Met	Cys	Phe	Pro	Gln	Lys	Gly	Leu	Glu	Gly	Tyr	Tyr	Pro	Asn	Ala
		35					40					45			
Pro	Ala	Thr	Pro	Ser	Leu	Gln	Lys	Val	Ile	Cys	Asp	Leu	Gln	Gly	Leu
		50				55					60				
Thr	Ala	Arg	Cys	Asp	Val	Ser	Cys	Cys	Gln	Ala	Glu	Arg	Gly	Leu	Gly
					70					75				80	
Glu	Pro	Cys	Arg	Asp	Val	Met	Thr	Ser	Tyr	Val	Leu	Gly	Asn	Lys	Val
				85					90					95	
Thr	Cys	Cys	Arg	Pro	Leu	Glu	Leu	Trp	Pro	Val	Lys	Thr	Pro	Gly	Asn
			100					105						110	
Pro	Met	Ala	Arg	Arg	Glu	Thr	Val	Leu							
		115					120								

<210> 7

<211> 480

<212> DNA

<213> Homo sapiens

<400> 7

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 agaaaacca cacctctcct cccctcccca gtggctgtgg ctttcctagg gacaatagga  
 120  
 tgaatgggct ttcagtgtgg ggacagcaaa acatgeacta gggcccagag tggcagttct  
 180  
 cttggtgtgg agagtgcctg ccacaggcct tggccagagc ccgtgagggga gtggtgtgtg  
 240  
 aaagggcacc tccacgtggg taagcgtgag gacttggaact tctctggcac tgagatggga  
 300  
 cctcctgcct gtgggagtc tctggccacc accctggggc cagtaaagggt tggagctaga  
 360



agggtcgtcc tccctgactt gagctctgag ggctttgcct gccagccag agcggcaagg  
 420  
 cacaggggac cctcggggac gcccatggcc accctgggga agacagggct cctcacgcgt  
 480

<210> 8  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
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 Gly Ser Ser Leu Gly Val Glu Ser Ala Cys His Arg Pro Trp Pro Glu  
 20 25 30  
 Pro Val Arg Glu Trp Cys Val Lys Gly His Leu His Val Gly Lys Arg  
 35 40 45  
 Glu Asp Leu Asp Phe Ser Gly Thr Glu Met Gly Pro Pro Ala Cys Gly  
 50 55 60  
 Ser His Leu Ala Thr Thr Leu Gly Pro Val Lys Val Gly Ala Arg Arg  
 65 70 75 80  
 Val Val Leu Pro Asp Leu Ser Ser Glu Gly Phe Ala Cys Pro Ala Arg  
 85 90 95  
 Ala Ala Arg His Arg Gly Pro Ser Gly Thr Pro Met Ala Thr Leu Gly  
 100 105 110  
 Lys Thr Gly Leu Leu Thr Arg  
 115

<210> 9  
 <211> 428  
 <212> DNA  
 <213> Homo sapiens

<400> 9  
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 120  
 tcccagggat gctggatgac ctctttcagt ccattgttct gtgcgccctg ctgctcttct  
 180  
 ggctgtgcgt gtaccacggg attcgtgtcc agggagaaaag aaagtgttta actttctatt  
 240  
 tgcctaaaatt cttcattggt ggactattgt ggttggtctc tggtacgcta ggaatatggc  
 300  
 aaacagttaa cgaattacat gatccaatgt accagtatcg agttgatacc ggaaattttc  
 360  
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 420  
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 428

<210> 10  
 <211> 138  
 <212> PRT

<213> Homo sapiens

<400> 10

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Met Arg Asp Trp Gly Ile Glu Gln Lys Trp Met Ser Val Leu Leu Pro
 1           5           10           15
Leu Leu Leu Leu Tyr Asn Asp Pro Phe Phe Pro Leu Ser Phe Leu Val
 20           25           30
Asn Ser Trp Leu Pro Gly Met Leu Asp Asp Leu Phe Gln Ser Met Phe
 35           40           45
Leu Cys Ala Leu Leu Leu Phe Trp Leu Cys Val Tyr His Gly Ile Arg
 50           55           60
Val Gln Gly Glu Arg Lys Cys Leu Thr Phe Tyr Leu Pro Lys Phe Phe
 65           70           75           80
Ile Val Gly Leu Leu Trp Leu Ala Ser Val Thr Leu Gly Ile Trp Gln
 85           90           95
Thr Val Asn Glu Leu His Asp Pro Met Tyr Gln Tyr Arg Val Asp Thr
 100          105          110
Gly Asn Phe Gln Gly Met Lys Val Phe Phe Met Val Val Ala Ala Val
 115          120          125
Tyr Ile Leu Tyr Leu Leu Phe Leu Ile Val
 130          135

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<210> 11

<211> 453

<212> DNA

<213> Homo sapiens

<400> 11

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gaatgttgca ggcaaactca agaccggtgg ccttggtgaa ggtccaggtc agctcggcgg
120
acttgccccg ctgcaccagc acgctgttgg ggtcgtcatg cttcatgccg cccatatcgc
180
catgccccat ggcggtgtgg tccatcttgc ccatgccggt ggccgtgagc atgccgctgg
240
cttgcatctt gagcatttct ttctggtgtt cggcgtgcat cgccgcatca cccagattga
300
attcgtgcag taactggcct ttgttgacca gcacaaagcg cacggtctca ccggctttta
360
catccagagc cttggg'gcga aaggaaatgt cctgcagggt gacttccacg gtgcgcgtgg
420
ctttatcggc cgggtgccggg tggccaaacg cgt
453

```

<210> 12

<211> 130

<212> PRT

<213> Homo sapiens

<400> 12

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Met Leu Gln Ala Asn Ser Arg Pro Val Ala Leu Val Lys Val Gln Val
 1           5           10           15
Ser Ser Ala Asp Leu Pro Gly Ser Thr Ser Thr Leu Leu Gly Ser Ser

```

[illegible]

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<210> 13
<211> 2034
<212> DNA
<213> Homo sapiens
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<400> 13
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120
tgggccctac catgctggca ttttctcca tgtgtcaaac acatgggttc agccagcgaa
180
gattccatgg gacctctctg tgtgggacgt gtgtcccca ccacaaatgg aacgttcctt
240
gtttgcatct ggaggggttg gtggtctctgc tggctggagc agcctggggc cagaggaagc
300
cgtatcaacc ggctctgcag cgcttcagcg agggtgcctt ggagtacctt gccaacctgg
360
accgagcccc agacccacg gtcaggaagg acgcctttgc caccgacatc ttcagcgcct
420
acgatgttct ctccatcag tggctgcaga gtcgagaagc caagctcctt cttgccgtgg
480
tggaggctct ggggcctatg agccatctgc tgcccagtga gaggttgga gagcagctgc
540
ccaagctcct ccctgggatt ctgcacctct acaagaagca cgcagagacc ttctacttgt
600
ccaagagcct gggccagatc ctcgaggcag ctgtgagtggt gggcagccgc aactggaga
660
cccagctgga tgccctcttg gctgcaactgc actcccagat ctgtgtgcct gtggagtcct
720
caagccccct ggtgatgagt aaccagaagg aggtgctgcg ctgcttcact gtgtggcctt
780
gcagctcgcc tgaccgccta ctggccttcc tgctgccag gctggacacc accaatgaga
840
ggacccgcgt gggcaccttg cagggggcca aacatgtcat caactcaact gctgctcaaa
900
tggaagataa aaagcccttt atcctgtctt ccatgaggct tcctctcttg aacaccaaca
960

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gcaaggtgaa gcgggcagtg gtgcaggtga ttagcgccca tggcccacca cggctacctg  
 1020  
 gagcagcctg gaggtgaggg gatgatcgag taaatcgtgc agcagtgcgc gctgcccccc  
 1080  
 gagcaggagc ctgagaagcc agggcccggc agcaaggacc ccaaggccga cagcgtgcgg  
 1140  
 gccatcagcg tgcgcaccct ctacctgggc agcaccaccg tggacaggat gagtcacgtc  
 1200  
 ctctggccat acctgctcca gttcctcacc cctgtgcgct tcaactggggc cctgactccg  
 1260  
 ctctgcagga gcctcgtgca tctggcgag aagaggcagg agggcggggc cgacgccttc  
 1320  
 ctcatccagt acgacgcccc tgcgagcctc ccgtctccct atgctgtaac cggaagactg  
 1380  
 ttggttggtg cttccagccc ctacctaggg gacggacgtg gggcagcggc gctgcgcctc  
 1440  
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 1500  
 ccgctgctgc tggggtacct ggatgagcac acagaagaga ccctgccaca ggaggagtgg  
 1560  
 gaggagaagc tggtgatggg gagggccggg gtacggccca tcctgggcct taagggtgtg  
 1620  
 tctggcctgg ggggtgctgg ggtggcagag gctgggccac ctgcctcgac ctcacctcgt  
 1680  
 ggtttggctg gggagccaag gatcaggcag catcaaggct gaagacccca gcagccttgc  
 1740  
 agcggggggc ttgctgtgac aaggcaccgg ccctctagca gtcgcagccc caagcgctcg  
 1800  
 gggcaacctc tcacctgcc tggtagacca actgtggcat ggctgtcccc tgaggggttg  
 1860  
 ctctgccgcc cccggcctcc gctggaaggc ggtctgcagc ccctgcagcc acagcacatg  
 1920  
 gggatgtgcc caggctccag ccagccctgt gaggggtcgg gctcccagcc cctcagtggc  
 1980  
 atcttggcct gcagttcctg cgagacaccc tggccatcat ttctgacaac gcgt  
 2034

<210> 14

<211> 222

<212> PRT

<213> Homo sapiens

<400> 14

Ile	Val	Gln	Gln	Cys	Ala	Leu	Pro	Pro	Glu	Gln	Glu	Pro	Glu	Lys	Pro
1				5					10					15	
Gly	Pro	Gly	Ser	Lys	Asp	Pro	Lys	Ala	Asp	Ser	Val	Arg	Ala	Ile	Ser
			20					25					30		
Val	Arg	Thr	Leu	Tyr	Leu	Val	Ser	Thr	Thr	Val	Asp	Arg	Met	Ser	His
		35				40					45				
Val	Leu	Trp	Pro	Tyr	Leu	Leu	Gln	Phe	Leu	Thr	Pro	Val	Arg	Phe	Thr
	50				55					60					
Gly	Ala	Leu	Thr	Pro	Leu	Cys	Arg	Ser	Leu	Val	His	Leu	Ala	Gln	Lys
65				70					75					80	
Arg	Gln	Glu	Ala	Gly	Ala	Asp	Ala	Phe	Leu	Ile	Gln	Tyr	Asp	Ala	His

```

      85              90              95
Ala Ser Leu Pro Ser Pro Tyr Ala Val Thr Gly Arg Leu Leu Val Val
      100              105              110
Ser Ser Ser Pro Tyr Leu Gly Asp Gly Arg Gly Ala Ala Ala Leu Arg
      115              120              125
Leu Leu Ser Val Leu His Pro Asn Ile His Pro Leu Leu Gly Gln His
      130              135              140
Trp Glu Thr Thr Val Pro Leu Leu Leu Gly Tyr Leu Asp Glu His Thr
      145              150              155              160
Glu Glu Thr Leu Pro Gln Glu Glu Trp Glu Glu Lys Leu Leu Met Val
      165              170              175
Arg Ala Gly Val Arg Pro Ile Leu Gly Leu Lys Val Leu Ser Gly Leu
      180              185              190
Gly Gly Ala Gly Val Ala Glu Ala Gly Pro Pro Ala Ser Thr Ser Pro
      195              200              205
Arg Gly Leu Ala Gly Glu Pro Arg Ile Arg Gln His Gln Gly
      210              215              220

```

<210> 15  
 <211> 363  
 <212> DNA  
 <213> Homo sapiens

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<400> 15
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120
ttgcaggaca ccaatgacac cttcatggcc aacatgcaga agaacggtag ctattcgatc
180
atcccgcgta tcgccggcgg cgagatcacc ccggacaaac tgatcgccct cggcgcggtg
240
gcgaagaaat acgatctgta caccaagatc accggcggcc agcggatcga cctgttcggc
300
gccagttgc acgaattgcc gcagatctgg ggcgagctgg tggatgccgg attcgagacc
360
ggt
363

```

<210> 16  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

```

<400> 16
Xaa Ala Leu Leu Ala Arg His Gly Lys Gly His Val Gly Cys Asp Ile
1      5      10      15
Cys Lys Pro Ala Val Gly Ser Ile Leu Ala Ser Cys Trp Asn Gln Pro
20      25      30
Ile Met Asp Pro Ala Leu Val Pro Leu Gln Asp Thr Asn Asp Thr Phe
35      40      45
Met Ala Asn Met Gln Lys Asn Gly Thr Tyr Ser Ile Ile Pro Arg Ile
50      55      60
Ala Gly Gly Glu Ile Thr Pro Asp Lys Leu Ile Ala Leu Gly Ala Val

```

```

65              70              75              80
Ala Lys Lys Tyr Asp Leu Tyr Thr Lys Ile Thr Gly Gly Gln Arg Ile
              85              90              95
Asp Leu Phe Gly Ala Gln Leu His Glu Leu Pro Gln Ile Trp Gly Glu
              100              105              110
Leu Val Asp Ala Gly Phe Glu Thr Gly
              115              120

```

<210> 17  
 <211> 682  
 <212> DNA  
 <213> Homo sapiens

```

<400> 17
gaattccatt ttgtggagta agaggtgact ggggtatagg gtacaaccca tagccatcca
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tgttcatctt tgttttgaat ataattggct agaagatata catatatcta tgtaacttcc
120
tctagcatcc tccagtatgg aggctgcatt aagactgcat gaaggagagg gagagaaggg
180
agaaacagag cagctggaca agaggacagg tatagggaat aagggagaag ccagtaaggc
240
aggaaagacc ctccgtgaca aaggggcagg gaacagaact caaacattta atggcaggta
300
acccaggtta gaatggtaaa ttgaaaggtg aatataaagg gagaatggtg aaatgaattt
360
tctgaaatta attgctgtgt ttatagtttt tagccatgca tcggaatcac ctcaggactc
420
cactcccaat caattatata tctgggggag gaccaaggcg ttggtatttt tcagaagctc
480
cactggtgat tctgacagca cagctaggat taagaaactg atcaatggga acagcatgcc
540
tgttgcagag gagcttcctt gggaaatgtc acacacagaa catcaatctt ccttccccac
600
tcctgagatc cctcattctt tggcaccagg aacagttgca attagtaaac cctgggtccc
660
tgctgtctca caaatcgcaa ga
682

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<210> 18  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

```

<400> 18
Met Asn Phe Leu Lys Leu Ile Ala Val Phe Ile Val Phe Ser His Ala
1              5              10              15
Ser Glu Ser Pro Gln Asp Ser Thr Pro Asn Gln Leu Tyr Ile Trp Gly
              20              25              30
Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp
              35              40              45
Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val
50              55              60
Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser

```

```

65              70              75              80
Phe Pro Thr Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala
              85              90              95
Ile Ser Lys Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg
              100              105              110

```

<210> 19  
 <211> 515  
 <212> DNA  
 <213> Homo sapiens

```

<400> 19
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60
cccccatctc aactatgtta gccagtctgg ctgttcactt agtcactaca gtttgcttct
120
cgtctgcagt gcagtcttgg gctataagaa aactggggcc actcaatacc tcccccttt
180
tggcccttct cctcctctgg tccatgggtg ggggtggggg gagcccagtt tcagcaccag
240
cagctggagc ccataaccaca ctcatttttc agttctggct gtgggagccc ctcccacagg
300
tttcagttcc ccaagcccca ggctgagtt ttttttattg caaaagctgg ttgttgttgt
360
ggctagctcc caggcgtgtg aggtgcagct tgctaagtaa gagctaggaa agagaatagg
420
gtcctgctgt aggtgtccag tctgaaggaa tgctgggat acttcctcaa gcagttcctt
480
ctcacagtct cctggctgct ccgcatgtca gatct
515

```

<210> 20  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

```

<400> 20
Met Gly Pro Ala Ser Leu Leu His Pro Ser Leu Gly Lys Asp His Ala
1      5      10      15
Pro Ile Ser Thr Met Leu Ala Ser Leu Ala Val His Leu Val Thr Thr
20     25     30
Val Cys Phe Ser Ser Ala Val Gln Ser Trp Ala Ile Arg Asn Thr Gly
35     40     45
Pro Leu Asn Thr Ser Pro Leu Leu Ala Leu Leu Leu Trp Ser Met
50     55     60
Gly Gly Val Gly Gly Ser Pro Val Ser Ala Pro Ala Ala Gly Ala His
65     70     75     80
Thr Thr Leu Ile Phe Gln Phe Trp Leu Trp Glu Pro Leu Pro Gln Val
85     90     95
Ser Val Pro Gln Ala Pro Gly Leu Ser Phe Phe Tyr Cys Lys Ser Trp
100    105    110
Leu Leu Leu Trp Leu Ala Pro Arg Arg Val Arg Cys Ser Leu Leu Ser
115    120    125
Lys Ser

```

130

<210> 21  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<400> 21  
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 60  
 tagacgcggt gcctatgggt gcggaggacc atggagtga gcgagtaaga ctagatgatg  
 120  
 caacaaatgt gcctgagggg gaaatggcac gagccagtgc caatgagggc atgacacctg  
 180  
 ttaaccacga caaataccct tctgtccttt taaatgaagc ggcccaggct tcattactgg  
 240  
 atacaatgac tgcttgcaact gatgggttca caattgagca attggagctt acacgatctc  
 300  
 tatgttatga aagagtatta gcacatcgat cctcatggga tcgttcagcc ctggctcaag  
 360  
 aattaaagca agttgtccaa ggcattccatn  
 390

<210> 22  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
 Met Val Ala Glu Asp His Gly Val Lys Arg Val Arg Leu Asp Asp Ala  
 1 5 10 15  
 Thr Asn Val Pro Glu Gly Glu Met Ala Arg Ala Ser Ala Asn Glu Gly  
 20 25 30  
 Met Thr Pro Val Asn His Asp Lys Tyr Pro Ser Val Leu Leu Asn Glu  
 35 40 45  
 Ala Ala Gln Ala Ser Leu Leu Asp Thr Met Thr Ala Cys Thr Asp Gly  
 50 55 60  
 Phe Thr Ile Glu Gln Leu Glu Leu Thr Arg Ser Leu Cys Tyr Glu Arg  
 65 70 75 80  
 Val Leu Ala His Arg Ser Ser Trp Asp Arg Ser Ala Leu Ala Gln Glu  
 85 90 95  
 Leu Lys Gln Val Val Gln Gly Ile His  
 100 105

<210> 23  
 <211> 385  
 <212> DNA  
 <213> Homo sapiens

<400> 23  
 ntctcggagg ccgacagcct ggcgggctgg aagccctcgg tgtaccacgt gctgctcatc  
 60  
 ctgggcctgt tcgcggtgct gctgtcctgc tgcgcctcgg ccatgtacac cagcgtggag  
 120



ggetgggact acgtggactc gctctacttc tgcttcgtca ccttcagcac catcggttc  
 180  
 ggggacctgg tgagcagcca gcacgcegcc taccggaacc aggggctcta cgcctgggc  
 240  
 aacttctct tcatcctgct cggcgtgtgc tgcatttact cgctcttcaa cgtcatctcc  
 300  
 atcctcatca agcagggtgct caactggatg ctgcgaagc tgagctgccg ctgctgcgcg  
 360  
 cgctgctgcc cggctcctgg cgcgc  
 385

&lt;210&gt; 24

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 24

Xaa Ser Glu Ala Asp Ser Leu Ala Gly Trp Lys Pro Ser Val Tyr His  
 1 5 10 15  
 Val Leu Leu Ile Leu Gly Leu Phe Ala Val Leu Leu Ser Cys Cys Ala  
 20 25 30  
 Ser Ala Met Tyr Thr Ser Val Glu Gly Trp Asp Tyr Val Asp Ser Leu  
 35 40 45  
 Tyr Phe Cys Phe Val Thr Phe Ser Thr Ile Gly Phe Gly Asp Leu Val  
 50 55 60  
 Ser Ser Gln His Ala Ala Tyr Arg Asn Gln Gly Leu Tyr Arg Leu Gly  
 65 70 75 80  
 Asn Phe Leu Phe Ile Leu Leu Gly Val Cys Cys Ile Tyr Ser Leu Phe  
 85 90 95  
 Asn Val Ile Ser Ile Leu Ile Lys Gln Val Leu Asn Trp Met Leu Arg  
 100 105 110  
 Lys Leu Ser Cys Arg Cys Cys Ala Arg Cys Cys Pro Ala Pro Gly Ala  
 115 120 125

&lt;210&gt; 25

&lt;211&gt; 337

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 25

ccatgggaga gaccgtgcat tttcttctag gtctgcgtgg gaagtcactg cagagtttcg  
 60  
 aggaggggag ttcccagctc tgtatttttg aagggtcagt cttgttgctt ggaccagtga  
 120  
 ggagccccgt gggatccaga ctcgagtggg tggagccggg gcaggtggga gcagagacac  
 180  
 tggaggaaag ctggtcgaat gcaactgtgta tttggaggca gaaccagcag agggctctct  
 240  
 gggttgagt tagggcaaaa gagaaagaag gcaccaagcc tggggtctgg gttttctctc  
 300  
 ttacacttgc tgggtggacg gtggtgccac tgaatga  
 337

&lt;210&gt; 26

<211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 26  
 Met Gly Glu Thr Val His Phe Leu Leu Gly Leu Arg Gly Lys Ser Leu  
 1 5 10 15  
 Gln Ser Phe Glu Glu Gly Ser Ser Gln Leu Cys Ile Phe Glu Gly Ser  
 20 25 30  
 Val Leu Leu Leu Gly Pro Val Arg Ser Pro Val Gly Ser Arg Leu Glu  
 35 40 45  
 Trp Val Glu Pro Gly Gln Val Gly Ala Glu Thr Leu Glu Glu Ser Trp  
 50 55 60  
 Ser Asn Ala Leu Cys Ile Trp Arg Gln Asn Gln Gln Arg Val Leu Trp  
 65 70 75 80  
 Val Glu Cys Arg Ala Lys Glu Lys Glu Gly Thr Lys Pro Gly Val Trp  
 85 90 95  
 Val Phe Ser Leu Thr Leu Ala Gly Trp Thr Val Val Pro Leu Asn  
 100 105 110

<210> 27  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 ccgacgtcga atatccatgc agccgcgcgcg aggatggaga gagcgatgga gcaactcaac  
 60  
 cgcctgacgc gtcgctgctgcg ccgcgcgcgc accgtggagt tgcccaggga taatgaaact  
 120  
 gctgtttata cattaatgcc aatgggttatg gctgatcaac acaggtctgt ttctgaacta  
 180  
 ctatcaaatt caaaatttga tgtcaattat gcattcggac gtgtgaaaag aagcttgctt  
 240  
 cacattgcag caaattgtgg atcgggtggaa tgcttggttt tgctgttaaa gaaaggagca  
 300  
 aatcctaact atcaagatat ttcaggctgt aca  
 333

<210> 28  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
 Pro Thr Ser Asn Ile His Ala Ala Ala Pro Arg Met Glu Arg Ala Met  
 1 5 10 15  
 Glu Gln Leu Asn Arg Leu Thr Arg Ser Leu Arg Arg Ala Arg Thr Val  
 20 25 30  
 Glu Leu Pro Glu Asp Asn Glu Thr Ala Val Tyr Thr Leu Met Pro Met  
 35 40 45  
 Val Met Ala Asp Gln His Arg Ser Val Ser Glu Leu Leu Ser Asn Ser  
 50 55 60  
 Lys Phe Asp Val Asn Tyr Ala Phe Gly Arg Val Lys Arg Ser Leu Leu

```

65              70              75              80
His Ile Ala Ala Asn Cys Gly Ser Val Glu Cys Leu Val Leu Leu Leu
              85              90              95
Lys Lys Gly Ala Asn Pro Asn Tyr Gln Asp Ile Ser Gly Cys Thr
              100              105              110

```

<210> 29  
 <211> 375  
 <212> DNA  
 <213> Homo sapiens

```

<400> 29
ncgccgtccg tgctggctat tatgacggcg ggtagcgacc agggcgagga ggtcaactcg
60
gagagctatt tgagcgccgt gacgccgctg agtcccaaag agattcgtca gctgccccgc
120
tacaatatca cgatcaagcg cgtcgtgaac atgacgggca agggccgcac gccgagctgg
180
tactcgctcg tcgtggctgg caatggtcgg ggctcgtgg gctatggcga aggcaaagat
240
actaacatca gccgcgcgaa caaaaaggcg ttccacgcgc cggtgaaaaa catggacttg
300
gtatcgggtcc accggtcgaa gagtggcgcc aacacgctcg agccccccgt cgagggccgc
360
tgggggcgcta cgcg
375

```

<210> 30  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

```

<400> 30
Xaa Pro Ser Val Leu Ala Ile Met Thr Ala Gly Ser Asp Gln Gly Glu
1          5          10          15
Glu Val Asn Ser Glu Ser Tyr Leu Ser Ala Val Thr Pro Leu Ser Pro
          20          25          30
Lys Glu Ile Arg Gln Leu Pro Arg Tyr Asn Ile Thr Ile Lys Arg Val
          35          40          45
Val Asn Met Thr Gly Lys Gly Arg Thr Pro Ser Trp Tyr Ser Leu Val
          50          55          60
Val Ala Gly Asn Gly Arg Gly Leu Val Gly Tyr Gly Glu Gly Lys Asp
65          70          75          80
Thr Asn Ile Ser Arg Ala Asn Lys Lys Ala Phe His Ala Ala Val Lys
          85          90          95
Asn Met Asp Leu Val Ser Val His Arg Ser Lys Ser Gly Ala Asn Thr
          100          105          110
Leu Glu Pro Pro Val Glu Gly Arg Trp Gly Ala Thr Arg
          115          120          125

```

<210> 31  
 <211> 375  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
 accggtcttg gcctcagctt tgctctgaaa ttgaagtcgg tgccaaaagt ggggaagagc  
 60  
 gggagcaggc acttacgagc ctgcgcgtca gggatgcttc ctggggccct gagagtgcag  
 120  
 agattccttg atccagagct gcggctgggc ggctgcagct gcgcctggga gtgcagggct  
 180  
 cccgccctgc cagctcaaaa ggaaatgggg gctcctgcct gttcctggct cctgttggcc  
 240  
 ctgcagagtg cacaaacctt gccgcgcttc ctccactgca gcttacgtct ttgcagcagc  
 300  
 cactcccgat gggctgccac tgccatctgt gagaccataa tgtgtgcaat ttgagactca  
 360  
 tggcctgcat tgttt  
 375

<210> 32  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 32  
 Met Gln Ala Met Ser Leu Lys Leu His Thr Leu Trp Ser His Arg Trp  
 1 5 10 15  
 Gln Trp Gln Pro Ile Gly Ser Gly Cys Cys Lys Asp Val Ser Cys Ser  
 20 25 30  
 Gly Gly Ser Ala Ala Arg Phe Val His Ser Ala Gly Pro Thr Gly Ala  
 35 40 45  
 Arg Asn Arg Gln Glu Pro Pro Phe Pro Phe Glu Leu Ala Gly Arg Glu  
 50 55 60  
 Pro Cys Thr Pro Arg Arg Ser Cys Ser Arg Pro Ala Ala Ala Leu Asp  
 65 70 75 80  
 Pro Gly Ile Ser Ala Leu Ser Gly Ala Gln Glu Ala Ser Leu Thr Arg  
 85 90 95  
 Arg Leu Val Ser Ala Cys Ser Arg Ser Ser Pro Leu Leu Ala Pro Thr  
 100 105 110  
 Ser Ile Ser Glu Gln Ser  
 115

<210> 33  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 33  
 ccattgcagcc caaccgttgg cgataaagtc cgtttaggcg ataccaatctt atgggcaacc  
 60  
 attgaacaag atttattaac caaaggtgat gagtgtaaat ttggtggcgg taaaagtgtg  
 120  
 cgtgatggta tggcgcaaag cggcaccgca actcgcgaca atccaaatgt attggatttt  
 180  
 gtgattacca atgtgatgat cattgatgcc aaattaggca ttatcaaagc cgatattggg  
 240

attcgcgatg gtcgtattgt cggatcggg caagcaggta accctgacac catggatgac  
 300  
 gtcacgccaac acatgattat cggtgctagc acagaagtac ataacgggtgc a  
 351

<210> 34  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
 Pro Cys Ser Pro Thr Val Gly Asp Lys Val Arg Leu Gly Asp Thr Asn  
 1 5 10 15  
 Leu Trp Ala Thr Ile Glu Gln Asp Leu Leu Thr Lys Gly Asp Glu Cys  
 20 25 30  
 Lys Phe Gly Gly Gly Lys Ser Val Arg Asp Gly Met Ala Gln Ser Gly  
 35 40 45  
 Thr Ala Thr Arg Asp Asn Pro Asn Val Leu Asp Phe Val Ile Thr Asn  
 50 55 60  
 Val Met Ile Ile Asp Ala Lys Leu Gly Ile Ile Lys Ala Asp Ile Gly  
 65 70 75 80  
 Ile Arg Asp Gly Arg Ile Val Gly Ile Gly Gln Ala Gly Asn Pro Asp  
 85 90 95  
 Thr Met Asp Asp Val Thr Pro Asn Met Ile Ile Gly Ala Ser Thr Glu  
 100 105 110  
 Val His Asn Gly Ala  
 115

<210> 35  
 <211> 355  
 <212> DNA  
 <213> Homo sapiens

<400> 35  
 nngctagctg caccaccacc tgttcatgca ggcagagcgg ccaccctca tggaagaaga  
 60  
 ggaatccact gtattgggca caggcttcct gctggacctt ggcaagcagg tgcttggtcg  
 120  
 gtaccaggaa gtccagcgtg tacctcagtg cgtcctcccg ataagtcctc tccaccacct  
 180  
 ggaacacctg gcccaacagg gtgggggctg ttgcctcaaa ggggtggatac agggcggcga  
 240  
 gagtgctctg cacacagtcc tccactggct caggctccat ggctcggcgc cgggccgcgt  
 300  
 ccgacgcttg gtcggggcggg cggggccggg cgcgccaccg cctcccttca cgcgt  
 355

<210> 36  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
 Xaa Leu Ala Ala Pro Pro Pro Val His Ala Gly Arg Ala Ala Thr Pro

```

      1           5           10           15
His Gly Arg Arg Gly Ile His Cys Ile Gly His Arg Leu Pro Ala Gly
      20           25           30
Pro Trp Gln Ala Gly Ala Trp Leu Val Pro Gly Ser Pro Ala Cys Thr
      35           40           45
Ser Val Arg Pro Pro Asp Lys Ser Ser Pro Pro Pro Gly Thr Pro Gly
      50           55           60
Pro Thr Gly Trp Gly Leu Leu Pro Gln Arg Val Asp Thr Gly Arg Arg
      65           70           75           80
Glu Cys Ser Ala His Ser Pro Pro Leu Ala Gln Ala Pro Trp Leu Gly
      85           90           95
Ala Gly Pro Arg Pro Thr Leu Gly Arg Ala Gly Gly Ala Gly Arg Ala
      100          105          110
Thr Ala Ser Leu His Ala
      115

```

<210> 37  
 <211> 492  
 <212> DNA  
 <213> Homo sapiens

```

<400> 37
acgcgtggcc ttcgtctgcc accaggaccg actcagcccc accgggtttc cggacccgcc
60
gcaaccatga caagggcgat gttgtgatct gggtggattc cttctccgac atgctcgagg
120
gatcggatct ctccggcgta gtcacgggtgc ttgccgaggc cggctatcgc ccacgggtcc
180
tcgccgacga cgtctgctgc gggttgacgt ggatcactac cggtcagctc gacgggtgctc
240
ggcgtcggct gcgcgtggt ctgcacgtgc tggcaccctc gtcagacgcc agcgtcccag
300
tcgttgggct agagccgtcc tgcactaccg tctggcggtga tgacgcactc cgctctctgc
360
cagatgatcc gcgcgtccac cgggtagcca gaaacatgca taccgtcgcc gagatgcttg
420
aggcagcaca gtggacccca ccctcgctag caggccacac cctcgctcgt cagccccatt
480
gtcatcccgc gg
492

```

<210> 38  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

```

<400> 38
Met Leu Glu Gly Ser Asp Leu Ser Ala Val Val Thr Val Leu Ala Glu
      1           5           10           15
Ala Gly Tyr Arg Pro Arg Val Leu Ala Asp Asp Val Cys Cys Gly Leu
      20           25           30
Thr Trp Ile Thr Thr Gly Gln Leu Asp Gly Ala Arg Arg Arg Leu Arg
      35           40           45
Ala Gly Leu Asp Val Leu Ala Pro Leu Ser Asp Ala Ser Val Pro Val

```

```

      50              55              60
Val Gly Leu Glu Pro Ser Cys Thr Thr Val Trp Arg Asp Asp Ala Leu
65              70              75              80
Arg Leu Leu Pro Asp Asp Pro Arg Val His Arg Val Ala Arg Asn Met
      85              90              95
His Thr Val Ala Glu Met Leu Glu Ala Ala Gln Trp Thr Pro Pro Ser
      100             105             110
Leu Ala Gly His Thr Leu Val Ala Gln Pro His Cys His Pro Ala
      115             120             125

```

<210> 39  
 <211> 412  
 <212> DNA  
 <213> Homo sapiens

```

<400> 39
aacgaaggtn ccgtacgcgc tctgaaagcc ctgcgtaaaag agcgttccga tcgccgggaa
60
gtgatngca ccgccaaaat gcaggtggtc gaagccgcga gttcaggcaa gattgtcttt
120
gaaatggaag acgtttatta cagcattgcc ggaaaacaac tggtagagcaa cttctctgcg
180
caagtcacgc gtggtgataa aattgcgctg attggcccga acggttgtgg taaaacgacg
240
ttgctgaaac tgatgttaag taagattcag gcagacagcg gccgtgttca ctgcggtact
300
aaactggaag ttgcgtactt cgaccagcac cgtgctgagc tggatcctga gcgtacgggtg
360
atggataacc tggccgaagg taagcaggaa gtgatggtaa atggccgtgt an
412

```

<210> 40  
 <211> 137  
 <212> PRT  
 <213> Homo sapiens

```

<400> 40
Asn Glu Gly Xaa Val Arg Ala Leu Lys Ala Leu Arg Lys Glu Arg Ser
1              5              10              15
Asp Arg Arg Glu Val Met Xaa Thr Ala Lys Met Gln Val Val Glu Ala
20             25             30
Ala Ser Ser Gly Lys Ile Val Phe Glu Met Glu Asp Val Tyr Tyr Ser
35             40             45
Ile Ala Gly Lys Gln Leu Val Ser Asn Phe Ser Ala Gln Val Met Arg
50             55             60
Gly Asp Lys Ile Ala Leu Ile Gly Pro Asn Gly Cys Gly Lys Thr Thr
65             70             75             80
Leu Leu Lys Leu Met Leu Ser Lys Ile Gln Ala Asp Ser Gly Arg Val
85             90             95
His Cys Gly Thr Lys Leu Glu Val Ala Tyr Phe Asp Gln His Arg Ala
100            105            110
Glu Leu Asp Pro Glu Arg Thr Val Met Asp Asn Leu Ala Glu Gly Lys
115            120            125
Gln Glu Val Met Val Asn Gly Arg Val

```

130

135

<210> 41  
 <211> 1080  
 <212> DNA  
 <213> Homo sapiens

<400> 41  
 gaattcaagt ggacacaggc tccacgcccg cgtctcaccg ataagagcta caagcacaac  
 60  
 tactatgacg agcgggtttc gctcgaagag cgtcttgagc gcactgtggc taaggatttc  
 120  
 gtcacgacgg aggtcgagcc catgtgggat gcggtgatg tcatgcggat gggtaaggat  
 180  
 ctcttcatcc agcacggtct gacgacaaat cggaagtcaa tggagtgggt taagcggtac  
 240  
 taccgccgatt tccgcgttca cgcggtgaat ttccctgggg atccgtaccc gatccatc  
 300  
 gacgcgacct ttgtgccgct tcgtccgggg ctcatcatca acaaccgaa tcgtccactg  
 360  
 ccgcaggagc agaggaagat cttcgaggcc aatgactggc agatcggtga tgctgctcag  
 420  
 ccggcgcacg acacgcctcc agaattgtgc tactcgtctg tgtggctatc aatgaactgc  
 480  
 ttggtacttg atccgaagac ggcatctgc gaggcttcgg aagttcatca gatggagcag  
 540  
 atggacaagc tgggtatgaa cgtcatcccg gtcgccttcc gtgacgcgta cccattcggg  
 600  
 ggaggtctcc actgcgccac agctgatgta tatcgcaag gtacctgtga ggactacttc  
 660  
 ccgaatcagg tcgacgaccc gaccttggtg tgagaaaacc ccgtggatcat gtcatgactg  
 720  
 acggatctcg gtggctcggg acggaactta cgttgtccgt taccgggccg ccgggtctga  
 780  
 tatggcagta tcacgcctag caaaaaggag catgtcatgg acatggagcc gggcatcatc  
 840  
 aacgtcaaac aggaagttcc aggcgtcggg acgatgaacc agaaagtggg attcgtgtcc  
 900  
 atgcttcttt ctgcaacggg tatgggggtg gtgggtactt tcgggcgtct cagcactcct  
 960  
 gtggatccca cgacgggcag taagtacatc atcgggtgatt ttttggccac tggtaggatg  
 1020  
 atagtcgggg tcctgggatt tctgcttatt atcgtcatac ttggaaaatg gtctgagctc  
 1080

<210> 42  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 42  
 Glu Phe Lys Trp Thr Gln Ala Pro Arg Pro Arg Leu Thr Asp Lys Ser  
 1 5 10 15  
 Tyr Lys His Asn Tyr Tyr Asp Glu Arg Val Ser Leu Glu Glu Arg Leu



```

      20      25      30
Glu Arg Thr Val Ala Lys Asp Phe Val Thr Thr Glu Val Glu Pro Met
      35      40      45
Trp Asp Ala Ala Asp Val Met Arg Met Gly Lys Asp Leu Phe Ile Gln
      50      55      60
His Gly Leu Thr Thr Asn Arg Lys Ser Met Glu Trp Phe Lys Arg Tyr
      65      70      75      80
Tyr Pro Asp Phe Arg Val His Ala Val Asn Phe Pro Gly Asp Pro Tyr
      85      90      95
Pro Ile His Ile Asp Ala Thr Phe Val Pro Leu Arg Pro Gly Leu Ile
      100      105      110
Ile Asn Asn Pro Asn Arg Pro Leu Pro Gln Glu Gln Arg Lys Ile Phe
      115      120      125
Glu Ala Asn Asp Trp Gln Ile Val Asp Ala Ala Gln Pro Ala His Asp
      130      135      140
Thr Pro Pro Glu Leu Cys Tyr Ser Ser Val Trp Leu Ser Met Asn Cys
      145      150      155      160
Leu Val Leu Asp Pro Lys Thr Val Ile Cys Glu Ala Ser Glu Val His
      165      170      175
Gln Met Glu Gln Met Asp Lys Leu Gly Met Asn Val Ile Pro Val Ala
      180      185      190
Phe Arg Asp Ala Tyr Pro Phe Gly Gly Gly Leu His Cys Ala Thr Ala
      195      200      205
Asp Val Tyr Arg Glu Gly Thr Cys Glu Asp Tyr Phe Pro Asn Gln Val
      210      215      220
Asp Asp Pro Thr Leu Val
      225      230

```

<210> 43  
 <211> 358  
 <212> DNA  
 <213> Homo sapiens

```

<400> 43
gggcccccca catagtggac acaggtttct gggatgtcag catggagtgc caagaggtgg
60
gtgaccacct ggtggggaat aaggcgcttc tgggacatag aggctgcctt ccagctgcgc
120
ctggcagagc tgttgacaca acagcatggt ctgcagtgcc gggccactgc caccacacc
180
gatgtccttt aaggatggat ttgggttttc ggattcgcgt ggcctatcag cgggagtccc
240
agatcctgaa ggaagtgcag agcccagagg ggatgatctc gctgagggac acagctgcct
300
ccctcgcct tgagagagac acaaggcagt tgccactgct caccagtgcc ctgcacgn
358

```

<210> 44  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

```

<400> 44
Met Glu Cys Gln Glu Val Gly Asp His Leu Val Gly Asn Lys Ala Leu

```

1		5		10		15									
Leu	Gly	His	Arg	Gly	Cys	Leu	Pro	Ala	Ala	Pro	Gly	Arg	Ala	Val	Asp
		20						25					30		
Thr	Thr	Ala	Trp	Ser	Ala	Val	Pro	Gly	His	Cys	His	Ala	His	Arg	Cys
		35						40				45			
Pro	Leu	Arg	Met	Asp	Leu	Gly	Phe	Arg	Ile	Arg	Val	Ala	Tyr	Gln	Arg
	50					55					60				
Glu	Ser	Gln	Ile	Leu	Lys	Glu	Val	Gln	Ser	Pro	Glu	Gly	Met	Ile	Ser
65					70					75				80	
Leu	Arg	Asp	Thr	Ala	Ala	Ser	Leu	Arg	Leu	Glu	Arg	Asp	Thr	Arg	Gln
				85					90					95	
Leu	Pro	Leu	Leu	Thr	Ser	Ala	Leu	His							
		100						105							

&lt;210&gt; 45

&lt;211&gt; 905

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 45

gtcgacgata aaggagtatt tgcgcagcag cagtatgatg ctctcgttga ggcggggttc  
 60  
 gcggctcctg gaatcccaga gcagtatggt ggcgacgggtg cggatgcgat tgcgtccgca  
 120  
 ataatcatgg aagaggtcgc tcgagtctgt gcgtcgtcgt ccaccgtcat atcgtccaat  
 180  
 gagcttggtta ccgtccctct cctcaaatac ggtagcggagg agcagaggaa acgttatctt  
 240  
 tctgaagttg cttcgggtaa ggcacttttc ggatatgcgc tctccgaggc tgatgctgga  
 300  
 tcagatccag ctgcacttaa gtgtcgagcc gacgaagatg gggacagttt cgtcctgaat  
 360  
 ggcggttaagg cttgggtcac ggaggctggc gaggccaagt acctggtgat atttgcggtt  
 420  
 actgaccag acgatccgcg ccacagaatc agcgcgttga tgggtccatgc agatgacccg  
 480  
 ggcattagct acggggctcc ggagcacaaa atggggatac gcgggtcagt taccagggaa  
 540  
 gtggttttca agaatacgcg tatccccaag gaacgagtaa ttggccgtcg agggcacggt  
 600  
 ctgagtgttg ctctaggtag gcttgataac tctcgtgtct cgattgctgc tcaagcagt  
 660  
 ggaattgccc aaggagcttt agacattgcc acggattacg tccagaagcg caagcagttt  
 720  
 ggccagccac tgtccaattt tgagggaatc cagttcatgc tcgcagacat ggcaatgcgt  
 780  
 ttggaggcgg cgcgagcgct gacatactct gcagctgac gtagtgggcg ccagactgac  
 840  
 gatgtgagtt acttcggcgc ggcggccaaa tgtttcgctt ccgacacagc gatggcagtg  
 900  
 tgcac  
 905

&lt;210&gt; 46

<211> 301  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 Val Asp Asp Lys Gly Val Phe Ala Gln Gln Gln Tyr Asp Ala Leu Val  
 1 5 10 15  
 Glu Ala Gly Phe Ala Ala Pro Gly Ile Pro Glu Gln Tyr Gly Gly Asp  
 20 25 30  
 Gly Ala Asp Ala Ile Ala Ser Ala Ile Ile Met Glu Glu Val Ala Arg  
 35 40 45  
 Val Cys Ala Ser Ser Ser Thr Val Ile Ser Ser Asn Glu Leu Gly Thr  
 50 55 60  
 Val Pro Leu Leu Lys Tyr Gly Ser Glu Glu Gln Arg Lys Arg Tyr Leu  
 65 70 75 80  
 Ser Glu Val Ala Ser Gly Lys Ala Leu Phe Gly Tyr Ala Leu Ser Glu  
 85 90 95  
 Ala Asp Ala Gly Ser Asp Pro Ala Ala Leu Lys Cys Arg Ala Asp Glu  
 100 105 110  
 Asp Gly Asp Ser Phe Val Leu Asn Gly Val Lys Ala Trp Val Thr Glu  
 115 120 125  
 Ala Gly Glu Ala Lys Tyr Leu Val Ile Phe Ala Val Thr Asp Pro Asp  
 130 135 140  
 Asp Pro Arg His Arg Ile Ser Ala Leu Met Val His Ala Asp Asp Pro  
 145 150 155 160  
 Gly Ile Ser Tyr Gly Ala Pro Glu His Lys Met Gly Ile Arg Gly Ser  
 165 170 175  
 Val Thr Arg Glu Val Val Phe Lys Asn Thr Arg Ile Pro Lys Glu Arg  
 180 185 190  
 Val Ile Gly Arg Arg Gly His Gly Leu Ser Val Ala Leu Gly Thr Leu  
 195 200 205  
 Asp Asn Ser Arg Val Ser Ile Ala Ala Gln Ala Val Gly Ile Ala Gln  
 210 215 220  
 Gly Ala Leu Asp Ile Ala Thr Asp Tyr Val Gln Lys Arg Lys Gln Phe  
 225 230 235 240  
 Gly Gln Pro Leu Ser Asn Phe Glu Gly Ile Gln Phe Met Leu Ala Asp  
 245 250 255  
 Met Ala Met Arg Leu Glu Ala Ala Arg Ala Leu Thr Tyr Ser Ala Ala  
 260 265 270  
 Asp Arg Ser Gly Arg Gln Thr Asp Asp Val Ser Tyr Phe Gly Ala Ala  
 275 280 285  
 Ala Lys Cys Phe Ala Ser Asp Thr Ala Met Ala Val Cys  
 290 295 300

<210> 47  
 <211> 379  
 <212> DNA  
 <213> Homo sapiens

<400> 47  
 aagcttgtag agctagtccg aagcggactg tccgtacgcc aagctgctaa aagatgtggg  
 60  
 atgcattctta ccgctgcgta tgccgtagct acggaagctg ggtgccatat ccggttaagt  
 120

cagtatgctc ggaaagtccg ccagacgcag ttaagagtgg aatacctgcg ccttcggctg  
 180  
 gcgagcctgc ctggtggtga tgctggcgcg gcagtaggaa ttgatcgctg actgcgttta  
 240  
 gatttcgaaa aaggactcac caaatcccag ggtcgacgag aagagttcat acccgtcggc  
 300  
 gaagacgcca gcacgtataa cagacttatg aaagcgctgc gccaacgcca tgatgtcatc  
 360  
 aaatccggaa agcttgccc  
 379

<210> 48

<211> 106

<212> PRT

<213> Homo sapiens

<400> 48

Met	His	Leu	Thr	Ala	Ala	Tyr	Ala	Val	Ala	Thr	Glu	Ala	Gly	Cys	His
1				5				10					15		
Ile	Arg	Leu	Ser	Gln	Tyr	Ala	Arg	Lys	Val	Arg	Gln	Thr	Gln	Leu	Arg
		20					25					30			
Val	Glu	Tyr	Leu	Arg	Leu	Arg	Leu	Ala	Ser	Leu	Pro	Gly	Gly	Asp	Ala
	35				40						45				
Gly	Ala	Ala	Val	Gly	Ile	Asp	Arg	Arg	Leu	Arg	Leu	Asp	Phe	Glu	Lys
	50				55				60						
Gly	Leu	Thr	Lys	Ser	Gln	Gly	Arg	Arg	Glu	Glu	Phe	Ile	Pro	Val	Gly
65				70					75				80		
Glu	Asp	Ala	Ser	Thr	Tyr	Asn	Arg	Leu	Met	Lys	Ala	Leu	Arg	Gln	Arg
			85					90					95		
His	Asp	Val	Ile	Lys	Ser	Gly	Lys	Leu	Ala						
		100						105							

<210> 49

<211> 309

<212> DNA

<213> Homo sapiens

<400> 49

tgatcatgat gctggcatgg actattctgg tccctgttcc tctctcacct gctgaaggac  
 60  
 atccctctaa tttttgtgtc tccttctgta tcatcaaatt ttccctctct actgagtctc  
 120  
 ttgcatctcc ttggaagcat gctgtactat gtcccatcct taaagaactc cccttgctctg  
 180  
 cacattaccc tctgccagct ggctcatttt tctgctcccc ttacagggga aactcttcaa  
 240  
 aaagtatatc ccacctcctt ccatctcatg ttctcttgaa cctgcagtac tgggtgctcc  
 300  
 ctctttttg  
 309

<210> 50

<211> 101

<212> PRT

<213> Homo sapiens

<400> 50

```

Met Met Leu Ala Trp Thr Ile Leu Val Pro Val Pro Leu Ser Pro Ala
 1           5           10           15
Glu Gly His Pro Ser Asn Phe Cys Val Ser Phe Cys Ile Ile Lys Phe
      20           25           30
Ser Leu Ser Thr Glu Ser Leu Ala Ser Pro Trp Lys His Ala Val Leu
      35           40           45
Cys Pro Ile Leu Lys Glu Leu Pro Leu Ser Ala His Tyr Pro Leu Pro
      50           55           60
Ala Gly Ser Phe Phe Cys Ser Pro Leu Gln Gly Asn Ser Ser Lys Ser
65           70           75           80
Tyr Leu His Leu Leu Pro Ser His Val Leu Leu Asn Leu Gln Tyr Trp
      85           90           95
Val Leu Pro Pro Phe
      100

```

<210> 51

<211> 512

<212> DNA

<213> Homo sapiens

<400> 51

```

agatccttga agaattgcc aactgtcttc ctcctgctt ataatttcct tattccctag
60
gatgtgatcc ttgttcttgg ggcctcacat ggcagctgga tctctggcga ttgcatctga
120
gttccagaca ccaggatgga aaagaaaaga aggaggggca agaggaaccc ccagatgctc
180
cttaagagct actgcgtggc attcccactt gcatctcatt tgctcgatcg ctgtcactgt
240
gccctaacga gctgcaagga cactggggaa atgagtctgt cttgtacttc atgtgccccct
300
caaaatcttc tgttgctgag ggagaagagg ccagccggta ttgaggaaca actagcactt
360
tctgcttccg cgteccaggg ggacgtgggt gtgttgaatc cacaccgggg gtgcggacct
420
ctgaggctgg gctggatggg acatcaggtg ggcctctgt ttcatttatg tgacctccca
480
tcaggctctc tggttggatc ctgctttcta ga
512

```

<210> 52

<211> 125

<212> PRT

<213> Homo sapiens

<400> 52

```

Met Glu Lys Lys Arg Arg Arg Gly Lys Arg Asn Pro Gln Met Leu Leu
 1           5           10           15
Lys Ser Tyr Cys Val Ala Phe Pro Leu Ala Ser His Leu Leu Asp Arg
      20           25           30
Cys His Cys Ala Leu Thr Ser Cys Lys Asp Thr Gly Glu Met Ser Leu

```

```

          35          40          45
Ser Cys Thr Ser Cys Ala Pro Gln Asn Leu Leu Leu Leu Arg Glu Lys
          50          55          60
Arg Pro Ala Gly Ile Glu Glu Gln Leu Ala Leu Ser Ala Ser Ala Ser
65          70          75          80
Gln Gly Asp Val Gly Val Leu Asn Pro His Arg Gly Cys Gly Pro Leu
          85          90          95
Arg Leu Gly Trp Met Gly His Gln Val Gly Pro Leu Phe His Leu Cys
          100          105          110
Asp Leu Pro Ser Gly Leu Leu Val Gly Ser Cys Phe Leu
          115          120          125

```

<210> 53  
 <211> 474  
 <212> DNA  
 <213> Homo sapiens

```

<400> 53
accggtacac ctacgtcacc cgtaaaaacc gacgcaatac ccggatcgcc tcgtcctcaa
60
aaaattcgat cccgtcgtgc gtcgtcacat tgagttcaag gagggccgct aatggccaaa
120
aagtccaaga ttgtcgccca gaagaaacgt gagaagctcg tagcccaata cgccgaaagg
180
cgcgccgaac tcaaggccat catgaagtgc ccaactgcct cattggacga acgcatggag
240
gcatcgcgta agctgtctcg cctgccgcgc gattcatccc ccgtgcggtt acgtaaccgt
300
gaccaagtcg acgggcgtcc ccgcggctac gttggcaagg ccggtgtgtc ccgtatccgt
360
ttccgtgaga tggcccaccg cggcgaactc cccggaatcg cgaagtcaag ctggtgaagc
420
catggcagta ccgaagcgaa agaagtcccg ttcgaccacg cgtcataggc gggc
474

```

<210> 54  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

```

<400> 54
Met Ala Lys Lys Ser Lys Ile Val Ala Gln Lys Lys Arg Glu Lys Leu
1          5          10          15
Val Ala Gln Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Met Lys
          20          25          30
Cys Pro Thr Ala Ser Leu Asp Glu Arg Met Glu Ala Ser Arg Lys Leu
          35          40          45
Ser Arg Leu Pro Arg Asp Ser Ser Pro Val Arg Leu Arg Asn Arg Asp
          50          55          60
Gln Val Asp Gly Arg Pro Arg Gly Tyr Val Gly Lys Ala Gly Val Ser
65          70          75          80
Arg Ile Arg Phe Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Ile
          85          90          95
Ala Lys Ser Ser Trp

```

100

<210> 55  
 <211> 378  
 <212> DNA  
 <213> Homo sapiens

<400> 55  
 ccatggccca ggacagccgg catatcggct acgactacgg tacaccggtg gcgccacagt  
 60  
 tcggcgcagc caagcccgca gcgtgctgcc aggcgcaagc gacaaacacc ggcccgtggg  
 120  
 tgggtgttcca ccatgtgcgt tgcacccacg acacctttct gatcgacgtc tttctcaacc  
 180  
 agcccgatgc caccgcgcag caggtcaatg ccgacaacce gcactacgtc gggcgtttca  
 240  
 gccgcacgg catggggctg gtggatgaca agggccgttg cattaccag ggcgtatcgc  
 300  
 gcgcgttgaa tcgggcgcgc agcaccaagg cgctgaacct gggaccgagt gacgcggcgc  
 360  
 agttatcggg gaggcgta  
 378

<210> 56  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 56  
 Met Ala Gln Asp Ser Arg His Ile Gly Tyr Asp Tyr Gly Thr Pro Val  
 1 5 10 15  
 Ala Pro Gln Phe Gly Ala Ala Lys Pro Ala Ala Cys Cys Gln Ala Gln  
 20 25 30  
 Ala Thr Asn Thr Gly Pro Trp Val Val Phe Asp His Val Arg Cys Thr  
 35 40 45  
 His Asp Thr Phe Leu Ile Asp Val Phe Leu Asn Gln Pro Asp Ala Thr  
 50 55 60  
 Ala Gln Gln Val Asn Ala Asp Asn Pro His Tyr Val Gly Arg Phe Ser  
 65 70 75 80  
 Arg Ile Gly Met Gly Leu Val Asp Asp Lys Gly Arg Cys Ile Thr Gln  
 85 90 95  
 Gly Val Ser Arg Ala Leu Asn Ala Ala Arg Ser Thr Lys Ala Leu Asn  
 100 105 110  
 Leu Gly Pro Ser Asp Ala Ala Gln Leu Ser Val Arg Arg  
 115 120 125

<210> 57  
 <211> 388  
 <212> DNA  
 <213> Homo sapiens

<400> 57  
 agaccacccc gacacagatc aggagtcgtc atgtccagaa agaagaaggc cggcatcctc  
 60

accgcaggcg gtgattgccc cgggctcaac gccgctatcc ggggatttgg caaggctgcc  
 120  
 atccgccagc acgacatgga gctcatcggt attcaggacg gctttcttgg attggcggga  
 180  
 aaccgcacca tctcccttgg ccgcgctgcc ctctcaggca tcttgacggt cggcggggacc  
 240  
 atcctgggaa ctagccgtga caaggtaaat cacatgatta tcgacggcga ggaacgggat  
 300  
 atgggtcccca ccaccgtcga gaattacgag aagctggggc ttgacgcttt ggtgactttg  
 360  
 ggtggcgggtg gcaccgcaa gaacgcgt  
 388

<210> 58  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

<400> 58  
 Arg Pro Thr Arg His Arg Ser Gly Val Val Met Ser Arg Lys Lys Lys  
 1 5 10 15  
 Val Gly Ile Leu Thr Ala Gly Gly Asp Cys Pro Gly Leu Asn Ala Ala  
 20 25 30  
 Ile Arg Gly Phe Gly Lys Ala Ala Ile Arg Gln His Asp Met Glu Leu  
 35 40 45  
 Ile Gly Ile Gln Asp Gly Phe Leu Gly Leu Ala Gly Asn Arg Thr Ile  
 50 55 60  
 Ser Leu Gly Pro Arg Ala Leu Ser Gly Ile Leu Thr Val Gly Gly Thr  
 65 70 75 80  
 Ile Leu Gly Thr Ser Arg Asp Lys Val Asn His Met Ile Ile Asp Gly  
 85 90 95  
 Glu Glu Arg Asp Met Val Pro Thr Thr Val Glu Asn Tyr Glu Lys Leu  
 100 105 110  
 Gly Leu Asp Ala Leu Val Thr Leu Gly Gly Gly Gly Thr Ala Lys Asn  
 115 120 125  
 Ala

<210> 59  
 <211> 417  
 <212> DNA  
 <213> Homo sapiens

<400> 59  
 ggtaccatcg gagctcgaca agaaatggtt ggggtgaagtc gtggcttctg ctccacccag  
 60  
 tgccctcatg ggtcagccca cctgaatatc ttcatgcctg tgcatttctc ctgatgttca  
 120  
 cgtgtgccct gtgtttttac gcattctgtga tcgtgcaccc acgcgtctca gagaggagcc  
 180  
 cgtttgggaa tccggagaat gtgcgctggc ggaagagcgt cacacactgg aagcaaacct  
 240  
 cagaccgcgt ggacaagacc aaggatgaaa tggaacacga ggccttggtg gaaggggaacc  
 300



tggcaaccga ggcaagccta gtggttctgg acacactgga gatcatcgtg cagacgggtga  
 360  
 tgctttcaga agccccgggag agcgtcttgg gggcagtgtg gaaggttgtg ctgtaca  
 417

<210> 60  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 60  
 Met Phe Thr Cys Ala Leu Cys Phe Tyr Ala Ser Val Ile Val His Pro  
 1 5 10 15  
 Arg Val Ser Glu Arg Ser Pro Phe Gly Asn Pro Glu Asn Val Arg Trp  
 20 25 30  
 Arg Lys Ser Val Thr His Trp Lys Gln Thr Ser Asp Arg Val Asp Lys  
 35 40 45  
 Thr Lys Asp Glu Met Glu His Glu Ala Leu Val Glu Gly Asn Leu Ala  
 50 55 60  
 Thr Glu Ala Ser Leu Val Val Leu Asp Thr Leu Glu Ile Ile Val Gln  
 65 70 75 80  
 Thr Val Met Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Ala Val Leu  
 85 90 95  
 Lys Val Val Leu Tyr  
 100

<210> 61  
 <211> 304  
 <212> DNA  
 <213> Homo sapiens

<400> 61  
 agatcttcac agccttagac ttttttcatg ggtgccttac agttttggag gtccttatcc  
 60  
 gcacacatat ttgcaggctt ggagagagtg tgtgggggca tgtactttcg gtgggtcaag  
 120  
 tatgaagaag caggccttat aaacacatat tctgacctta acctgtactt cagaagagga  
 180  
 ccgctgactc accaaggagg cctgaaggac aaggcagcat ctctgtcttc acatgagtcc  
 240  
 tcccctagac cgggcccctg gccaggcctg accacagagc tcccattgcc tttcctgcac  
 300  
 gcgt  
 304

<210> 62  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 62  
 Met Gly Ala Leu Gln Phe Trp Arg Ser Leu Ser Ala His Ile Phe Ala  
 1 5 10 15

```

Gly Leu Glu Arg Val Cys Gly Gly Met Tyr Phe Arg Trp Val Lys Tyr
20          25          30
Glu Glu Ala Gly Leu Ile Asn Thr Tyr Ser Asp Leu Asn Leu Tyr Phe
          35          40          45
Arg Arg Gly Pro Leu Thr His Gln Gly Gly Leu Lys Asp Lys Ala Ala
          50          55          60
Ser Leu Ser Ser His Glu Ser Ser Pro Arg Pro Gly Pro Trp Pro Gly
65          70          75          80
Leu Thr Thr Glu Leu Pro Leu Pro Phe Leu His Ala
          85          90

```

<210> 63  
 <211> 577  
 <212> DNA  
 <213> Homo sapiens

```

<400> 63
cgcgctcaagg ggggtctacac cgggacgatt aacgcctcgg tgggagtatt catcaccgcg
60
ctgacgggtgc tagctgggtg gctcacccta gccgggcgta tcagtgtcgg ggaactcgtc
120
accgtgggtcg ggctggccca aacctcggc cctccgctgc gagcactggg cgtcgacacc
180
gcgacgatgt tggccaccgc ccacgcctcc ggggaccgat tctgtgagtt gcgtgatagc
240
ccggcagcct ggcagatcca ccccgacgac ggtgcccgc caacaccggg tgatggcccg
300
gtggagtgc acatcccgtt cagggatttc cagcttgacg tcgccggcgg caccatgtg
360
ggtatcatgg cgcctcaatc ggtctgtgac gccttgccg aggcgataga ccacggctcc
420
gagaccgtct tgaatggggg tcccgccagt cgctcaacc ctgcccacg gcgtcgtctg
480
gtgctgggtg ctccccgctc cccgaactg ttcgacgata ctgcccggtc gaacatcgtg
540
cttgacagcc agacgactgt cgccaggctg aatgcat
577

```

<210> 64  
 <211> 192  
 <212> PRT  
 <213> Homo sapiens

```

<400> 64
Arg Val Lys Gly Val Tyr Thr Gly Thr Ile Asn Ala Ser Val Gly Val
1          5          10          15
Phe Ile Thr Ala Leu Thr Val Leu Ala Gly Trp Leu Thr Leu Ala Gly
          20          25          30
Arg Ile Ser Val Gly Glu Leu Val Thr Val Val Gly Leu Ala Gln Thr
          35          40          45
Leu Gly Pro Pro Leu Arg Ala Leu Gly Val Asp Thr Ala Thr Met Leu
          50          55          60
Ala Thr Ala His Ala Ser Gly Asp Arg Phe Cys Glu Leu Arg Asp Ser
65          70          75          80

```

```

Pro Ala Ala Trp Gln Ile His Pro Asp Asp Gly Ala Arg Thr Thr Pro
      85              90              95
Gly Asp Gly Pro Val Glu Leu His Ile Pro Val Arg Asp Phe Gln Leu
      100            105            110
Asp Val Ala Gly Gly Thr His Val Gly Ile Met Ala Pro Gln Ser Val
      115            120            125
Cys Asp Ala Leu Ala Glu Ala Ile Asp His Gly Ser Glu Thr Val Leu
      130            135            140
Asn Gly Val Pro Ala Ser Arg Leu Asn Pro Ala Gln Arg Arg Arg Leu
      145            150            155            160
Val Leu Val Ala Pro Arg Ser Pro Glu Leu Phe Asp Asp Thr Ala Arg
      165            170            175
Ala Asn Ile Val Leu Asp Ser Gln Thr Thr Val Ala Arg Leu Asn Ala
      180            185            190

```

<210> 65  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

```

<400> 65
gtcgaccgcg ccttgggatc gctcgaaggg gccagcctgg accaggtagc ggaagaagtc
60
aagaaggccg ctttcaagat caccgcgcc gggcaactag tgggcacat ggctccgag
120
cgcttggcg tacccttcgg catcatcgac ctttcgcttg cccctactgc cgaattggga
180
gattcggggg ccacatcct tgagcatatg ggattggacc aagtaggcac gcacggcaca
240
actgctgctt tggtctgct taacgacgcc gtaaagaaag gcggcatgat ggctgcccc
300
cgcgtcggcg gtttgtctgg ctcttcac cgggctcc
339

```

<210> 66  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

```

<400> 66
Val Asp Arg Ala Leu Gly Ser Leu Glu Gly Ala Ser Leu Asp Gln Val
1      5      10      15
Ala Glu Glu Val Lys Lys Ala Ala Phe Lys Ile Thr Arg Ala Gly Gln
      20      25      30
Leu Val Gly Thr Met Ala Ser Glu Arg Leu Gly Val Pro Phe Gly Ile
      35      40      45
Ile Asp Leu Ser Leu Ala Pro Thr Ala Glu Leu Gly Asp Ser Gly Ala
      50      55      60
His Ile Leu Glu His Met Gly Leu Asp Gln Val Gly Thr His Gly Thr
      65      70      75      80
Thr Ala Ala Leu Ala Leu Asn Asp Ala Val Lys Lys Gly Gly Met
      85      90      95
Met Ala Cys Pro Arg Val Gly Gly Leu Ser Gly Ser Phe Ile Pro Gly
      100      105      110

```

Ser

<210> 67  
 <211> 446  
 <212> DNA  
 <213> Homo sapiens

<400> 67  
 tgatcataaa ccacgcgtca ccgaggggat gtggcacacc tacctgcgcg tcgcagatgc  
 60  
 cgcacaggca cgggtcaggg gcgttcgcgg cgccagctgg cacaacttcg cgaccggtga  
 120  
 caaggggtcc ttcgacgcca acgagcttgc cgtaactcct gatactgaca ccgtcatcca  
 180  
 gggagtcggg cccgccttag ccctcctcga ttcagcgtgg ggacgccaga tccacgtgga  
 240  
 gacaacaggg tgtcccagtg ccgtggtctg gaatccacgc tcctcgtcga cacatgccga  
 300  
 taacccgaca gcccaggcat ggcgcgattt cgtatgcgtc gagaccgggg cctgcaagga  
 360  
 caatgcggtc attgttgccc cacacagcga cctcaccatg tccacacgga ttagcgtcga  
 420  
 aacgttgtga tcgctgcatg gatatt  
 446

<210> 68  
 <211> 133  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
 Met Trp His Thr Tyr Leu Arg Val Ala Asp Ala Ala Gln Ala Arg Val  
 1 5 10 15  
 Arg Gly Val Arg Gly Ala Ser Trp His Asn Phe Ala Thr Gly Asp Lys  
 20 25 30  
 Gly Ser Phe Asp Ala Asn Glu Leu Ala Val Thr Pro Asp Thr Asp Thr  
 35 40 45  
 Val Ile Gln Gly Val Gly Pro Ala Leu Ala Leu Leu Asp Ser Ala Trp  
 50 55 60  
 Gly Arg Gln Ile His Val Glu Thr Thr Gly Cys Pro Ser Ala Val Val  
 65 70 75 80  
 Trp Asn Pro Arg Ser Ser Ser Thr His Ala Asp Asn Pro Thr Ala Gln  
 85 90 95  
 Ala Trp Arg Asp Phe Val Cys Val Glu Thr Gly Ala Cys Lys Asp Asn  
 100 105 110  
 Ala Val Ile Val Ala Pro His Ser Asp Leu Thr Met Ser Thr Arg Ile  
 115 120 125  
 Ser Val Glu Thr Leu  
 130

<210> 69  
 <211> 552  
 <212> DNA

<213> Homo sapiens

<400> 69

```

nnaagggttaa ggagaaaagc aaggaccttg caaagagagc ctctgtgccg gagaggctgg
60
ccctcaagga ggagccaaaa gaagacccca gtggagcagc tgtgcccag atgccaaaaa
120
agtcctccaa gattgccagc ttcattccca aaggggggaa gctcaacagt gccaagaagg
180
agcnccatgg ccccttcctt cagtggaata ccaaaccag gaatgaaaag catgcccggg
240
aaatccccaa gtgcccagc gccttccaag gaaggggagc ggagccggag tgggaagctg
300
agctcaggac tccccagca gaagccccag ctggacggca gacactccag ttcctcttcc
360
agcctggcgt cctcagaagg aaaaggccca ggagggacca ccctgaacca cagcatcagc
420
agccagactg tcagtgggtc tgcggggacc acccagacca caggaagcaa tnnaccgtca
480
gtgttcagct acctcagccc cagcagcaat acaaccatcc caacactgcc acggttgac
540
ctttcctgta ca
552

```

<210> 70

<211> 184

<212> PRT

<213> Homo sapiens

<400> 70

```

Xaa Arg Val Arg Arg Lys Ala Arg Thr Leu Gln Arg Glu Pro Leu Cys
1      5      10      15
Arg Arg Gly Trp Pro Ser Arg Arg Ser Gln Lys Lys Thr Pro Val Glu
20     25     30
Gln Leu Cys Pro Arg Cys Gln Lys Ser Pro Pro Arg Leu Pro Ala Ser
35     40     45
Ser Pro Lys Gly Gly Ser Ser Thr Val Pro Arg Arg Ser Xaa Met Ala
50     55     60
Pro Ser Leu Ser Gly Ile Pro Lys Pro Gly Met Lys Ser Met Pro Gly
65     70     75     80
Lys Ser Pro Ser Ala Pro Ala Pro Ser Lys Glu Gly Glu Arg Ser Arg
85     90     95
Ser Gly Lys Leu Ser Ser Gly Leu Pro Gln Gln Lys Pro Gln Leu Asp
100    105    110
Gly Arg His Ser Ser Ser Ser Ser Ser Leu Ala Ser Ser Glu Gly Lys
115    120    125
Gly Pro Gly Gly Thr Thr Leu Asn His Ser Ile Ser Ser Gln Thr Val
130    135    140
Ser Gly Ser Val Gly Thr Thr Gln Thr Thr Gly Ser Asn Xaa Pro Ser
145    150    155    160
Val Phe Ser Tyr Leu Ser Pro Ser Ser Asn Thr Thr Ile Pro Thr Leu
165    170    175
Pro Arg Leu His Leu Ser Cys Thr
180

```

<210> 71  
 <211> 316  
 <212> DNA  
 <213> Homo sapiens

<400> 71  
 cgcggttgaaa tggcggttcga acttaaacgt ttacatattg actccgtgcc attaaacatt  
 60  
 ttgaatcctg ttaaaggagac tccatttgaa agcaacgaag ctttacgtcc tttaaatac  
 120  
 ttacgtacct tcgccgtatt ccgtttcatc ttgccaaacg cattgatagc aactgcaggt  
 180  
 ggccgcgaag taaatctacg agacttacaa gcttatgctc taaaagggtg cctaaacggt  
 240  
 atcatgggtg gtggctactt aactactggc ggtcggtcac ctcaagacga tctccaaatg  
 300  
 attcaagact tggagt  
 316

<210> 72  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 72  
 Arg Val Glu Met Ala Phe Glu Leu Lys Arg Leu His Ile Asp Ser Val  
 1 5 10 15  
 Pro Leu Asn Ile Leu Asn Pro Val Lys Gly Thr Pro Phe Glu Ser Asn  
 20 25 30  
 Glu Ala Leu Arg Pro Leu Asn Ile Leu Arg Thr Phe Ala Val Phe Arg  
 35 40 45  
 Phe Ile Leu Pro Asn Ala Leu Ile Arg Thr Ala Gly Gly Arg Glu Val  
 50 55 60  
 Asn Leu Arg Asp Leu Gln Ala Tyr Ala Leu Lys Gly Gly Leu Asn Gly  
 65 70 75 80  
 Ile Met Val Gly Gly Tyr Leu Thr Thr Gly Gly Arg Ser Pro Gln Asp  
 85 90 95  
 Asp Leu Gln Met Ile Gln Asp Leu Glu  
 100 105

<210> 73  
 <211> 384  
 <212> DNA  
 <213> Homo sapiens

<400> 73  
 nntaccggca agatcctggc cgaagggtgac gtcgaggttt ctgaggctat cgactttgct  
 60  
 gcttggtatg tcgaccgagc cgaggagctc gagggcgctg acggtgcca gtttgtgccg  
 120  
 ccacgagtga ccgtcgctac cccgccgtgg aacttcgccc tgtctattac cgccggatcc  
 180

acccttgccg ctctggccgc cggatcgta gtactactca agcccgctcc acaggccccg  
 240  
 cactgtgctg ccgtcatctc tgaatgctg tgggaggctg ggatccccgc ggacgttctg  
 300  
 cagctcgctg atgttgagga aaatgaggct ggtaaacc tggtagacca ccccgaggtc  
 360  
 gatcgggtca tcctcacggg aggt  
 384

<210> 74  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 74  
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 Pro Trp Asn Phe Ala Leu Ser Ile Thr Ala Gly Ser Thr Leu Ala Ala  
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 <211> 405  
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 <213> Homo sapiens

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<210> 76

<211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 76  
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 Arg Gly Val Trp Cys Asn Asn Leu Val Tyr Asn Ile His Leu Leu Thr  
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 65 70 75 80  
 Pro Ser Ala Cys Gly Thr Ala Arg Glu Val Gly Thr Phe Ser His Arg  
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<210> 78

<211> 799

<212> PRT

<213> Homo sapiens

<400> 78

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Leu	His	Leu	Gly	Val	Pro	His	Gly	Ala	Ile	Pro	Gly	Ser	Glu	Arg	Ala
		20					25						30		
Thr	Ala	Ser	Ile	Ile	Gly	Asp	Val	Met	Gly	Pro	Thr	Leu	Asn	His	Leu
		35				40						45			
Asn	Asn	Leu	Leu	Arg	Leu	Pro	Phe	Gly	Cys	Gly	Glu	Gln	Asn	Met	Ile
	50				55					60					
His	Phe	Ala	Pro	Asn	Val	Phe	Val	Leu	Lys	Tyr	Leu	Gln	Lys	Thr	Gln
65				70				75						80	
Gln	Leu	Ser	Pro	Glu	Val	Glu	Arg	Glu	Thr	Thr	Asp	Tyr	Leu	Val	Gln
			85					90						95	
Gly	Tyr	Gln	Arg	Gln	Leu	Thr	Tyr	Lys	Arg	Gln	Asp	Gly	Ser	Tyr	Ser
		100					105						110		
Ala	Phe	Gly	Glu	Arg	Asp	Ala	Ser	Gly	Ser	Met	Trp	Leu	Thr	Ala	Phe
	115					120						125			
Val	Leu	Lys	Ser	Phe	Ala	Gln	Ala	Arg	Ser	Phe	Ile	Phe	Val	Asp	Pro
	130				135						140				
Arg	Glu	Leu	Ala	Ala	Ala	Lys	Ser	Trp	Ile	Ile	Gln	Gln	Gln	Gln	Ala
145				150					155					160	
Asp	Gly	Ser	Phe	Leu	Ala	Val	Gly	Arg	Val	Leu	Asn	Lys	Asp	Ile	Gln
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Gly	Gly	Ile	His	Gly	Ile	Val	Pro	Leu	Thr	Ala	Tyr	Val	Val	Val	Ala
		180					185						190		
Leu	Leu	Glu	Thr	Gly	Thr	Ala	Ser	Glu	Glu	Glu	Arg	Gly	Ser	Thr	Asp
	195						200					205			
Lys	Ala	Arg	His	Phe	Leu	Glu	Ser	Ala	Ala	Pro	Leu	Ala	Met	Asp	Pro
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Tyr	Ser	Cys	Ala	Leu	Thr	Thr	Tyr	Ala	Leu	Thr	Leu	Leu	Arg	Ser	Pro
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Ala	Ala	Pro	Glu	Ala	Leu	Arg	Lys	Leu	Arg	Ser	Leu	Ala	Ile	Met	Arg
			245					250						255	
Asp	Gly	Val	Thr	His	Trp	Ser	Leu	Ser	Asn	Ser	Trp	Asp	Val	Asp	Lys
		260					265						270		
Gly	Thr	Phe	Leu	Ser	Phe	Ser	Asp	Arg	Val	Ser	Gln	Ser	Val	Val	Ser
	275					280						285			
Ala	Glu	Val	Glu	Met	Thr	Ala	Tyr	Ala	Leu	Leu	Thr	Tyr	Thr	Leu	Leu
	290				295						300				
Gly	Asp	Val	Ala	Ala	Ala	Leu	Pro	Val	Val	Lys	Trp	Leu	Ser	Gln	Gln

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Asn Leu Thr Val Ser Leu Ala Ser Thr Asn Leu Asp Tyr Gln Glu Thr
          355          360          365
Phe Glu Leu His Arg Thr Asn Gln Lys Val Leu Gln Thr Ala Ala Ile
          370          375          380
Pro Ser Leu Pro Thr Gly Leu Phe Val Ser Ala Lys Gly Asp Gly Cys
385          390          395          400
Cys Leu Met Gln Ile Asp Val Thr Tyr Asn Val Pro Asp Pro Val Ala
          405          410          415
Lys Pro Ala Phe Gln Leu Leu Val Ser Leu Gln Glu Pro Glu Ala Gln
          420          425          430
Gly Arg Pro Pro Met Pro Ala Ser Ala Ala Glu Gly Ser Arg Gly
          435          440          445
Asp Trp Pro Pro Ala Asp Asp Asp Asp Pro Ala Ala Asp Gln His His
          450          455          460
Gln Glu Tyr Lys Val Met Leu Glu Val Cys Thr Arg Trp Leu His Ala
465          470          475          480
Gly Ser Ser Asn Met Ala Val Leu Glu Val Pro Leu Leu Ser Gly Phe
          485          490          495
Arg Ala Asp Ile Glu Ser Leu Glu Gln Leu Leu Leu Asp Lys His Met
          500          505          510
Gly Met Lys Arg Tyr Glu Val Ala Gly Arg Arg Val Leu Phe Tyr Phe
          515          520          525
Asp Glu Ile Pro Ser Arg Cys Leu Thr Cys Val Arg Phe Arg Ala Leu
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Arg Glu Cys Val Val Gly Arg Thr Ser Ala Leu Pro Val Ser Val Tyr
          545          550          555          560
Asp Tyr Tyr Glu Pro Ala Phe Glu Ala Thr Arg Phe Tyr Asn Val Ser
          565          570          575
Thr His Ser Pro Leu Ala Arg Glu Leu Cys Ala Gly Pro Ala Cys Asn
          580          585          590
Glu Val Glu Arg Ala Pro Ala Arg Gly Pro Gly Trp Phe Pro Gly Glu
          595          600          605
Ser Gly Pro Ala Val Ala Pro Glu Glu Gly Ala Ala Ile Ala Arg Cys
          610          615          620
Gly Cys Asp His Asp Cys Gly Ala Gln Gly Asn Pro Val Cys Gly Ser
          625          630          635          640
Asp Gly Val Val Tyr Ala Ser Ala Cys Arg Leu Arg Glu Ala Ala Cys
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Arg Gln Ala Ala Pro Leu Glu Pro Ala Pro Pro Ser Cys Cys Ala Leu
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Glu Gln Arg Leu Pro Ala Ser Ser Ser Thr Tyr Gly Asp Asp Leu
          675          680          685
Ala Ser Val Ala Pro Gly Pro Leu Gln Gln Asp Val Lys Leu Asn Gly
          690          695          700
Ala Gly Leu Glu Val Glu Asp Ser Asp Pro Glu Pro Glu Gly Glu Ala
          705          710          715          720
Glu Asp Arg Val Thr Ala Gly Pro Arg Pro Pro Val Ser Ser Gly Asn
          725          730          735
Leu Glu Ser Ser Thr Gln Ser Ala Ser Pro Phe His Arg Trp Gly Gln

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<210> 79
<211> 346
<212> DNA
<213> Homo sapiens
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<210> 80
<211> 101
<212> PRT
<213> Homo sapiens
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<400> 80
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      20                    25              30
Asp Val Gly Leu Ser Glu Gly Ala Val Lys Tyr Phe Gln Ser Arg Thr
    35                40              45
Asn Asp Phe Met Ala Leu Ser Ile Asp Ala Val Ala Ser Ala Asp Ala
  50                55              60
Tyr Ser Val Gly Phe Pro Gly Phe Gly Gly Met Asn Leu Ala Pro Ile
65                70              75              80
Ser Glu Glu Ala Ala Ala Glu Met Glu Glu Pro Tyr Ile Tyr His Phe
      85                90              95
Pro Asp Gly Asn Ala
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<210> 81
<211> 429
<212> DNA
<213> Homo sapiens
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<400> 81

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 429

<210> 82  
 <211> 79  
 <212> PRT  
 <213> Homo sapiens

<400> 82  
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 His Val His Val Cys Ala Pro Val Cys Met Ser Val Cys Thr Arg  
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<210> 83  
 <211> 411  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
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 411

<210> 84  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
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 Gly Leu Thr Lys Val Gln Lys Ile Val Ala Ala Ser Glu Phe Leu Arg  
 20 25 30  
 Asn Asp Leu Ile Gly Leu Gly Ile Asp Lys Ala Lys Ile Glu Ile Ile  
 35 40 45  
 His Asn Gly Ile Asp His Arg Pro Phe Phe Pro Gln Leu Gln Ile Asp  
 50 55 60  
 Ala Glu Thr Val Thr Ile Lys Pro Phe Ala Ile Lys Arg Pro Tyr Phe  
 65 70 75 80  
 Ile Tyr Gly Ser Arg Leu Ser Gly Pro Glu Lys Lys His Ile Glu Leu  
 85 90 95  
 Ile Lys Ala Phe Ala Leu Phe Lys Glu Arg Thr Lys Ser Pro His Pro  
 100 105 110  
 Leu Val Ile Ala Gly Ala Glu Gly Pro Ser Ser Glu Glu Val His  
 115 120 125

<210> 85  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
 nnacgcgtgc cgcgcaaggg aaccatgttc gtgtcgggtgc gcgaaaccga caaggcgcgc  
 60  
 atcctcgacg cggtgaaact gctgagttcg ctcggttca aggtgatcgc cacctcgggc  
 120  
 acccagcgtt tcctggtgga gaacggagta ccggcggaag agatcaacaa ggtgctggaa  
 180  
 ggccgcccgc acattgttga cgcaattacc aacggcgagg tgcaactcgt tttcaatacc  
 240  
 accgaggggc cacaggcgct ggctgacagc cgctcgttgc gacgcgctgc cctcttgc  
 300  
 aaagtgccat attacaccac tctttcaggt gca  
 333

<210> 86  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 86  
 Xaa Arg Val Pro Arg Lys Gly Thr Met Phe Val Ser Val Arg Glu Thr  
 1 5 10 15  
 Asp Lys Ala Arg Ile Leu Asp Ala Val Lys Leu Leu Ser Ser Leu Gly  
 20 25 30  
 Phe Lys Val Ile Ala Thr Ser Gly Thr Gln Arg Phe Leu Val Glu Asn



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      35          40          45
Gly Val Pro Ala Glu Lys Ile Asn Lys Val Leu Glu Gly Arg Pro His
      50          55          60
Ile Val Asp Ala Ile Thr Asn Gly Glu Val Gln Leu Val Phe Asn Thr
65          70          75          80
Thr Glu Gly Pro Gln Ala Leu Ala Asp Ser Arg Ser Leu Arg Arg Ala
      85          90          95
Ala Leu Leu His Lys Val Pro Tyr Tyr Thr Thr Leu Ser Gly Ala
      100          105          110

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&lt;210&gt; 87

&lt;211&gt; 355

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 87

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acgcgtgagg aaatgggggc cgcaggcctg gatcgcaagg tatggcagtg cccggtcgtc
60
ctcctgagcg atgttcattc ggtaggggta cagggtgacg ggcgtactta tggttctccc
120
attgtgcttc gcccggtgac gagtgaggac gccatgactg cggactgggc acgtatccca
180
tatgacgtac tggaaaagat ctcgactcgc attacgaatg cgtgtccgca aatcaaccgg
240
gtggactactg atatcacatc taaaccgccc gccaccatcg agtgggaatg agccccgtct
300
caccgtgaac atgacatggc ccgcaccttt cttggggcgg gccatgccgt gtttag
355

```

&lt;210&gt; 88

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 88

```

Thr Arg Glu Glu Met Gly Ala Ala Gly Leu Asp Arg Lys Val Trp Gln
  1          5          10          15
Cys Pro Val Val Leu Leu Ser Asp Val His Ser Val Gly Val Gln Gly
      20          25          30
Asp Gly Arg Thr Tyr Gly Ser Pro Ile Val Leu Arg Pro Val Thr Ser
      35          40          45
Glu Asp Ala Met Thr Ala Asp Trp Ala Arg Ile Pro Tyr Asp Val Leu
      50          55          60
Glu Lys Ile Ser Thr Arg Ile Thr Asn Ala Cys Pro Gln Ile Asn Arg
65          70          75          80
Val Val Leu Asp Ile Thr Ser Lys Pro Pro Ala Thr Ile Glu Trp Glu
      85          90          95

```

&lt;210&gt; 89

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 89

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 60  
 agggcaagag ttatataata gacgggtgta tgggtttaag gtatacatgg tgatgagaca  
 120  
 ggtgattgga taaggccaga gggttgggcg gggttctgcc cctgctgaag cctgggtggg  
 180  
 cccaggctctg tgatctggga ccggaacaac acatctgctc tgggcctgct ggatgtggcg  
 240  
 caagccctgg aacagaacca cagcctcaag tccatgccgc tgccactgaa tgacgtaacc  
 300  
 caggctcatc gcagccggcc agaactcaca actcgagcgg tccatcagat c  
 351

&lt;210&gt; 90

&lt;211&gt; 61

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

Ser	Leu	Val	Gly	Pro	Arg	Ser	Val	Ile	Trp	Asp	Arg	Asn	Asn	Thr	Ser
1				5					10					15	
Ala	Leu	Gly	Leu	Leu	Asp	Val	Ala	Gln	Ala	Leu	Glu	Gln	Asn	His	Ser
			20				25						30		
Leu	Lys	Ser	Met	Pro	Leu	Pro	Leu	Asn	Asp	Val	Thr	Gln	Ala	His	Arg
		35					40					45			
Ser	Arg	Pro	Glu	Leu	Thr	Thr	Arg	Ala	Val	His	Gln	Ile			
		50					55					60			

&lt;210&gt; 91

&lt;211&gt; 327

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 91

nggtgggtcc tctcgcagga caggtaatcc tgagacctac gcagctccct ggagctctgc  
 60  
 acgtcgaagc ccagcagggc ctccctgcagg tccctggggc agccagcaca cacaagtc  
 120  
 cggaaggggc ttagactcc ctgccagcgg ctttcccggg gaaggcacc acgcccagct  
 180  
 gcctcttgca ggtactgctc gggctctggtg ggagggcagc cgtgtccagc acaccctgtg  
 240  
 tgtgcagtc tctccctgcc ccactgccga acgagccctc cacggtgaag ccattgggga  
 300  
 acgtgacctt gcccttcccc atgaggt  
 327

&lt;210&gt; 92

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 92

Met Gly Lys Gly Lys Val Thr Phe Pro Asn Gly Phe Thr Val Glu Gly

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      1             5             10             15
Ser Phe Gly Ser Gly Ala Gly Arg Gly Leu His Thr Gln Gly Val Leu
      20             25             30
Asp Thr Ala Ala Leu Pro Pro Asp Pro Ser Ser Thr Cys Lys Arg Gln
      35             40             45
Leu Gly Val Gly Ala Phe Pro Gly Lys Ala Ala Gly Arg Glu Ser Thr
      50             55             60
Ala Pro Ser Gly Thr Leu Cys Val Leu Ala Ala Pro Gly Thr Cys Arg
      65             70             75             80
Arg Pro Cys Trp Ala Ser Thr Cys Arg Ala Pro Gly Ser Cys Val Gly
      85             90             95
Leu Arg Ile Thr Cys Pro Ala Arg Gly Pro Thr
      100             105

```

&lt;210&gt; 93

&lt;211&gt; 394

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 93

```

nccgcgtacg acaagcagta cctcgagggg cgttacggtg cggacccata cctgagcaac
60
atgctcgaat gggacggcgg acatgagcaa taggccgcca aagcacagcg agaggaaggc
120
ggcgcgctct gcggcctcgc ggatgaagga ggggtggtcg cgcaagagac gccccgcgcc
180
ttttgtaccg ataaatcccg ggcgccacct gatcgtgacc gaggggtacga aaacggaacc
240
gctctatttc gaggctatca ggttgctgtt caacaaccgt tatcacggcc agtgggtgac
300
aatggaagtt gtcgttaccg gcaagcatat caggggactt ctcgatcgtg cagtcactct
360
ggcgggaagaa agtgccacag gattcactca cgta
394

```

&lt;210&gt; 94

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 94

```

Met Leu Ala Gly Asn Asp Asn Phe His Cys His Pro Leu Ala Val Ile
      1             5             10             15
Thr Val Val Asp Thr Gln Pro Asp Ser Leu Glu Ile Glu Arg Phe Arg
      20             25             30
Phe Arg Thr Leu Gly His Asp Gln Val Ala Pro Gly Ile Tyr Arg Tyr
      35             40             45
Lys Arg Arg Gly Ala Ser Leu Ala Arg Pro Pro Leu Leu His Pro Arg
      50             55             60
Gly Arg Arg Ala Arg Arg Leu Pro Leu Ala Val Leu Trp Arg Pro Ile
      65             70             75             80
Ala His Val Arg Arg Pro Ile Arg Ala Cys Cys Ser Gly Met Gly Pro
      85             90             95
His Arg Asn Ala Pro Arg Gly Thr Ala Cys Arg Thr Arg

```

100

105

<210> 95  
 <211> 531  
 <212> DNA  
 <213> Homo sapiens

<400> 95  
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 tgcttggatc ctaaaatgga ctggtcttgg gtgtgtaacc ccggtgaagt tatagcctcc  
 120  
 ccaaattgag gtgacagaag gaagacaaga ggtgtaagct ggagagggaa gggaagaaat  
 180  
 cagtggcttt ggccagcctc tgtgccaccc agtacgacag aggagtggga actggccctc  
 240  
 tggggctctg cttggccata ggcactgcac attgtgccac ctgctcatca cctcctctag  
 300  
 tctcacactg agcatcggag tacctgttgt gcagacagga aaactgagga gctctgagag  
 360  
 gctgagcatg gagctcacc ccatgcatag ggtgtgggaa gagggcacag gaggcctcat  
 420  
 ccatggggga aagggttgag gatggacatg ggtggggaga gggcatagac atcccttctc  
 480  
 aatctctgtt cccaccacat ttcataaggag atgagttagg agatgacagc t  
 531

<210> 96  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 96  
 Met Arg Pro Pro Val Pro Ser Ser His Thr Leu Trp His Gly Val Ser  
 1 5 10 15  
 Ser Met Leu Ser Leu Ser Glu Leu Leu Ser Phe Pro Val Cys Thr Thr  
 20 25 30  
 Gly Thr Pro Met Leu Ser Val Arg Leu Glu Glu Val Met Ser Arg Trp  
 35 40 45  
 His Asn Val Gln Cys Leu Trp Pro Ser Arg Ala Pro Glu Gly Gln Phe  
 50 55 60  
 Pro Leu Leu Cys Arg Thr Gly Trp His Arg Gly Trp Pro Lys Pro Leu  
 65 70 75 80  
 Ile Ser Ser Leu Pro Ser Pro Ala Tyr Thr Ser Cys Leu Pro Ser Val  
 85 90 95  
 Thr Ser Ile Trp Gly Gly Tyr Asn Phe Thr Gly Val Thr His Pro Arg  
 100 105 110  
 Pro Val His Phe Arg Ile Gln Ala Lys Phe Pro Glu  
 115 120

<210> 97  
 <211> 405  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 97

ggtcggggcca gtcgaacttc attcccgcctt cgagggtctt gctgcggatg ggccgtacgc  
 60  
 tcgcggtgcc ttgcgcgcgg gctggtaggt ggagaagccg cgcgagtacg cgccgtagag  
 120  
 cgacatcgtg tctgagacgt cgaagctcag gccagcctt ggcgctccagg cgcgctcggg  
 180  
 cggtcggccc tcttgcggca attgattcag cgcaatcccg gccatcacat gccagcgtt  
 240  
 gtccagggtc atgaaatcct gggcataggc gcgcgaggag cgcagcggcg aattggacag  
 300  
 gcgctcgata ttgggcgtga tgtccgaaga cgggaacggg acccgggggg agaagacgtt  
 360  
 gcccgggaaa agatcccccg acgccatcgt ggtgtcgacc gagat  
 405

&lt;210&gt; 98

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 98

Met	Ala	Ser	Gly	Asp	Leu	Phe	Pro	Gly	Asn	Val	Phe	Ser	Pro	Arg	Val
1				5					10					15	
Pro	Phe	Pro	Ser	Ser	Asp	Ile	Thr	Pro	Asn	Ile	Glu	Arg	Leu	Ser	Asn
			20					25					30		
Ser	Pro	Leu	Arg	Ser	Ser	Arg	Ala	Tyr	Ala	Gln	Asp	Phe	Met	Thr	Leu
		35					40				45				
Asp	Lys	Arg	Trp	His	Val	Met	Ala	Gly	Ile	Ala	Leu	Asn	Gln	Leu	Pro
	50					55				60					
Gln	Glu	Gly	Gly	Pro	Thr	Glu	Arg	Ala	Trp	Thr	Pro	Lys	Leu	Gly	Leu
65				70					75					80	
Ser	Phe	Asp	Val	Ser	Asp	Thr	Met	Ser	Leu	Tyr	Gly	Ala	Tyr	Ser	Arg
			85					90					95		
Gly	Phe	Ser	Thr	Tyr	Gln	Pro	Ala	Arg	Lys	Ala	Pro	Arg	Ala	Tyr	Gly
			100					105					110		
Pro	Ser	Ala	Ala	Arg	Pro	Ser	Lys	Arg	Glu						
			115					120							

&lt;210&gt; 99

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 99

acgcgtccgc tcccgatgtc gttgacgagc tgcgctcagc gatgacggta ctcacccatc  
 60  
 tgccccgacg acccagcaaa cgccccggc tgttctcat tgaccacgcc gaccggatcg  
 120  
 tcgatcccat cactcgggat ttgctggaat ccttggttcg cgaagccggc gaggctgcgg  
 180  
 tgatcttggg tgcccagcgt cgcggctgca tcgattgggt cccccacag atcatccaca  
 240

acctggccga acaccatttt gagtcgtcct ctggagggtac tcgatgatga ctgaacgttc  
 300  
 ccattccacg atcagggttaa ggtggccggc ggtgggtggtt ctgctcctcg ttccgctgct  
 360  
 ggtgggtcgcc ggattggtcc gggacgacct ggcataccac cgaccgggtg ggccgggtga  
 420  
 aagcggccgt cgtcaacgag gacaaggccg tcaagggtcg tggacaactg gttccgatgg  
 480  
 gccgccaaact caccgccgcc ttgatggact ctggctcgca caccactgat ggccacaccg  
 540  
 tcgac  
 545

<210> 100

<211> 101

<212> PRT

<213> Homo sapiens

<400> 100

Met	Gly	Thr	Phe	Ser	His	His	Arg	Val	Pro	Pro	Glu	Asp	Asp	Ser	Lys
1				5					10					15	
Trp	Cys	Ser	Ala	Arg	Leu	Trp	Met	Ile	Cys	Gly	Glu	Ser	Gln	Ser	Met
			20					25					30		
Arg	Pro	Arg	Arg	Trp	Ala	Pro	Lys	Ile	Thr	Ala	Ala	Ser	Pro	Ala	Ser
			35				40					45			
Arg	Thr	Arg	Asp	Ser	Ser	Lys	Ser	Arg	Val	Met	Gly	Ser	Thr	Ile	Arg
			50			55				60					
Ser	Ala	Trp	Ser	Met	Arg	Asn	Ser	Arg	Gly	Arg	Leu	Leu	Gly	Arg	Arg
65					70				75					80	
Gly	Arg	Trp	Val	Ser	Thr	Val	Ile	Ala	Glu	Arg	Ser	Ser	Ser	Thr	Thr
			85					90						95	
Ser	Gly	Ala	Asp	Ala											
			100												

<210> 101

<211> 619

<212> DNA

<213> Homo sapiens

<400> 101

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 60  
 tcatgcacga tccggacttc gatccgatcc ccatgggtgaa caaggagctt gacgccttcg  
 120  
 aagctgcccgg ggggtgactat ctcatcctcg ccacggattc cggacgcaag ggatacacga  
 180  
 ccgcccgtcc tcacgaggcc ggcggaaaac gctattacca acctggacca gatccgcgaa  
 240  
 gtctgcgcca gccgcaacgt caccgcctgt ctacaccccc attggggaac gatgggtccag  
 300  
 aaccgtgacg aagtgatccg cgtgctcgag aactcctcga tcgggctgtg cctggacact  
 360  
 ggtcatctgg cctgtggtgg taccgatgtc gttgagctgg tgcgtaagta cgccaaccgc  
 420

gtcgacattg tccacgcaa agatgtccat aaggagatgg ccgacaagct ttgacctggc  
 480  
 gagatcacct ggtccgaagg cattcgcgcc gggatgttcg caccatcgg cgacggtgat  
 540  
 atcgactttg cagccatcgt gaggtcctt gatgaagccg ggttcgatgg ttattacgtc  
 600  
 ctagagcagg acatcatga  
 619

<210> 102

<211> 173

<212> PRT

<213> Homo sapiens

<400> 102

Thr	Arg	Ser	Leu	Thr	Pro	Ser	Lys	Leu	Pro	Gly	Val	Thr	Ile	Ser	Ser
1				5					10					15	
Ser	Pro	Arg	Ile	Pro	Asp	Ala	Arg	Asp	Thr	Arg	Pro	Pro	Val	Leu	Thr
			20					25					30		
Arg	Pro	Ala	Glu	Asn	Ala	Ile	Thr	Asn	Leu	Asp	Gln	Ile	Arg	Glu	Val
		35					40					45			
Cys	Ala	Ser	Arg	Asn	Val	Thr	Ala	Cys	Leu	His	Pro	His	Trp	Gly	Thr
		50				55				60					
Met	Val	Gln	Asn	Arg	Asp	Glu	Val	Ile	Arg	Val	Leu	Glu	Asn	Ser	Ser
65					70					75				80	
Ile	Gly	Leu	Cys	Leu	Asp	Thr	Gly	His	Leu	Ala	Cys	Gly	Gly	Thr	Asp
			85						90					95	
Val	Val	Glu	Leu	Val	Arg	Lys	Tyr	Ala	Asn	Arg	Val	Asp	Ile	Val	His
			100					105					110		
Ala	Lys	Asp	Val	His	Lys	Glu	Met	Ala	Asp	Lys	Leu	Leu	Pro	Gly	Glu
		115					120					125			
Ile	Thr	Trp	Ser	Glu	Gly	Ile	Arg	Ala	Gly	Met	Phe	Ala	Pro	Ile	Gly
	130					135					140				
Asp	Gly	Asp	Ile	Asp	Phe	Ala	Ala	Ile	Val	Arg	Leu	Leu	Asp	Glu	Ala
145					150					155				160	
Gly	Phe	Asp	Gly	Tyr	Tyr	Val	Leu	Glu	Gln	Asp	Ile	Met			
			165						170						

<210> 103

<211> 321

<212> DNA

<213> Homo sapiens

<400> 103

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 120  
 actgggggga gacccttgcc gctgggggga gaccgagcc attgggggga gacccttgcc  
 180  
 atggggaaag acccctgcca ttgggggaga ntacctgcca ttgggggaga tccctgccgt  
 240  
 tggggggaga tccctgctgt tggggggaga ntccctcctg taggggaaga cccctgcagg  
 300

agtgggtggg gcgaagaccc c  
321

<210> 104  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 104  
Xaa His Gly Gly Arg Gln Gln Pro Cys Gly Gly Asp Pro Ser His Trp  
1 5 10 15  
Gly Glu Thr Pro Ala Ile Gly Gly Arg Pro Leu Pro Trp Gly Lys Thr  
20 25 30  
Pro Ala Met Gly Gln Thr Pro Ala Thr Gly Gly Arg Pro Leu Pro Leu  
35 40 45  
Gly Gly Asp Pro Ser His Trp Gly Glu Thr Pro Ala Met Gly Lys Asp  
50 55 60  
Pro Cys His Trp Gly Arg Xaa Pro Ala Ile Gly Gly Asp Pro Cys Arg  
65 70 75 80  
Trp Gly Glu Ile Pro Ala Val Gly Gly Arg Xaa Pro Pro Val Gly Glu  
85 90 95  
Asp Pro Cys Arg Ser Gly Trp Gly Glu Asp Pro  
100 105

<210> 105  
<211> 344  
<212> DNA  
<213> Homo sapiens

<400> 105  
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60  
ccgggtcaac gaggggtttgg cgcacgggtcc actccgtggc gcccggggtg atgtgcaaca  
120  
gggcggggccc gcgcgcggcc gggcctgatt ccagcctctc gtgctcgtcc cagtacccat  
180  
ccagcgcattc gcccagcggc tcggcatccc agccgtggtc gccgtcgagc gccccaggg  
240  
cctcaatgtc gtcacggcg gccagttcca cccggcgga catctcgttg cggaccatga  
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cccggaaggc gcgggaattc tcggtcagtt tcggcggtgc cggc  
344

<210> 106  
<211> 62  
<212> PRT  
<213> Homo sapiens

<400> 106  
Cys Ala Thr Gly Arg Ala Arg Ala Arg Pro Gly Leu Ile Pro Ala Ser  
1 5 10 15  
Arg Ala Arg Pro Ser Thr His Pro Ala His Arg Pro Ser Gly Arg His  
20 25 30  
Pro Ser Arg Gly Arg Arg Arg Ala Pro Pro Gly Pro Gln Cys Arg His



35 40 45  
 Arg Arg Pro Val Pro Pro Gly Gly Thr Ser Arg Cys Gly Pro  
 50 55 60

<210> 107  
 <211> 549  
 <212> DNA  
 <213> Homo sapiens

<400> 107  
 acgcgttcct cggacgctgc tagtttgagc gcacaggcat tgggcggggc tcacggggga  
 60  
 gccgcttaat aaccgaccaa catgaaactc aagggtgccc ccttcctagc ggggaccctg  
 120  
 cacagacccg aaaataaggg gttttgctct gccctcctca gttcacgtgg gcaccttgga  
 180  
 acactgaaga aggcattttc cgaactcact gtccctacga cttattctcc gcactgtttt  
 240  
 cgcctccttc gccctgttct cgtgactgac aggagcaggg gtcacaagca ggcagcccga  
 300  
 gagctctgct cacctggaaa agcatttttg tgtagcttaa atgtgaaggc ctcaggcagt  
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 540  
 agggtaggc  
 549

<210> 108  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 108  
 Met Lys Leu Lys Gly Cys Pro Phe Leu Ala Gly Thr Leu His Arg Pro  
 1 5 10 15  
 Glu Asn Lys Gly Phe Cys Ser Ala Leu Leu Ser Ser Arg Gly His Leu  
 20 25 30  
 Gly Thr Leu Lys Lys Ala Phe Ser Glu Leu Thr Val Leu Arg Thr Tyr  
 35 40 45  
 Ser Pro His Cys Phe Arg Leu Leu Arg Pro Val Leu Val Thr Asp Arg  
 50 55 60  
 Ser Arg Gly His Lys Gln Ala Ala Arg Glu Leu Cys Ser Pro Gly Lys  
 65 70 75 80  
 Ala Phe Leu Cys Ser Leu Asn Val Lys Ala Ser Gly Ser Gly Leu Leu  
 85 90 95  
 Ser Ser Ser Thr Cys Ala His Leu His Ser Phe Met  
 100 105

<210> 109  
 <211> 748

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

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60
aagtcagaag acttatttgt tctggtacct attctgctgt taataaattg ataatgagt
120
gatattgggg taagttacca atttacttta cagcccttaa gtaaataatc tgctttcttc
180
agcatcatag acttttgaag aggattaatt aagcgcttaa aaaacctgta gactctatta
240
cagtcagtga aaggaataat tctctttaca aagtaaatgc agttgtttta ttttagacaa
300
gagtgttcta aacttcgtga agagttaagg cttcaacatg aagaggataa gaagtcagca
360
atgtctcaac ttttgcagtt gaaagatcga gagaaaaatg cagcaagaga ttcattggcag
420
aagaaagtag aagatctctt aaaccagatt tccttgctga aacagaatct ggagatacag
480
ctttcccagt ctcagacttc tttgcaacaa ctgcaagccc agtttacgca agaacgacag
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660
gctcttgaaa atcatttaca acagaagcat tctgcagagc ttcaatcact aaaagatgca
720
cacagagagt caatggaggg cttccgga
748

```

&lt;210&gt; 110

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 110

```

Met Gln Leu Phe Tyr Phe Arg Gln Glu Cys Ser Lys Leu Arg Glu Glu
1      5      10      15
Leu Arg Leu Gln His Glu Glu Asp Lys Lys Ser Ala Met Ser Gln Leu
20     25     30
Leu Gln Leu Lys Asp Arg Glu Lys Asn Ala Ala Arg Asp Ser Trp Gln
35     40     45
Lys Lys Val Glu Asp Leu Leu Asn Gln Ile Ser Leu Leu Lys Gln Asn
50     55     60
Leu Glu Ile Gln Leu Ser Gln Ser Gln Thr Ser Leu Gln Gln Leu Gln
65     70     75     80
Ala Gln Phe Thr Gln Glu Arg Gln Arg Leu Thr Gln Glu Leu Glu Glu
85     90     95
Leu Glu Glu Gln His Gln Gln Arg His Lys Ser Leu Lys Glu Ala His
100    105    110
Val Leu Ala Phe Gln Thr Met Glu Glu Glu Lys Glu Lys Glu Gln Arg
115    120    125
Ala Leu Glu Asn His Leu Gln Gln Lys His Ser Ala Glu Leu Gln Ser

```

130 135 140  
 Leu Lys Asp Ala His Arg Glu Ser Met Glu Gly Phe Arg  
 145 150 155

<210> 111  
 <211> 429  
 <212> DNA  
 <213> Homo sapiens

<400> 111  
 ggcgcgccag agagtgcaca atgggtgtcag gatatgggag ccaccggaat cattaaccat  
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 cgtgaaccgc tcgccccgca ggtcaacgac ttcgggatca ccgggttcga cggcattctc  
 120  
 tcggcttatn nacgccacca gcatncgact ttggctgaga tcatcgacc gttcggacat  
 180  
 ctggtcatga tcgacggaac cgactcattc gatctcatgg ccttcaagtc aaagtcgtta  
 240  
 acggtgacca gcgagtcgat gttcagccgt ccacagtctc cgacgcccga cgtcgccgaa  
 300  
 caaggccggg cactggccag catcgccgac ctcgtcgaga aggggcagat ccgtccgacg  
 360  
 atgaccgccg atatcgaggg tctgacaacc cagcatgtgc gtgaggccac cgcagccgtc  
 420  
 gagtcgggc  
 429

<210> 112  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 112  
 Ala Arg Pro Glu Ser Ala Gln Trp Cys Gln Asp Met Gly Ala Thr Gly  
 1 5 10 15  
 Ile Ile Asn His Arg Glu Pro Leu Ala Pro Gln Val Asn Asp Phe Gly  
 20 25 30  
 Ile Thr Gly Phe Asp Gly Ile Leu Ser Ala Tyr Xaa Arg His Gln His  
 35 40 45  
 Xaa Thr Leu Ala Glu Ile Ile Ala Pro Phe Gly His Leu Val Met Ile  
 50 55 60  
 Asp Gly Thr Asp Ser Phe Asp Leu Met Ala Phe Lys Ser Lys Ser Leu  
 65 70 75 80  
 Thr Val Thr Ser Glu Ser Met Phe Ser Arg Pro Gln Phe Ala Thr Pro  
 85 90 95  
 Asp Val Ala Glu Gln Gly Arg Ala Leu Ala Ser Ile Ala Asp Leu Val  
 100 105 110  
 Glu Lys Gly Gln Ile Arg Pro Thr Met Thr Arg His Ile Glu Gly Leu  
 115 120 125  
 Thr Thr Gln His Val Arg Glu Ala Thr Ala Ala Val Glu Ser Gly  
 130 135 140

<210> 113  
 <211> 382

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 113

gtgcactgga cggatgctgg ggaactgagg cctgcccttc tccactcctg ctgcctctgt  
 60  
 gtggaccgcc tgccacctgg cttcaacgat gtggacgctc tgtgccgggc gctgtcagct  
 120  
 gtccacagcc ccaccttctg ccagctggcg tgcggccagg atgggcagct gaagggcttc  
 180  
 gcggtgctgg agtatgagac ggctgagatg gcggaggagg cacagcagca ggcggacggc  
 240  
 ctgtccctgg ggggcagcca cctgcgagtc tccttctgcg cccctgggac ccccgggcgc  
 300  
 agtatgctgg ccgctctcat cgttgccag gccacggccc tcaatcgggg gcagggagtc  
 360  
 ctccccgagc ccaacatcct gc  
 382

&lt;210&gt; 114

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 114

Met	Leu	Gly	Ser	Gly	Arg	Thr	Pro	Cys	Pro	Arg	Leu	Arg	Ala	Val	Ala
1				5					10					15	
Trp	Ala	Thr	Met	Arg	Ala	Ala	Ser	Ile	Leu	Arg	Pro	Gly	Val	Pro	Gly
			20					25					30		
Ala	Gln	Lys	Glu	Thr	Arg	Arg	Trp	Leu	Pro	Pro	Arg	Asp	Arg	Pro	Ser
		35					40					45			
Ala	Cys	Cys	Cys	Ala	Ser	Ser	Ala	Ile	Ser	Ala	Val	Ser	Tyr	Ser	Ser
	50					55					60				
Thr	Ala	Lys	Pro	Phe	Ser	Cys	Pro	Ser	Trp	Pro	His	Ala	Ser	Trp	Gln
65					70					75				80	
Lys	Val	Gly	Leu	Trp	Thr	Ala	Asp	Ser	Ala	Arg	His	Arg	Ala	Ser	Thr
			85					90						95	
Ser	Leu	Lys	Pro	Gly	Gly	Arg	Arg	Ser	Thr	Gln	Arg	Gln	Gln	Glu	Trp
			100					105						110	
Arg	Arg	Ala	Gly	Leu	Ser	Ser	Pro	Ala	Ser	Val	Gln	Cys			
			115				120					125			

&lt;210&gt; 115

&lt;211&gt; 4798

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 115

ctcccccca gtctgtctta agtactgatg ccagagaggt ctgcctaagc tcagtgtgtg  
 60  
 catttcactc cctgtttgga gccatgagtg gccccctgtt gccttcaaga ctgaagccat  
 120  
 ccccatcctt cctccacca acctagaggc ttgcttcgt aaatgctggc cctttccttc  
 180

atgggctcca ccctctgagt gtgtcatgaa ctcttccact tccttgccctt ggttcgtatt  
240  
gggtcctctg cccgaggtca gagatttga cgagcccttc tcctccatct tcacagtctc  
300  
catttaccat tagatgccag gccagacag ttgatgaaa atgtaagaaa cggaccaag  
360  
tataagaaaa agctagatct gtccatttta tttctagttt ttggaagaga tgtggataca  
420  
gagaaatatt actctactat tgaaaaaat atatatcagt ctgattataa atgtcaactc  
480  
atactaagtc aatatcaggg aagcagtgtg gagaaggatg tggcaaactg gagattgctg  
540  
tttccataga aagagggcag ctaatgctta tctccagacc attgttatgc agtaatgtag  
600  
actccatttc accagattta attcttaagg agaaactgga aacttgtatt attatttgat  
660  
tattactttt ggcagttaat tttaaaaatc accgtttagg ccaaaacaac atgacatttg  
720  
tctgggctac aagggaactct tagcgactct tagcttgcaac ttacctttct aatctcaggg  
780  
ctttttacaa agcccttctc tgaattccct gaagatatgc tagcttgaag gctcactgca  
840  
tactctcaac tccccagcca ctccctgtt tccctcttat accagttaat actttgatgt  
900  
tattttttca gtccatttta atcttttaga ctggaggttc cttgaggggtg gggcctaatt  
960  
cttgttttta tcttcccat agcaattatc aagttatctg ctccctttgg cacctaagaa  
1020  
atattagttg ggggtgataac tgaatggctg tccttctgcc ttcgttactg cttttgtgga  
1080  
tgttattttt tttgaccctt attccaccctg tgtgcagtgg agaggatggg tgttgatatt  
1140  
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1200  
gcaaggaagt caaggaattg gggtttgaac ccaagtcgtc tcagttccat tccattgtcc  
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1380  
cccgtgctcc agtcaggaca ctggctctgag tacttccgga attttgctga ctctgtctt  
1440  
cagaaaatcc ctcaagacag accaactca gaggttctcc tgaagcaccg ctttggtgctc  
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cgggagcggc caccacagt catcatggac ctgatccaga ggaccaagga tgccgtgcgg  
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1740  
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1800

gaggaggagg aagaggagga ggaggaagaa ggccctgaag cccgggagat ggccatgatg  
1860  
caggagggggg agcacacagt cacctctcac agctccatta tccaccggct gccgggctct  
1920  
gacaacctat atgatgaccc ctaccagcca gagataaccc ccagccctct ccagccgcct  
1980  
gcagccccag ctcccacttc caccacctct tccgcccgcc gccgggcta ctgccgtaac  
2040  
cgagaccact ttgccaccat ccgaaccgcc tccctggta gccgtcagat ccaggagcat  
2100  
gagcaggact ctgcgctgcg ggagcagctg agcggctata agcggatgag acgacagcac  
2160  
cagaagcagc tgctggccct ggagtcacgg ctgaggggtg aacgggagga gcacagtga  
2220  
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2280  
gcccgccggc accaggccat aggtgagaag gaggcacgag ctgccaggc cgaggagcgg  
2340  
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2580  
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2640  
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2700  
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2940  
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3300  
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3420

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 4080  
 ccattagctc tgttggcaag ggtctgggtc ctgtgcaagg gctggaactg gcgtctggca  
 4140  
 cgggccagcc agggtttagc atccacttg ccccgctggg ccatccacac actggccagc  
 4200  
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 4260  
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 4320  
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 4380  
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 4440  
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 4560  
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 4680  
 tctttgattt tgtttttctg tctcccttcc aacctgtccc cttccccca ccaaaaaag  
 4740  
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 4798

&lt;210&gt; 116

&lt;211&gt; 1062

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 116

Met Met Gly Thr Ser Gln Gly His Val Ala Arg Lys Ser Arg Asn Trp

1	5	10	15
Gly Leu Asn Pro Ser Arg Leu Ser Ser Ile Pro Leu Ser Ser Thr Pro			
	20	25	30
Cys His Leu Ser Pro Ser Ser Leu Ser Pro Phe Ser Val Ala Glu Arg			
	35	40	45
Lys Pro Pro Leu Phe Asn Met Asn Ala Met Ser Ala Leu Tyr His Ile			
	50	55	60
Ala Gln Asn Glu Ser Pro Val Leu Gln Ser Gly His Trp Ser Glu Tyr			
	65	70	75
Phe Arg Asn Phe Val Asp Ser Cys Leu Gln Lys Ile Pro Gln Asp Arg			
	85	90	95
Pro Thr Ser Glu Val Leu Leu Lys His Arg Phe Val Leu Arg Glu Arg			
	100	105	110
Pro Pro Thr Val Ile Met Asp Leu Ile Gln Arg Thr Lys Asp Ala Val			
	115	120	125
Arg Glu Leu Asp Asn Leu Gln Tyr Arg Lys Met Lys Lys Ile Leu Phe			
	130	135	140
Gln Glu Ala Pro Asn Gly Pro Gly Ala Glu Ala Pro Glu Glu Glu Glu			
	145	150	155
Glu Ala Glu Pro Tyr Met His Arg Ala Gly Thr Leu Thr Ser Leu Glu			
	165	170	175
Ser Ser His Ser Val Pro Ser Met Ser Ile Ser Ala Ser Ser Gln Ser			
	180	185	190
Ser Ser Val Asn Ser Leu Ala Asp Ala Ser Asp Asn Glu Glu Glu Glu			
	195	200	205
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Pro Glu Ala Arg			
	210	215	220
Glu Met Ala Met Met Gln Glu Gly Glu His Thr Val Thr Ser His Ser			
	225	230	235
Ser Ile Ile His Arg Leu Pro Gly Ser Asp Asn Leu Tyr Asp Asp Pro			
	245	250	255
Tyr Gln Pro Glu Ile Thr Pro Ser Pro Leu Gln Pro Pro Ala Ala Pro			
	260	265	270
Ala Pro Thr Ser Thr Thr Ser Ser Ala Arg Arg Arg Ala Tyr Cys Arg			
	275	280	285
Asn Arg Asp His Phe Ala Thr Ile Arg Thr Ala Ser Leu Val Ser Arg			
	290	295	300
Gln Ile Gln Glu His Glu Gln Asp Ser Ala Leu Arg Glu Gln Leu Ser			
	305	310	315
Gly Tyr Lys Arg Met Arg Arg Gln His Gln Lys Gln Leu Leu Ala Leu			
	325	330	335
Glu Ser Arg Leu Arg Gly Glu Arg Glu Glu His Ser Ala Arg Leu Gln			
	340	345	350
Arg Glu Leu Glu Ala Gln Arg Ala Gly Phe Gly Ala Glu Ala Glu Lys			
	355	360	365
Leu Ala Arg Arg His Gln Ala Ile Gly Glu Lys Glu Ala Arg Ala Ala			
	370	375	380
Gln Ala Glu Glu Arg Lys Phe Gln Gln His Ile Leu Gly Gln Gln Lys			
	385	390	395
Lys Glu Leu Ala Ala Leu Leu Glu Ala Gln Lys Arg Thr Tyr Lys Leu			
	405	410	415
Arg Lys Glu Gln Leu Lys Glu Glu Leu Gln Glu Asn Pro Ser Thr Pro			
	420	425	430
Lys Arg Glu Lys Ala Glu Trp Leu Leu Arg Gln Lys Glu Gln Leu Gln			



435 440 445  
 Gln Cys Gln Ala Glu Glu Glu Ala Gly Leu Leu Arg Arg Gln Arg Gln  
 450 455 460  
 Tyr Phe Glu Leu Gln Cys Arg Gln Tyr Lys Arg Lys Met Leu Leu Ala  
 465 470 475 480  
 Arg His Ser Leu Asp Gln Asp Leu Leu Arg Glu Asp Leu Asn Lys Lys  
 485 490 495  
 Gln Thr Gln Lys Asp Leu Glu Cys Ala Leu Leu Leu Arg Gln His Glu  
 500 505 510  
 Ala Thr Arg Glu Leu Glu Leu Arg Gln Leu Gln Ala Val Gln Arg Thr  
 515 520 525  
 Arg Ala Glu Leu Thr Arg Leu Gln His Gln Thr Glu Leu Gly Asn Gln  
 530 535 540  
 Leu Glu Tyr Asn Lys Arg Arg Glu Gln Glu Leu Arg Gln Lys His Ala  
 545 550 555 560  
 Ala Gln Val Arg Gln Gln Pro Lys Ser Leu Lys Val Arg Ala Gly Gln  
 565 570 575  
 Arg Pro Pro Gly Leu Pro Leu Pro Ile Pro Gly Ala Leu Gly Pro Pro  
 580 585 590  
 Asn Thr Gly Thr Pro Ile Glu Gln Gln Pro Cys Ser Pro Gly Gln Glu  
 595 600 605  
 Ala Val Leu Asp Gln Arg Met Leu Gly Glu Glu Glu Glu Ala Val Gly  
 610 615 620  
 Glu Arg Arg Ile Leu Gly Lys Glu Gly Ala Thr Leu Glu Pro Lys Gln  
 625 630 635 640  
 Gln Arg Ile Leu Gly Glu Glu Ser Gly Ala Pro Ser Pro Ser Pro Gln  
 645 650 655  
 Lys His Gly Ser Leu Val Asp Glu Glu Val Trp Gly Leu Pro Glu Glu  
 660 665 670  
 Ile Glu Glu Leu Arg Val Pro Ser Leu Val Pro Gln Glu Arg Ser Ile  
 675 680 685  
 Val Gly Gln Glu Glu Ala Gly Thr Trp Ser Leu Trp Gly Lys Glu Asp  
 690 695 700  
 Glu Ser Leu Leu Asp Glu Glu Phe Glu Leu Gly Trp Val Gln Gly Pro  
 705 710 715 720  
 Ala Leu Thr Pro Val Pro Glu Glu Glu Glu Glu Glu Glu Gly Ala  
 725 730 735  
 Pro Ile Gly Thr Pro Arg Asp Pro Gly Asp Gly Cys Pro Ser Pro Asp  
 740 745 750  
 Ile Pro Pro Glu Pro Pro Pro Thr His Leu Arg Pro Cys Pro Ala Ser  
 755 760 765  
 Gln Leu Pro Gly Leu Leu Ser His Gly Leu Leu Ala Gly Leu Ser Phe  
 770 775 780  
 Ala Val Gly Ser Ser Ser Gly Leu Leu Pro Leu Leu Leu Leu Leu  
 785 790 795 800  
 Leu Pro Leu Leu Ala Ala Gln Gly Gly Gly Gly Leu Gln Ala Ala Leu  
 805 810 815  
 Leu Ala Leu Glu Val Gly Leu Val Gly Leu Gly Ala Ser Tyr Leu Leu  
 820 825 830  
 Leu Cys Thr Ala Leu His Leu Pro Ser Ser Leu Phe Leu Leu Leu Ala  
 835 840 845  
 Gln Gly Thr Ala Leu Gly Ala Val Leu Gly Leu Ser Trp Arg Arg Gly  
 850 855 860  
 Leu Met Gly Val Pro Leu Gly Leu Gly Ala Ala Trp Leu Leu Ala Trp

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<210> 117
<211> 471
<212> DNA
<213> Homo sapiens
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```
<210> 118
<211> 157
<212> PRT
<213> Homo sapiens
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&lt;400&gt; 118

Xaa Ala Leu Thr Ile Cys Leu Ala Gly Val Val Ile Cys Ala Val Gly  
 1 5 10 15  
 Val Val Asp Asp Leu Leu Asp Leu Pro Ala Leu Ala Lys Ala Ala Gly  
 20 25 30  
 Gln Val Leu Ala Ala Gly Ile Val Val Thr Gly Gly Val Arg Met Phe  
 35 40 45  
 Trp Ile Pro Leu Pro Asn Ser Ile Ile Ala Leu Gly Thr Pro Thr Ser  
 50 55 60  
 Ile Leu Val Thr Val Phe Phe Ile Val Leu Cys Ala Asn Ala Val Asn  
 65 70 75 80  
 Phe Ile Asp Gly Leu Asp Gly Leu Ala Ser Gly Val Val Ala Ile Gly  
 85 90 95  
 Ser Leu Ala Phe Phe Ser Tyr Thr Tyr Leu Leu Ala His Glu Gln Asp  
 100 105 110  
 Phe Val Val Ala Thr Thr Thr Ser Leu Ile Thr Ala Ala Thr Ala Gly  
 115 120 125  
 Ala Cys Leu Gly Phe Leu Pro His Asn Trp His Pro Ala Arg Met Phe  
 130 135 140  
 Met Gly Asp Ser Gly Ala Leu Leu Leu Gly Leu Leu Leu  
 145 150 155

&lt;210&gt; 119

&lt;211&gt; 302

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 119

ntcaaacatg agcagtcgtg gggccgagg ccgcggtggc tattatcgcg agctttatgg  
 60  
 tagccgaggt cgaggcagta aatctaataa aactttcgca aaaaattcgg atgtctactc  
 120  
 tcagaaaaag actcgaacag tacgaggcac ctccgaagat ttagcacgat cgctccataa  
 180  
 gcttcatatg cgcccgtagc ctgcgtatca tgacattgag ggtatgtggg ctttcccagc  
 240  
 ctttactttt tatctggatc atgcacaagc agaccatac gctgccccaa ataaggcacg  
 300  
 cn  
 302

&lt;210&gt; 120

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 120

Met Ser Ser Arg Gly Gly Arg Gly Gly Tyr Tyr Arg Glu Leu  
 1 5 10 15  
 Tyr Gly Ser Arg Gly Arg Gly Ser Lys Ser Asn Glu Thr Phe Ala Lys  
 20 25 30  
 Asn Ser Asp Val Tyr Ser Gln Lys Lys Thr Arg Thr Val Arg Gly Thr  
 35 40 45  
 Ser Glu Asp Leu Ala Arg Ser Leu His Lys Leu His Met Arg Pro Tyr

50					55					60					
Pro	Ala	Tyr	His	Asp	Ile	Glu	Gly	Met	Trp	Ala	Phe	Pro	Ala	Phe	Thr
65					70					75					80
Phe	Tyr	Leu	Asp	His	Ala	Gln	Ala	Asp	Pro	Tyr	Ala	Ala	Pro	Asn	Lys
				85					90					95	
Ala	Arg														

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<210> 121
<211> 318
<212> DNA
<213> Homo sapiens
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<400> 121
ngcatggggg gccctgggac cgcacttggtg cccctttttt ttttagggaa aaaattgagc
60
cctaaaggat ttgccgcatt acaggaaagt tttttggtaa gtttggggtt gtttctgtgc
120
tgtgtgagaa ggagtagaag cagctccagt agagtgggcc ttttcatttt tatccagagg
180
aaatttgtag gctgtggcta ttacttcctt ttttttcttt tttttttttg tttagagaca
240
gagtctgnct ctgtcgccag gctggagtga agtggcacga tctcagctca ctgcaacctc
300
tgcctcccag gttcaagc
318
```

```
<210> 122
<211> 89
<212> PRT
<213> Homo sapiens
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```
<400> 122
Xaa Met Gly Gly Pro Gly Thr Ala Leu Val Pro Leu Phe Phe Leu Gly
      1              5              10              15
Lys Lys Leu Ser Pro Lys Gly Phe Ala Ala Leu Gln Glu Ser Phe Leu
      20              25              30
Val Ser Leu Gly Leu Phe Leu Cys Cys Val Arg Arg Ser Arg Ser Ser
      35              40              45
Ser Ser Arg Val Gly Leu Phe Ile Phe Ile Gln Arg Lys Phe Val Gly
      50              55              60
Cys Gly Tyr Tyr Phe Leu Phe Phe Leu Phe Phe Cys Leu Glu Thr
      65              70              75              80
Glu Ser Xaa Ser Val Ala Arg Leu Glu
      85
```

```
<210> 123
<211> 338
<212> DNA
<213> Homo sapiens
```

```
<400> 123
acgcgtctag ggtagaaatc aactccagta actgtcatc aacctcagca atgctgggga
60
```

cgggcagagg cagggcagct gtgtgccaca ttctgccag ggctggtcag gccccggctc  
 120  
 tcaccactcc tcctccctgc tttgaacctg tggaacaaag ggcccctgca ccccaactca  
 180  
 ttctcttttg ccacataagg gcctcaagtc atgctgtccc ctctgcctgg gttgcttttt  
 240  
 ctccctctgc ttgggtcact gttcacacca ctggccactt tcctcagga agggccctca  
 300  
 ctgcccacac acctaaacat gcccctgct cctccata  
 338

<210> 124  
 <211> 96  
 <212> PRT  
 <213> Homo sapiens

<400> 124  
 Met Leu Gly Thr Gly Arg Gly Arg Ala Ala Val Cys His Ile Pro Ala  
 1 5 10 15  
 Arg Ala Gly Gln Ala Pro Ala Leu Thr Thr Pro Pro Pro Cys Phe Glu  
 20 25 30  
 Pro Val Glu Gln Arg Ala Pro Ala Pro Gln Leu Ile Pro Leu Cys His  
 35 40 45  
 Ile Arg Ala Ser Ser His Ala Val Pro Ser Ala Trp Val Ala Phe Ser  
 50 55 60  
 Pro Ser Ala Trp Val Thr Val His Thr Thr Gly His Phe Pro Gln Gly  
 65 70 75 80  
 Arg Ala Leu Thr Ala His Thr Pro Lys His Ala Pro Cys Ser Ser Ile  
 85 90 95

<210> 125  
 <211> 280  
 <212> DNA  
 <213> Homo sapiens

<400> 125  
 ccatggacct ggccagccac catcacctgc ctctgcctc acccaccctg ggtgcctgcc  
 60  
 ggcaaggatt ggagggcaga ctgctggagc gtgagaccag gccaatctgt ctttctggga  
 120  
 accttcagcc tccaactgga gctgactgtc aactttcggg tgagaagtca ctttctgca  
 180  
 ttcccaccac actatctatc tgtgcaatac ggcagcgtga cagcactcac cttattgagg  
 240  
 gtttctgctg tcctggccca ttctggatag gctgatcta  
 280

<210> 126  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 126  
 Met Asp Leu Ala Ser His His His Leu Pro Pro Ala Ser Pro Thr Leu

```

      1           5           10           15
Gly Ala Cys' Arg Gln Gly Leu Glu Gly Arg Leu Leu Glu Arg Glu Thr
      20           25           30
Arg Pro Ile Cys Leu Ser Gly Asn Leu Gln Pro Pro Thr Gly Ala Asp
      35           40           45
Cys Gln Leu Ser Gly Glu Lys Ser Leu Phe Cys Ile Pro Thr Thr Leu
      50           55           60
Ser Ile Cys Ala Ile Arg Gln Arg Asp Ser Thr His Leu Ile Glu Gly
65           70           75           80
Phe Cys Cys Pro Gly Pro Phe Trp Ile Gly Leu Ile
      85           90

```

<210> 127  
 <211> 444  
 <212> DNA  
 <213> Homo sapiens

```

<400> 127
cgcgatgatcg ccgtggcgga gggccgcggc gccgactcga tcgcccagct gacaaccgag
60
ctgcaaagcc gtcactgccc tgcggagcag atcacgtccg tcagcatcga catgtcgcca
120
gcgttcacga ggggctgcgc cgagcacctg cccaacgcgc gcgtcacctt cgacaagttc
180
cacgtcatcg ggcacgcaa tgcggccgtg gacaggatgc gccgcatcga gcagcgcage
240
gacaagtccc tcaaggggat gcgctggctg ctgctgaaga accgcgccag cctcaagccc
300
gaggctgccc ccgatctgga tgccctgac gccaggatgg cactgtgctg caccgcgcgc
360
gcctgggtct acaaggagca gctgcgcgag atcctcgcgc gcaagcagat caacgtggca
420
cgcgacatgc tcaagcactg gtgc
444

```

<210> 128  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

```

<400> 128
Arg Val Ile Ala Val Ala Glu Gly Arg Gly Ala Asp Ser Ile Ala Gln
      1           5           10           15
Leu Thr Thr Glu Leu Gln Ser Arg His Cys Pro Ala Glu Gln Ile Thr
      20           25           30
Ser Val Ser Ile Asp Met Ser Pro Ala Phe Ile Arg Gly Cys Ala Glu
      35           40           45
His Leu Pro Asn Ala Arg Val Thr Phe Asp Lys Phe His Val Ile Gly
      50           55           60
His Ala Asn Ala Ala Val Asp Arg Met Arg Arg Ile Glu Gln Arg Ser
65           70           75           80
Asp Lys Ser Leu Lys Gly Met Arg Trp Ser Leu Leu Lys Asn Arg Ala
      85           90           95
Ser Leu Lys Pro Glu Ala Ala Ala Asp Leu Asp Ala Leu Ile Ala Arg

```

100 105 110  
 Met Ala Thr Val Arg Thr Ala Arg Ala Trp Val Tyr Lys Glu Gln Leu  
 115 120 125  
 Arg Glu Ile Leu Ala Arg Lys Gln Ile Asn Val Ala Arg Asp Met Leu  
 130 135 140  
 Lys His Trp Cys  
 145

<210> 129  
 <211> 291  
 <212> DNA  
 <213> Homo sapiens

<400> 129  
 gaggaggac gtaccgtccc cgttatagcc aagctcgaga agccgcaagc tatcgagaac  
 60  
 ttggacgaga ttattgacgt ctttgacgcc gtcattggtg cccgtggcga tatggccgctc  
 120  
 gagtgccgcg tcgaggaagt tccgctgatc caaaagcaga tcatcgagaa ggctcgttta  
 180  
 caggctaagc ccgtcattgt ggccaccag atgcttgagt cgatgatcca cgctccccgt  
 240  
 ccgacccgcg ctgaggccgc cgacgtcgcg aacgccatcc ttgacggcgc g  
 291

<210> 130  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 130  
 Glu Glu Gly Arg Thr Val Pro Val Ile Ala Lys Leu Glu Lys Pro Gln  
 1 5 10 15  
 Ala Ile Glu Asn Leu Asp Glu Ile Ile Asp Val Phe Asp Ala Val Met  
 20 25 30  
 Val Ala Arg Gly Asp Met Ala Val Glu Cys Pro Leu Glu Glu Val Pro  
 35 40 45  
 Leu Ile Gln Lys Gln Ile Ile Glu Lys Ala Arg Leu Gln Ala Lys Pro  
 50 55 60  
 Val Ile Val Ala Thr Gln Met Leu Glu Ser Met Ile His Ala Pro Arg  
 65 70 75 80  
 Pro Thr Arg Ala Glu Ala Ala Asp Val Ala Asn Ala Ile Leu Asp Gly  
 85 90 95  
 Ala

<210> 131  
 <211> 416  
 <212> DNA  
 <213> Homo sapiens

<400> 131  
 tccggagcgt ccgtggccct catgggtgtg tcagcgtggt tgctgtctcg ggccgcagag  
 60

attccaccgg tgctctacct ggaggccgca gccgtcgggg ttcgattctt cggcatctcc  
 120  
 cgcggtgtct tccgctacgc cgaacgtctg gtaggccacg acctggctct gcggatgcag  
 180  
 ggggcattgc ggatgcgggt ctacgaccgg ctgtcacgta ccnaccctgc tggggnnacgt  
 240  
 cgccgggggtg acctgctggg acgggttact gccgacgtcg acgcggtgtt ggacatggtc  
 300  
 gtgcgggtga tcgttccggc gtgcgcgtca agcctcgtca tcattggcac cacggtcctt  
 360  
 ctttgtccga gagaagggtg agttttctta gccggattcc aacacagcct gggggg  
 416

<210> 132  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
 Ser Gly Ala Ser Val Ala Leu Met Gly Val Ser Ala Trp Leu Leu Ser  
 1 5 10 15  
 Arg Ala Ala Glu Ile Pro Pro Val Leu Tyr Leu Glu Ala Ala Val  
 20 25 30  
 Gly Val Arg Phe Phe Gly Ile Ser Arg Gly Val Phe Arg Tyr Ala Glu  
 35 40 45  
 Arg Leu Val Gly His Asp Leu Ala Leu Arg Met Gln Gly Ala Leu Arg  
 50 55 60  
 Met Arg Val Tyr Asp Arg Leu Ser Arg Thr Xaa Pro Ala Gly Xaa Arg  
 65 70 75 80  
 Arg Arg Gly Asp Leu Leu Val Arg Val Thr Ala Asp Val Asp Ala Val  
 85 90 95  
 Leu Asp Met Val Val Arg Val Ile Val Pro Ala Cys Ala Ser Ser Leu  
 100 105 110  
 Val Ile Ile Gly Thr Thr Val Leu Leu Cys Pro Arg Glu Gly  
 115 120 125

<210> 133  
 <211> 327  
 <212> DNA  
 <213> Homo sapiens

<400> 133  
 gccgttgcta tcgctgctgg tatgcgtgca gacgtcactg tttttgatat caatatcgct  
 60  
 gcgttgaaga gactcgccga catctaccag ggctcgtgttc acacagtagt atccaccgc  
 120  
 gccgaaattg cgaaggcgct agaaaccgct gacgttgtga tcggttctgt ccttattccg  
 180  
 ggtagttcta ccccgaaagt tggtactacc gatatgggtg ctacatgca gcctgggtct  
 240  
 gttcttattg atattgctat agaccaaggc ggctgcttcg aggattcgca cccaccact  
 300  
 tacgatgacc ccactttcac tgtgcac  
 327



<210> 134  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 134  
 Ala Val Ala Ile Ala Ala Gly Met Arg Ala Asp Val Thr Val Phe Asp  
 1 5 10 15  
 Ile Asn Ile Ala Ala Leu Lys Arg Leu Ala Asp Ile Tyr Gln Gly Arg  
 20 25 30  
 Val His Thr Val Val Ser Thr Arg Ala Glu Ile Ala Lys Ala Leu Glu  
 35 40 45  
 Thr Ala Asp Val Val Ile Gly Ser Val Leu Ile Pro Gly Ser Ser Thr  
 50 55 60  
 Pro Lys Leu Val Thr Thr Asp Met Val Ala His Met Gln Pro Gly Ser  
 65 70 75 80  
 Val Leu Ile Asp Ile Ala Ile Asp Gln Gly Gly Cys Phe Glu Asp Ser  
 85 90 95  
 His Pro Thr Thr Tyr Asp Asp Pro Thr Phe Thr Val His  
 100 105

<210> 135  
 <211> 560  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
 taagatgtgg tcctgccctg ttcctgaagg ggctgcagct ctgatggaaa atacagggat  
 60  
 ttacactcag ggctacagcc acggggggct gaggcccaag gctgcaatct cgggggaagg  
 120  
 ggaagtggc ttttcttgtt ggattggaaa catcctcttg gaggcaaaga cttttcttg  
 180  
 atcttacaga cttcccgga tttttagatt agaattattg gggcaaagga ggctgtcttg  
 240  
 ttttaaagca atgctacata gacacagtgg ggaagacctg gttcgacggc agataagcag  
 300  
 tgggtgatgg gcttgaggag gagagtcagg gcaaagtcta agactgagca gaaaggaatt  
 360  
 ccccatctc ccatggataa gtacgttcta gaacattctc tttgggtcta atactctgaa  
 420  
 atgacatctt gtcttcatgc tcgagagaga attacttcac tggctccact tggagtgcc  
 480  
 gtgttcagac accaagcctg actgggaggg ttccgttttc ttaaacacctt cccaccgccg  
 540  
 acttccaagt cccacgcgt  
 560

<210> 136  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 136

```

Met Trp Ser Cys Pro Val Pro Glu Gly Ala Ala Ala Leu Met Glu Asn
 1           5           10           15
Thr Gly Ile Tyr Thr Gln Gly Tyr Ser His Gly Gly Leu Arg Pro Lys
      20           25           30
Ala Ala Ile Ser Gly Glu Gly Glu Val Gly Phe Ser Trp Trp Ile Gly
      35           40           45
Asn Ile Leu Leu Glu Ala Lys Thr Phe Pro Gly Ser Tyr Arg Leu Pro
      50           55           60
Gly Ile Phe Arg Leu Glu Tyr Trp Gly Gln Arg Arg Leu Ser Cys Phe
      65           70           75           80
Lys Ala Met Leu His Arg His Ser Gly Glu Asp Leu Val Arg Arg Gln
      85           90           95
Ile Ser Ser Gly
          100

```

&lt;210&gt; 137

&lt;211&gt; 429

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

```

accggttgga tggcctgcag gccaaagcgt tcctgcaaac tcagcaggcc ttcagcgcaa
60
gaggcaaaca gctggtcgcg cacctgcttg aggtccaccg attgcgcata gcccttgagc
120
aaggcgcgcc agttggtttt gtcggccact tggctgcgga acaggtcttc gacaaaaccg
180
gactgctggc gggtcgcaac gcgcatgata ggcagcgcct ggctggcgcc ctggctgagc
240
cagcgcgctg gcagttgggt ggcccgggtg ataccgacct tgatccccga cgaattggcc
300
aggtacacca catggtcggt catgcagaat gtttcgcccc agccgggata acggcaagtg
360
ccggcgctgt aatggcaacg ttcggggctc atgatgcaca ggtcacactg ggccagcttg
420
gtcatgccc
429

```

&lt;210&gt; 138

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 138

```

Met Thr Lys Leu Ala Gln Cys Asp Leu Cys Ile Met Ser Pro Glu Arg
 1           5           10           15
Cys His Tyr Asp Ala Gly Thr Cys Arg Asp Pro Gly Trp Gly Glu Thr
      20           25           30
Phe Cys Met Thr Asp His Val Val Tyr Leu Ala Asn Ser Ser Gly Ile
      35           40           45
Lys Val Gly Ile Thr Arg Ala Thr Gln Leu Pro Thr Arg Trp Leu Asp
      50           55           60
Gln Gly Ala Ser Gln Ala Leu Pro Ile Met Arg Val Ala Thr Arg Gln

```

65					70					75				80	
Gln	Ser	Gly	Phe	Val	Glu	Asp	Leu	Phe	Arg	Ser	Gln	Val	Ala	Asp	Lys
				85					90					95	
Thr	Asn	Trp	Arg	Ala	Leu	Leu	Lys	Gly	Asp	Ala	Gln	Ser	Val	Asp	Leu
			100					105					110		
Lys	Gln	Val	Arg	Asp	Gln	Leu	Phe	Ala	Ser	Cys	Ala	Glu	Gly	Leu	Leu
		115				120						125			
Ser	Leu	Gln	Glu	Arg	Phe	Gly	Leu	Gln	Ala	Ile	Gln	Pro			
	130					135					140				

<210> 139  
 <211> 341  
 <212> DNA  
 <213> Homo sapiens

<400> 139  
 acgcgtcggt tgaaggcttg atccgcacgt ccaattcgct ttgcgccaat gcgccgcagc  
 60  
 ttgtgaacag cagaatcaag ccgctggtaa atcttctctgg gagcttcata ggccggggatg  
 120  
 ctacacgagc tggggagaca ctttgaaccc ggaattgtct gaataattct gtctcaaacc  
 180  
 tttgcagcct gtaacgactg aggggttcgga tggaaaaaca catgctccag gatgggaccg  
 240  
 acggccactt caccgatctc ttcatagccc tggcgtttgt agaaatccag gtagcgcgaa  
 300  
 tcgccagcgt cgagcacgac gcctgatgag tgcgggtcat t  
 341

<210> 140  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 140															
Met	Thr	Arg	Thr	His	Gln	Ala	Ser	Cys	Ser	Thr	Leu	Ala	Ile	Arg	Ala
1				5					10				15		
Thr	Trp	Ile	Ser	Thr	Asn	Ala	Arg	Ala	Met	Lys	Arg	Ser	Val	Lys	Trp
			20					25					30		
Pro	Ser	Val	Pro	Ser	Trp	Ser	Met	Cys	Phe	Ser	Ile	Arg	Thr	Leu	Ser
		35				40						45			
Arg	Tyr	Arg	Leu	Gln	Arg	Phe	Glu	Thr	Glu	Leu	Phe	Arg	Gln	Phe	Arg
	50				55						60				
Val	Gln	Ser	Val	Ser	Pro	Ala	Arg	Val	Ala	Ser	Pro	Pro	Met	Lys	Leu
65					70					75				80	
Pro	Gly	Arg	Phe	Thr	Ser	Gly	Leu	Ile	Leu	Leu	Phe	Thr	Ser	Cys	Gly
			85					90					95		
Ala	Leu	Ala	Gln	Ser	Glu	Leu	Asp	Val	Arg	Ile	Lys	Pro	Ser	Asn	Asp
		100						105					110		

Ala

<210> 141  
 <211> 324

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 141

gaattcctct tggatagctt cgggtaaattg ggtacagcaa atatcaggag cgcaaccgca  
 60  
 acctttactt actggtacat gaacaccatt tacattacag ctatcgctact caccacacgt  
 120  
 catgtgaaca gacacataac tgaaagggtt ataaaccaca gtctcacggt acgtatgacc  
 180  
 gtcaactgtg aacaccgcta agtaatagcc tgcggggggt tgcatagaact cctttgacca  
 240  
 tgcgtaataa atacgtccgt cattagtcac acctgatggg gcgaaacaaa aagaacggca  
 300  
 gcagttatca ccgcccatac gcgt  
 324

&lt;210&gt; 142

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

Met	Gly	Gly	Asp	Asn	Cys	Cys	Arg	Ser	Phe	Cys	Phe	Ala	Pro	Ser	Gly
1				5					10					15	
Val	Thr	Asn	Asp	Gly	Arg	Ile	Tyr	Tyr	Ala	Trp	Ser	Lys	Glu	Phe	Met
		20					25					30			
Gln	Ala	Pro	Ala	Gly	Tyr	Tyr	Leu	Ala	Val	Phe	Thr	Val	Asp	Gly	His
	35					40					45				
Thr	Tyr	Arg	Glu	Thr	Val	Val	Tyr	Lys	Pro	Phe	Ser	Tyr	Val	Ser	Val
	50				55					60					
His	Met	Thr	Trp	Gly	Glu	Tyr	Asp	Ser	Cys	Asn	Val	Asn	Gly	Val	His
65				70					75					80	
Val	Pro	Val	Ser	Lys	Gly	Cys	Gly	Cys	Ala	Pro	Asp	Ile	Cys	Cys	Thr
			85				90						95		
His	Leu	Pro	Glu	Ala	Ile	Gln	Glu	Glu	Phe						
			100				105								

&lt;210&gt; 143

&lt;211&gt; 1325

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 143

nacgcgtgga tctgccagct gagcctggag ctgtgcaggc agctgccttg ctacgatgag  
 60  
 gcacccagg agaagaactt cctgtacaaa tgcataggca ccaccctggg tgctgcttca  
 120  
 agtaaggagg tggtagaggaa gcaccttcaa gagctgctgg agacggccag ataccaggag  
 180  
 gaggcagaac gcgagggcct cgcctgctgc ttcgggatct gtgccatctc ccacctcgag  
 240  
 gacacgctgg cccagctgga ggacttcgtg aggtcagagg tcttcagaaa atccattggc  
 300

attctcaaca tttttaagga tcgaagtgag aacgaagtgg agaaggtgaa gagtgctctg  
 360  
 atcctgtgct atgggcacgt ggcgccccgg gccccccggg agctggtgct ggccaaggtg  
 420  
 gagtcagaca tcctccggaa catcntgcca gcacttcagc acnncaagga cccagccctg  
 480  
 aagctgtgcc ttgtccagag tgtgtgcatg gtcagccgcg ccatctgcag cagcaccag  
 540  
 gctggctcct tccacttcac ccggaaagca gagctggtgg cacagatgat ggagttcatc  
 600  
 agggcagagc ccccgactc cttgaggaca cctattcgga agaaagccat gctcacctgc  
 660  
 acttacttgg tctccgtgga gccagcgctg gacgagcagg cccgggcgga tgtgatccat  
 720  
 ggctgcctgc acagcatcat ggccctgctg cctgagccca aggaggagga cggaggctgc  
 780  
 cagaagtccc tgtatctgga gacactgcac gcccttgagg atctgctgac gagcctcctg  
 840  
 cagcggaaca tgacccccca aggcctgcag atcatgattg agcacctgag cccatggatc  
 900  
 aagtccccaa gaggtcacgt agcggcgctg gccctaggcc tgagcgccct cctcgtgcgc  
 960  
 tacttcctgg agcacctgcg tgtcagtggc gcccaagtag ataccaggtt tccatctgag  
 1020  
 cccaggatcc tgtgcaatgg ccctggtgcc cttccacaac ctgggccttc tcatcggcct  
 1080  
 cttctcccca cgggtgtgcgg acctgtggcc tgccacccgc caggaggccg tggactgtgt  
 1140  
 ctactcctg ctgtacctcc agctcggcta tgagggttc tcccgggact accgcgatga  
 1200  
 cgtggcggag cggtcctca gcctcaagga cggcctcgtg caccctgacc ccgccattct  
 1260  
 cttccacacc tgccacagtg taggccagat tattgccaag cgcctcccc cagcccttca  
 1320  
 cgcgt  
 1325

&lt;210&gt; 144

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 144

Xaa Ala Trp Ile Cys Gln Leu Ser Leu Glu Leu Cys Arg Gln Leu Pro  
 1 5 10 15  
 Cys Tyr Asp Glu Ala Pro Gln Glu Lys Asn Phe Leu Tyr Lys Cys Ile  
 20 25 30  
 Gly Thr Thr Leu Gly Ala Ala Ser Ser Lys Glu Val Val Arg Lys His  
 35 40 45  
 Leu Gln Glu Leu Leu Glu Thr Ala Arg Tyr Gln Glu Glu Ala Glu Arg  
 50 55 60  
 Glu Gly Leu Ala Cys Cys Phe Gly Ile Cys Ala Ile Ser His Leu Glu  
 65 70 75 80  
 Asp Thr Leu Ala Gln Leu Glu Asp Phe Val Arg Ser Glu Val Phe Arg

```
<210> 145
<211> 802
<212> DNA
<213> Homo sapiens
```

```
<400> 145
cgcccgctcta ggtccggctc agtgcgctgt tgctcgccgt agaacacgag gctgcgcaag
60
cataagcaga cgtagagagt ggtcacatcc atgtcgatgg tgtgcgcgta atgaaggtct
120
acatcaccct ggtgaaggcc tgcaccacta gcgtcggcac catttccccg cgtcggacaa
180
gacatcatgc cccatatctt gacagaatgt ctgacatgag tatgccacgc cgagcagcac
240
```

cagaggacga caccgatctg gccgacgccg cccgttcacg gccagatac ctcacccctg  
 300  
 tcatttggtg cggtatcgtc gctgtcctcg gactaggcat ttccgggtat cttgcgtggt  
 360  
 ggtcattgtg cgatcaagct gccgggggtct gtcagcgtgg tgaaccggtt atgtactggt  
 420  
 gttcgggtgt ctctctggcc attctcggac tcattatcgg ggtcttgacg cagatctggc  
 480  
 tggagaagcg ctggtggcac atgcttgcca tcgtcatccc ggctgttttc atcgtcgccg  
 540  
 gtatcttttt ctggctcgcc gtctaagaag gggcgtcaca gattccacaa acgacacagg  
 600  
 tattgatctc cgttttatcg gctcctagca gccgtggtca acgtatcgct atcaagcgat  
 660  
 acaggactcg tcgttcgcat cgttgttggt ctgctgggaa acaatcccag cgatctactc  
 720  
 ggctaccgcc agacagttca ctcacaaccc ctcacgccg cgacagacac aaatcccatt  
 780  
 ctcgatagac ggcccacacc ac  
 802

&lt;210&gt; 146

&lt;211&gt; 151

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 146

Met	Lys	Val	Tyr	Ile	Thr	Leu	Val	Lys	Ala	Cys	Thr	Thr	Ser	Val	Gly
1				5					10					15	
Thr	Ile	Ser	Pro	Arg	Arg	Thr	Arg	His	His	Ala	Pro	Tyr	Leu	Asp	Arg
			20					25					30		
Met	Ser	Asp	Met	Ser	Met	Pro	Arg	Arg	Ala	Ala	Pro	Glu	Asp	Asp	Thr
		35					40					45			
Asp	Leu	Ala	Asp	Ala	Ala	Arg	Ser	Trp	Arg	Arg	Tyr	Leu	Ile	Leu	Val
	50					55					60				
Ile	Cys	Gly	Val	Ile	Val	Ala	Val	Leu	Gly	Leu	Gly	Ile	Phe	Gly	Tyr
65					70				75					80	
Leu	Ala	Trp	Trp	Ser	Leu	Cys	Asp	Gln	Ala	Ala	Gly	Val	Cys	Gln	Arg
			85					90					95		
Gly	Glu	Pro	Val	Met	Tyr	Trp	Cys	Ser	Val	Val	Ser	Leu	Ala	Ile	Leu
		100					105					110			
Gly	Leu	Ile	Ile	Gly	Val	Leu	Thr	Gln	Ile	Trp	Leu	Glu	Lys	Arg	Trp
	115					120					125				
Trp	His	Met	Leu	Ala	Ile	Val	Ile	Pro	Ala	Val	Phe	Ile	Val	Ala	Gly
	130					135					140				
Ile	Phe	Phe	Trp	Leu	Ala	Val									
145					150										

&lt;210&gt; 147

&lt;211&gt; 368

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 147

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 <213> Homo sapiens

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 Arg Lys Val Ile Gly Gln Lys Val Pro Cys Val Ala Val Thr Gly Ser  
 35 40 45  
 Glu Lys Val Leu His Lys Lys Asp Tyr Trp Asp Leu Ala Thr Pro Met  
 50 55 60  
 Pro Ile Ala Trp Gly Thr Thr Asp Arg Thr Val Ile Ala Asp Ala Arg  
 65 70 75 80  
 Arg Thr Ile Pro Thr Thr Glu Trp Asp Ile Leu Ala Arg Leu Arg Pro  
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 300



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 <213> Homo sapiens

<400> 150  
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 Ser Ser Val Val Ile Trp His Asp Ala Val Asp Gly Ile Val Tyr Arg  
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 Ser Ala Asp Glu Gly Lys Ser Trp Ala Pro Ile Lys Gly Pro Glu Gln  
 50 55 60  
 Gly Gln Ala His Leu Phe Val Leu His Pro Tyr Asp Lys Thr Gln Ala  
 65 70 75 80  
 Tyr Ile Leu Thr Arg Ser Thr Gln His Trp Arg Thr Ser Asn Arg Gly  
 85 90 95  
 Glu Thr Trp Gln Ser Phe Ser Thr Pro His Pro Pro Thr Thr Leu Lys  
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 Thr Gly Gln Ala Cys Thr Val  
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 <211> 448  
 <212> DNA  
 <213> Homo sapiens

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 180  
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 gcttccacgg cacggcctcg tgcaaaatcg cgggtttcgg ggccttgag caaattgcgc  
 300  
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 360  
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<210> 152

<211> 149  
 <212> PRT  
 <213> Homo sapiens

<400> 152  
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 35 40 45  
 Cys Pro Val Ser Ala Pro Pro Ser Ser Pro Pro Glu Gly Lys Thr Trp  
 50 55 60  
 Ala Leu Arg Glu Pro Cys Gly Met Phe Phe Val Ile Asn Cys Thr Ser  
 65 70 75 80  
 Ala Ser Thr Ala Arg Pro Arg Ala Lys Ser Arg Val Ser Gly Pro Trp  
 85 90 95  
 Ser Lys Leu Arg Leu Ser Ala Ala Thr Ser Gly Gly Gln Gly Glu Gly  
 100 105 110  
 Phe Ala Ala Glu Thr Ala Ala Ser Gln His Arg Ala Ile Leu Gly Cys  
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 Cys Met Asp Ile Arg  
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 <211> 440  
 <212> DNA  
 <213> Homo sapiens

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<210> 154  
 <211> 69  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 154

Gly Arg His Ala Gly Val Cys Pro Ser Val Cys Pro Trp Val His Val  
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 Gly Pro Cys Ile Cys Val Tyr Ile Cys Gly Asp Met Tyr Met Cys Val  
 35 40 45  
 Cys Met Asn Arg Cys Lys Trp Gly Ala Leu Arg Cys Val Cys Val Cys  
 50 55 60  
 Ser Cys Thr Arg Val  
 65

&lt;210&gt; 155

&lt;211&gt; 344

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 155

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 344

&lt;210&gt; 156

&lt;211&gt; 92

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 156

Met Ala Glu Leu Met Ala Asp Ala Ala Thr Gly Thr Lys Pro Ser Tyr  
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 Leu Gln Arg Ser Ser Ser Ile Thr Ser Phe Glu Val Asp Arg Glu  
 20 25 30  
 Gln Arg His Ser Asp Asn Ala Pro Gln Glu Val Lys Ser Ser Leu Ser  
 35 40 45  
 Asp His Gly Arg Arg Ala Ser Ala Gln Gly Glu Leu Gly Thr Ser Gln  
 50 55 60  
 Ala Thr Pro Pro Arg Ser Met Pro Pro Pro Val Ser Ser Ala Ser Ser  
 65 70 75 80  
 Thr Ser Pro Leu Pro Ile Ser Ile Ile Ser Asp Leu  
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&lt;210&gt; 157

&lt;211&gt; 6816

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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tgaacaaagc aaattggaag gttctgggttc cggtttagat agctacctgc cggaacttgc  
300  
caagagtga agagaagcag aaatcaaact gaaaagtga agcagagtca aactttttta  
360  
tttggacca gatgccaga agcttgactt ctcacagct gagccagaag tgaagtcatt  
420  
tgaagagaag tttggaaaaa ggatccttgt caagtgaat gatttatctt tcaatttga  
480  
atgctgtgtt gccgaaaatg aagaaggacc cactacaaat gttgaacctt tctttgttac  
540  
tctatccctg tttgacataa aatacaaccg gaagatttct gccgatttcc acgtagacct  
600  
gaaccatttc tcagtgaggc aaatgatgc caccacgtcc cggcgctga tgaatggcag  
660  
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aagcagggaa tattttcagt cacttgtcct catccagata tatttcttgt ggccagaatt  
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<210> 158  
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 <212> PRT  
 <213> Homo sapiens

<400> 158  
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 Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly  
 35 40 45  
 Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr  
 50 55 60  
 Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys  
 65 70 75 80  
 Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys  
 85 90 95  
 His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro  
 100 105 110  
 Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn  
 115 120 125  
 Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln  
 130 135 140  
 Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg  
 145 150 155 160  
 Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr  
 165 170 175  
 Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His  
 180 185 190  
 Leu Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly  
 195 200 205  
 Ser Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp  
 210 215 220  
 Leu Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile  
 225 230 235 240  
 Pro Val Ser Ala Asn Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu  
 245 250 255  
 Gly Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly



				260												270
Lys	Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	
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Gln	Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	
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Ser	Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	
305					310					315					320	
Leu	His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	
				325					330						335	
Leu	Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	
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Glu	Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	
		370				375					380					
Lys	Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	
385					390					395					400	
Leu	Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	
				405					410						415	
Thr	Ser	Asn	Lys	Leu	Leu	Lys	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	
			420					425					430			
Ile	Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	
		435					440					445				
Leu	Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Val	Glu	Thr	
		450				455					460					
Val	Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Arg	Asp	Asn	
465					470					475					480	
Pro	Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	
				485					490						495	
Arg	Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	
			500					505					510			
Asn	Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	
		515					520						525			
Tyr	Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	
		530				535					540					
Pro	Leu	Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	
545					550					555					560	
Gln	Asp	Leu	Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	
				565					570					575		
His	Phe	Leu	Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	
			580					585					590			
Glu	Phe	Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	
		595					600									

690	695	700
Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser		
705	710	715
Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu		
	725	730
Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn		
	740	745
Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu		
	755	760
Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu		
	770	775
Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe		
	785	790
Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg		
	805	810
Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly		
	820	825
Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp		
	835	840
Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu		
	850	855
Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe		
	865	870
Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys		
	885	890
Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr		
	900	905
Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe		
	915	920
Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys		
	930	935
Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr		
	945	950
Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr		
	965	970
Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser		
	980	985
Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe		
	995	1000
Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu		
	1010	1015
Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg		
	1025	1030
Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn		
	1045	1050
Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr		
	1060	1065
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg		
	1075	1080
Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val		
	1090	1095
His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val		
	1105	1110
Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg		
	1115	1120

1125										1130					1135						
Arg	Ser	Arg	Gly	Gly	Val	Phe	Arg	Gln	Gly	Cys	Thr	Ala	Phe	Arg	Val						
			1140					1145					1150								
Ile	Thr	Pro	Asn	Ile	Asp	Glu	Glu	Ala	Ser	Met	Met	Glu	Asp	Val	Gly						
		1155				1160						1165									
Met	Gln	Asp	Val	His	Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu						
		1170				1175				1180											
Gln	Cys	Ala	Asp	Gly	Leu	Trp	Lys	Ala	Glu	Arg	Tyr	Glu	Leu	Ile	Ala						
1185				1190					1195						1200						
Asp	Ile	Tyr	Lys	Leu	Ile	Ile	Pro	Ile	Tyr	Glu	Lys	Arg	Arg	Asp	Phe						
			1205					1210						1215							
Glu	Arg	Leu	Ala	His	Leu	Tyr	Asp	Thr	Leu	His	Arg	Ala	Tyr	Ser	Lys						
		1220					1225					1230									
Val	Thr	Glu	Val	Met	His	Ser	Gly	Arg	Arg	Leu	Leu	Gly	Thr	Tyr	Phe						
		1235					1240					1245									
Arg	Val	Ala	Phe	Phe	Gly	Gln	Ala	Ala	Gln	Tyr	Gln	Phe	Thr	Asp	Ser						
		1250				1255				1260											
Glu	Thr	Asp	Val	Glu	Gly	Phe	Phe	Glu	Asp	Glu	Asp	Gly	Lys	Glu	Tyr						
1265				1270					1275						1280						
Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Pro	Leu	Ser	Glu	Ile	Ser	Gln	Arg						
			1285					1290						1295							
Leu	Leu	Lys	Leu	Tyr	Ser	Asp	Lys	Phe	Gly	Ser	Glu	Asn	Val	Lys	Met						
		1300					1305					1310									
Ile	Gln	Asp	Ser	Gly	Lys	Val	Asn	Pro	Lys	Asp	Leu	Asp	Ser	Lys	Tyr						
		1315					1320					1325									
Ala	Tyr	Ile	Gln	Val	Thr	His	Val	Ile	Pro	Phe	Phe	Asp	Glu	Lys	Glu						
		1330				1335				1340											
Leu	Gln	Glu	Arg	Lys	Thr	Glu	Phe	Glu	Arg	Ser	His	Asn	Ile	Arg	Arg						
1345				1350					1355						1360						
Phe	Met	Phe	Glu	Met	Pro	Phe	Thr	Gln	Thr	Gly	Lys	Arg	Gln	Gly	Gly						
			1365					1370						1375							
Val	Glu	Glu	Gln	Cys	Lys	Arg	Arg	Thr	Ile	Leu	Thr	Ala	Ile	His	Cys						
		1380					1385					1390									
Phe	Pro	Tyr	Val	Lys	Lys	Arg	Ile	Pro	Val	Met	Tyr	Gln	His	His	Thr						

1555  
Ser Ser Val Val  
1570

1560

1565

<210> 159  
<211> 540  
<212> DNA  
<213> Homo sapiens

<400> 159  
gccggctctg ccatgtgctt actctgagcc acctaacctc ggcgtgcttc agtttactca  
60  
tccgctcatc tgcagaatgg gtgatgctgt cggtacttcg tggcatacag gaaagtgtccc  
120  
agcatgggtca gcctcagtga gaggtggcca gtggggagtg gtggccactg tacacctggc  
180  
acagcccaga gatgcatgtg ccactctgtt gtgtgcttca accaaggggc gctctggcag  
240  
ggcttgggtg ggacttccca aagggtcatgg aaaagtcccc agtcaatgag atccatggag  
300  
acccatggga gtgggggtca gccccagcct aagaggacct ccagccctgc cctgtgcccc  
360  
aggacacacc aggcactgtc ccttgctgcc ttcccagaca acctgtacct tccaggccac  
420  
cagttctcgt ccatgacaaa gaaaggagcc ttctaaataa gtgcccgcga gaggtgtcac  
480  
gcttccctgc cccttccggg tggacctggg tttaaagag aagctgccag tgcaacgcgt  
540

<210> 160  
<211> 110  
<212> PRT  
<213> Homo sapiens

<400> 160  
Met Val Ser Leu Ser Glu Arg Trp Pro Val Gly Ser Gly Gly His Cys  
1 5 10 15  
Thr Pro Gly Thr Ala Gln Arg Cys Met Cys His Ser Val Val Cys Phe  
20 25 30  
Asn Gln Gly Ala Leu Trp Gln Gly Leu Gly Gly Thr Ser Gln Arg Ala  
35 40 45  
Trp Lys Ser Ser Gln Ser Met Arg Ser Met Glu Thr His Gly Ser Gly  
50 55 60  
Gly Gln Pro Gln Pro Lys Arg Thr Pro Ser Pro Ala Leu Cys Pro Arg  
65 70 75 80  
Thr His Gln Ala Leu Ser Leu Val Ala Phe Pro Asp Asn Leu Tyr Pro  
85 90 95  
Pro Gly His Gln Phe Ser Ser Met Thr Lys Lys Gly Ala Phe  
100 105 110

<210> 161  
<211> 351  
<212> DNA  
<213> Homo sapiens

<400> 161  
 nnacgcgtac gtctttcggc cgaagaagga acgtgggcag gggcctcctt cgctggccgc  
 60  
 cgcgcttggc tcgcagcgac gatgaagggc gacgacagca gcaagatcac ccacaagatc  
 120  
 gcccgggcca agcgcgaggg ccgcgtatgg tggagctttg agtacttccc gccgcgcacg  
 180  
 ccgcagggca tgcagaattt gtatgaccgt atcgagcgca tgagtcagct gggccccgag  
 240  
 tttgtggaca ttacgtggaa tgccgggggc cggacgtcgg atatgacgac gcagctggtc  
 300  
 aagacgggtgc atgcgtactt tgggtgcgag acgtgcatgc atctgacgtg c  
 351

<210> 162  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Xaa Arg Val Arg Leu Ser Ala Glu Glu Gly Thr Trp Ala Gly Ala Ser  
 1 5 10 15  
 Phe Ala Gly Arg Arg Ala Trp Leu Ala Ala Thr Met Lys Gly Asp Asp  
 20 25 30  
 Ser Ser Lys Ile Thr His Lys Ile Ala Arg Ala Lys Arg Glu Gly Arg  
 35 40 45  
 Val Trp Trp Ser Phe Glu Tyr Phe Pro Pro Arg Thr Pro Gln Gly Met  
 50 55 60  
 Gln Asn Leu Tyr Asp Arg Ile Glu Arg Met Ser Gln Leu Gly Pro Glu  
 65 70 75 80  
 Phe Val Asp Ile Thr Trp Asn Ala Gly Gly Arg Thr Ser Asp Met Thr  
 85 90 95  
 Thr Gln Leu Val Lys Thr Val His Ala Tyr Phe Gly Val Glu Thr Cys  
 100 105 110  
 Met His Leu Thr Cys  
 115

<210> 163  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 163  
 gcgtgctcca tcggcacctt gcagatgggc gaattcgctg aaaacgtcgc cggtaggcgtc  
 60  
 gacacctaca ccctgcgtca gcccatcggc gtatgcgcag gcatactcc gttcaacttc  
 120  
 ccggcgatga ttccactgtg gatgttcccg atggcgattg cctgcggtaa cactttcgtg  
 180  
 ctcaaaccgt ccgaacaaga ccctctgtcg acgatgctgc tggtagaact ggcgctggaa  
 240  
 gccggtgtgc cggccggcgt gctcaacgtg gtgcacggcg gcaaggatgt ggtggatgcg  
 300

ctgtgcaccc ataaagatat caaggcagtt tctttcgtcg gttcgaccgc cgttgggtacc  
360

<210> 164

<211> 120

<212> PRT

<213> Homo sapiens

<400> 164

Ala	Cys	Ser	Ile	Gly	Thr	Leu	Gln	Met	Gly	Glu	Phe	Ala	Glu	Asn	Val
1				5					10					15	
Ala	Gly	Gly	Val	Asp	Thr	Tyr	Thr	Leu	Arg	Gln	Pro	Ile	Gly	Val	Cys
			20					25					30		
Ala	Gly	Ile	Thr	Pro	Phe	Asn	Phe	Pro	Ala	Met	Ile	Pro	Leu	Trp	Met
			35				40					45			
Phe	Pro	Met	Ala	Ile	Ala	Cys	Gly	Asn	Thr	Phe	Val	Leu	Lys	Pro	Ser
	50					55					60				
Glu	Gln	Asp	Pro	Leu	Ser	Thr	Met	Leu	Leu	Val	Glu	Leu	Ala	Leu	Glu
65					70					75				80	
Ala	Gly	Val	Pro	Ala	Gly	Val	Leu	Asn	Val	Val	His	Gly	Gly	Lys	Asp
				85				90						95	
Val	Val	Asp	Ala	Leu	Cys	Thr	His	Lys	Asp	Ile	Lys	Ala	Val	Ser	Phe
			100					105					110		
Val	Gly	Ser	Thr	Ala	Val	Gly	Thr								
			115				120								

<210> 165

<211> 728

<212> DNA

<213> Homo sapiens

<400> 165

gctagcagcc ttcaccctcc tagaggggca ggctcggcga caaggggcgg ggggtgccccg  
60  
tcccagcgag ggacgcccgg ggctgggggt gccgggtcgag cccggggcaa cagcttcacc  
120  
aagtttggca accgcaacgt cttcatgaag gacaacagct cttcttccag cacagactcc  
180  
cgctccccgt cctcctccag gtccccgacg cgccacttcc gcagaagtga ctcccactca  
240  
gactccgaca gtcctactc agggaatgag tgtcaccctg tgggcccgcag gaaccgcgcc  
300  
cctaagggcc ggggcggctg agggggcccat atggatcggg gccgaggcag ggcgcagcgt  
360  
gggaagaggc acgatctggc gccaccaag cgcagtcgaa agaagatggc ggcgctggag  
420  
tgtgaggacc cggagcgaga gctgaagaag cagaagcggg cagcccgtt ccagcacgga  
480  
cactcccgcc gcctgcgct cgagcccctg gtgctgcaga tgagcagcct ggagagcagt  
540  
ggggctgacc ctgactggca ggagctgcag atcgtgggca cctgccctga catcaccaag  
600  
cactacctgc gcctcacctg tgcccccgac ccgtccaccg tgcgccctgt ggcattccct  
660

gtggcaggtt ttgaaaaagt cgctgtgcat ggtcaagtgc cactggaaag agaagcagga  
 720  
 ctacgcgt  
 728

<210> 166  
 <211> 242  
 <212> PRT  
 <213> Homo sapiens

<400> 166  
 Ala Ser Ser Leu His Pro Pro Arg Gly Ala Gly Ser Ala Thr Arg Gly  
 1 5 10 15  
 Gly Gly Ala Pro Ser Gln Arg Gly Thr Pro Gly Ala Gly Gly Ala Gly  
 20 25 30  
 Arg Ala Arg Gly Asn Ser Phe Thr Lys Phe Gly Asn Arg Asn Val Phe  
 35 40 45  
 Met Lys Asp Asn Ser Ser Ser Ser Thr Asp Ser Arg Ser Arg Ser  
 50 55 60  
 Ser Ser Arg Ser Pro Thr Arg His Phe Arg Arg Ser Asp Ser His Ser  
 65 70 75 80  
 Asp Ser Asp Ser Ser Tyr Ser Gly Asn Glu Cys His Pro Val Gly Arg  
 85 90 95  
 Arg Asn Pro Pro Pro Lys Gly Arg Gly Gly Arg Gly Ala His Met Asp  
 100 105 110  
 Arg Gly Arg Gly Arg Ala Gln Arg Gly Lys Arg His Asp Leu Ala Pro  
 115 120 125  
 Thr Lys Arg Ser Arg Lys Lys Met Ala Ala Leu Glu Cys Glu Asp Pro  
 130 135 140  
 Glu Arg Glu Leu Lys Lys Gln Lys Arg Ala Ala Arg Phe Gln His Gly  
 145 150 155 160  
 His Ser Arg Arg Leu Arg Leu Glu Pro Leu Val Leu Gln Met Ser Ser  
 165 170 175  
 Leu Glu Ser Ser Gly Ala Asp Pro Asp Trp Gln Glu Leu Gln Ile Val  
 180 185 190  
 Gly Thr Cys Pro Asp Ile Thr Lys His Tyr Leu Arg Leu Thr Cys Ala  
 195 200 205  
 Pro Asp Pro Ser Thr Val Arg Pro Val Ala Phe Pro Val Ala Gly Phe  
 210 215 220  
 Glu Lys Val Ala Val His Gly Gln Val Pro Leu Glu Arg Glu Ala Gly  
 225 230 235 240  
 Leu Arg

<210> 167  
 <211> 510  
 <212> DNA  
 <213> Homo sapiens

<400> 167  
 nnacgcgtgg aaccagaact caggcccggtg tgaggagtct ggtttggaac acacggggcc  
 60  
 gcaacacaga attgtcaggt cctgtgccgt gaccaccaac cctcggggcca tgccaggtgc  
 120

tgggtagggg caggtggctc ccgccaggcg cctgctggcc tgaccgcact ccgtccacag  
 180  
 gtcctcatgg gcgtcctccg gctgggcttc gtgtccgcct acctctcaca gccactgctc  
 240  
 gatggctttg ccatgggggc ctccgtgacc atcctgacct cgcagctcaa acacctgctg  
 300  
 ggcgtagcga tcccgcggca ccagggggcc ggcatggtgg tcctcacatg gctgagcctg  
 360  
 ctgcgcggcg ccgggcaggc caacgtgtgc gacgtggta ccagcacggt gtgcctggcg  
 420  
 gtgctgctag ccgcgaagga gctctcagac cgctaccgac accgcctgag ggtgccgctg  
 480  
 cccacggagc tgctggtcat cgtggtggcc  
 510

<210> 168  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 168  
 Gly Ala Gly Gly Ser Arg Gln Ala Pro Ala Gly Leu Thr Ala Leu Arg  
 1 5 10 15  
 Pro Gln Val Leu Met Gly Val Leu Arg Leu Gly Phe Val Ser Ala Tyr  
 20 25 30  
 Leu Ser Gln Pro Leu Leu Asp Gly Phe Ala Met Gly Ala Ser Val Thr  
 35 40 45  
 Ile Leu Thr Ser Gln Leu Lys His Leu Leu Gly Val Arg Ile Pro Arg  
 50 55 60  
 His Gln Gly Pro Gly Met Val Val Leu Thr Trp Leu Ser Leu Leu Arg  
 65 70 75 80  
 Gly Ala Gly Gln Ala Asn Val Cys Asp Val Val Thr Ser Thr Val Cys  
 85 90 95  
 Leu Ala Val Leu Leu Ala Ala Lys Glu Leu Ser Asp Arg Tyr Arg His  
 100 105 110  
 Arg Leu Arg Val Pro Leu Pro Thr Glu Leu Leu Val Ile Val Val Ala  
 115 120 125

<210> 169  
 <211> 537  
 <212> DNA  
 <213> Homo sapiens

<400> 169  
 gaattccacc gcatgtcgtg tctggacgta tgtaggtcgc ggtagtgtgc gaccgccggt  
 60  
 gccttaaagg agagcgggca tcggcggttc agtacgagag gggaagggtg gcggatactt  
 120  
 attgtcggtg cggcatcgtc catccacacc gtctgatggg tcaatggact ggtcaagcgg  
 180  
 ggtcacgagg ttcacctggc atcagtccat ccggcggggc gtactccat tgatccccga  
 240  
 gttcggatcc acctggcccc acacggcggg aaggcaaaat acgtcgtcaa tgccggctgg  
 300



ctgcgatcag tggcggctgg ggtgcaacct gacatcgta acgtccacta tgcgaccggt  
 360  
 tatggtctgc tcgctcgtct tgcccatatt gacgccccga cgctgctgtc ggtgtgggga  
 420  
 agtgacgttt acgattcccc ccgggcaaat cccctcatgc gtcacatggt ccgatccaac  
 480  
 ttggtctcag ctactcggat cgcacgcaca agccactgca tggcgcgtgt cacgcgt  
 537

<210> 170  
 <211> 164  
 <212> PRT  
 <213> Homo sapiens

<400> 170  
 Cys Ala Thr Ala Gly Ala Leu Lys Glu Ser Gly His Arg Arg Cys Ser  
 1 5 10 15  
 Thr Arg Gly Glu Gly Val Arg Ile Leu Ile Val Gly Ala Ala Ser Ser  
 20 25 30  
 Ile His Thr Val Arg Trp Val Asn Gly Leu Val Lys Arg Gly His Glu  
 35 40 45  
 Val His Leu Ala Ser Val His Pro Ala Gly Arg His Ser Ile Asp Pro  
 50 55 60  
 Arg Val Arg Ile His Leu Ala Pro His Gly Gly Lys Ala Lys Tyr Val  
 65 70 75 80  
 Val Asn Ala Gly Trp Leu Arg Ser Val Ala Ala Gly Val Gln Pro Asp  
 85 90 95  
 Ile Val Asn Val His Tyr Ala Thr Gly Tyr Gly Leu Leu Ala Arg Leu  
 100 105 110  
 Ala His Ile Asp Ala Pro Thr Leu Leu Ser Val Trp Gly Ser Asp Val  
 115 120 125  
 Tyr Asp Ser Pro Arg Ala Asn Pro Leu Met Arg His Met Val Arg Ser  
 130 135 140  
 Asn Leu Val Ser Ala Thr Arg Ile Ala Ser Thr Ser His Cys Met Ala  
 145 150 155 160  
 Arg Val Thr Arg

<210> 171  
 <211> 391  
 <212> DNA  
 <213> Homo sapiens

<400> 171  
 ctagacaagc tcgcgcgggt gggcttcgac actcttggtc tacagacctt cctaactgcg  
 60  
 ggggagaagg agtcccgcgc atggacgatt cacaagggcg acaccgcccc tgaggctgct  
 120  
 ggcgtcatcc ataccgactt ccagaagggg ttcacaaagg cccaggtggt gtccttcggc  
 180  
 gaccttggtg aatttggcgg cgaaaaggag gccagggctg ctgggaagct gcggttgagg  
 240  
 ggcaaggagt acgttatgca ggacgggtgac gtagtggaat tccgatttaa cgtgtagctc  
 300

tggtttgata cttacttggc ttaaccgcat ctgagatccg tcatatcttt ggcgtagcct  
 360  
 tattggtatg aataacatgc cgtagccaaa g  
 391

<210> 172  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 172  
 Leu Asp Lys Leu Ala Arg Val Gly Phe Asp Thr Leu Gly Leu Gln Thr  
 1 5 10 15  
 Phe Leu Thr Ala Gly Glu Lys Glu Ser Arg Ala Trp Thr Ile His Lys  
 20 25 30  
 Gly Asp Thr Ala Pro Glu Ala Ala Gly Val Ile His Thr Asp Phe Gln  
 35 40 45  
 Lys Gly Phe Ile Lys Ala Gln Val Val Ser Phe Gly Asp Leu Val Glu  
 50 55 60  
 Phe Gly Gly Glu Lys Glu Ala Gln Ala Ala Gly Lys Leu Arg Leu Glu  
 65 70 75 80  
 Gly Lys Glu Tyr Val Met Gln Asp Gly Asp Val Val Glu Phe Arg Phe  
 85 90 95  
 Asn Val

<210> 173  
 <211> 309  
 <212> DNA  
 <213> Homo sapiens

<400> 173  
 ccattggagtg tcccttgtgc gagcattttg agagctatac caacacccat ccctgcaggt  
 60  
 cccagagccg agccatttct caggagagca ggaagggagc aggccgaggg gtgctcccag  
 120  
 ccagccccgg aaccgaggt ctggggacgc agccgaccag ccctccttgt ctgggcctct  
 180  
 gtttcctctt cgacacaggg aagcagggag gggccgatca gcgacttagg cctgttggct  
 240  
 gtggtgggggt cccctgcgtt tctgggaagc cacggaccct gggatgtacc tgggtttcat  
 300  
 tcgcagtga  
 309

<210> 174  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

<400> 174  
 Met Glu Cys Pro Leu Cys Glu His Phe Glu Ser Tyr Thr Asn Thr His  
 1 5 10 15  
 Pro Cys Arg Ser Gln Ser Arg Ala Ile Ser Gln Glu Ser Arg Lys Gly

[illegible]

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<210> 175
<211> 8484
<212> DNA
<213> Homo sapiens
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<400> 175  
nnacttttttt tttttttttt catttatgct atggagaaac cagcatggag atgtcatggg  
60  
agagcatgca caggccccgc cctagggagt ggtgatgtgt ttggggaggt gcttgtttcc  
120  
aggtccatcc cacacgttgt ccagttggat cctatggcag gctggtgtg gctttctctc  
180  
tcttgcttct ctctctctc cagataaggg tctgcaggat cttctgctta gcaagtgggtg  
240  
gccaaaggact ggtggatggg tggttggaag cagcgcacat gctccacagt ggaactgtct  
300  
gtctccacgg acttcatgta tttgttcagg atggcaaaaa cctcattgtt caagatctga  
360  
tacttctga tccggtcggc catcttcttc aggggcacat tcttaatgat ttcattcttc  
420  
ccgtcttgcc tctgcacttt tagcagggtg taacagaagt cgaacaggtc aaagcgacgc  
480  
tgctggccca gcaggacaat gatggagcaa ccagcccagt tcaagccatc gccgaaacac  
540  
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Pro Leu Ile Glu Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg
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Glu Gly Asp Leu Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met
          1220          1225          1230
Phe Glu Val Ile Leu Thr Arg Ile Arg Ser Phe Leu Asp Asp Pro Ile
          1235          1240          1245
Trp Arg Gly Pro Leu Pro Ser Asn Gly Val Met His Val Asp Glu Cys
          1250          1255          1260
Val Glu Phe His Arg Leu Trp Ser Ala Met Gln Phe Val Tyr Cys Ile
1265          1270          1275          1280
Pro Val Gly Thr His Glu Phe Thr Val Glu Gln Cys Phe Gly Asp Gly
          1285          1290          1295
Leu His Trp Ala Gly Cys Met Ile Ile Val Leu Leu Gly Gln Gln Arg
          1300          1305          1310
Arg Phe Ala Val Leu Asp Phe Cys Tyr His Leu Leu Lys Val Gln Lys
          1315          1320          1325
His Asp Gly Lys Asp Glu Ile Ile Lys Asn Val Pro Leu Lys Lys Met
          1330          1335          1340
Val Glu Arg Ile Arg Lys Phe Gln Ile Leu Asn Asp Glu Ile Ile Thr
1345          1350          1355          1360
Ile Leu Asp Lys Tyr Leu Lys Ser Gly Asp Gly Glu Gly Thr Pro Val
          1365          1370          1375
Glu His Val Arg Cys Phe Gln Pro Pro Ile His Gln Ser Leu Ala Ser
          1380          1385          1390
Ser

```

<210> 177  
 <211> 417  
 <212> DNA  
 <213> Homo sapiens

<400> 177  
 acgcgtgatg tcacactgcc tctgccgctg ggtcctaatt cgattgcacg caccatggct  
 60  
 gcagttcgtg gcgcgcatag tttctggcat gcttcgcgca tcctggagac cgatcccgcc  
 120  
 gctgccgtga aaccgcctaa aaatgtgaag cgattgccca aagccgtgtc cgtggagcaa  
 180  
 atgcaaaagc tccttgccat acccagtctt aagactccta ccggcctgcg taatcgagcg  
 240  
 atacttgagt tcttatatgc taccggcgcg cgcgtgagcg agatgctggc aacagacctg  
 300  
 gacgatatac acctgggcga aaaaccccgcg gatgaaaacg gggaatctat tgcacttccc  
 360  
 gggatatgtgc gcctttttgg aaagggaggt aaagagcgtt tagtcccttt gggatcc  
 417

<210> 178  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

<400> 178  
 Thr Arg Asp Val Thr Leu Pro Leu Pro Leu Gly Pro Asn Ser Ile Ala  
 1 5 10 15  
 Arg Thr Met Ala Val Arg Gly Ala His Ser Phe Trp His Ala Ser  
 20 25 30  
 Arg Ile Leu Glu Thr Asp Pro Ala Ala Val Lys Pro Pro Lys Asn  
 35 40 45  
 Val Lys Arg Leu Pro Lys Ala Val Ser Val Glu Gln Met Gln Lys Leu  
 50 55 60  
 Leu Ala Ile Pro Ser Leu Lys Thr Pro Thr Gly Leu Arg Asn Arg Ala  
 65 70 75 80  
 Ile Leu Glu Phe Leu Tyr Ala Thr Gly Ala Arg Val Ser Glu Met Leu  
 85 90 95  
 Ala Thr Asp Leu Asp Asp Ile His Leu Gly Glu Lys Pro Arg Asp Glu  
 100 105 110  
 Asn Gly Glu Ser Ile Ala Leu Pro Gly Tyr Val Arg Leu Phe Gly Lys  
 115 120 125  
 Gly Gly Lys Glu Arg Leu Val Pro Leu Gly Ser  
 130 135

<210> 179  
 <211> 362  
 <212> DNA  
 <213> Homo sapiens

<400> 179  
 acgcgtcgaa ggtgccggtg ggggcgatca ataacatcgc gcaatccctg gaagagcctc  
 60

aggtgattgc ccgtgggttg atggtggaag atccccgcatc cccaagaatc cgggaattcg  
 120  
 ccattgggcc gggcagcccc aatccaaaat gtcggggcac gcccagtggg agtatggtaa  
 180  
 ggggcccggca ccgatgttgg nggcagcata cggatggaag tgctgggcga ggcctgggt  
 240  
 ttgccggcag agcaactggg gcagctcaag gcgggcgggg tgatcgagca gttggattga  
 300  
 gcaatggcgg ccgcgaagcc cgccatttac cttgatgact gtttagcgcg cggattcttt  
 360  
 aa  
 362

<210> 180  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 180  
 Met Ala Gly Phe Ala Ala Ala Ile Ala Gln Ser Asn Cys Ser Ile Thr  
 1 5 10 15  
 Pro Pro Ala Leu Ser Cys Pro Ser Cys Ser Ala Gly Lys Pro Arg Arg  
 20 25 30  
 Ser Pro Ser Thr Ser Ile Arg Met Leu Pro Pro Thr Ser Val Pro Ala  
 35 40 45  
 Pro Tyr His Thr Pro Thr Gly Arg Ala Pro Thr Phe Trp Ile Arg Ala  
 50 55 60  
 Ala Arg Pro Asn Gly Glu Phe Pro Asp Ser Trp Gly Cys Gly Ile Phe  
 65 70 75 80  
 His His Gln Pro Thr Gly Asn His Leu Arg Leu Phe Gln Gly Leu Arg  
 85 90 95  
 Asp Val Ile Asp Arg Pro His Arg His Leu Arg Arg  
 100 105

<210> 181  
 <211> 297  
 <212> DNA  
 <213> Homo sapiens

<400> 181  
 gcgttgatca tgtccgaccc aggcttgatc atgctggtac gccgtcactt cccgtgcatg  
 60  
 ccgattcact tgtcgggtaca ggccaatacg gtgaattggg ccagcgtcga gttctggcaa  
 120  
 cagcaaggta tctgccgggt aatcctgtcg cgggaattgt cactggaaga aatcggcgaa  
 180  
 atccgccaac aggtgccggc catggagctg gaagtgtttg tgcacggtgc cctgtacatg  
 240  
 gcctattccg ggcgctgttt gttgtccggc tatatgaaca agcgcgatgc caaccaa  
 297

<210> 182  
 <211> 99  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 182

Ala Leu Ile Met Ser Asp Pro Gly Leu Ile Met Leu Val Arg Arg His  
 1 5 10 15  
 Phe Pro Cys Met Pro Ile His Leu Ser Val Gln Ala Asn Thr Val Asn  
 20 25 30  
 Trp Ala Ser Val Glu Phe Trp Gln Gln Gly Ile Cys Arg Val Ile  
 35 40 45  
 Leu Ser Arg Glu Leu Ser Leu Glu Glu Ile Gly Glu Ile Arg Gln Gln  
 50 55 60  
 Val Pro Ala Met Glu Leu Glu Val Phe Val His Gly Ala Leu Tyr Met  
 65 70 75 80  
 Ala Tyr Ser Gly Arg Cys Leu Leu Ser Gly Tyr Met Asn Lys Arg Asp  
 85 90 95  
 Ala Asn Gln

&lt;210&gt; 183

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 183

cgggacgtca ccatgaagcc gaccggctcg ggggatgtgg cgaacaaggt catcacccat  
 60  
 attccgttta acatcgcttc ccaggcgact catccattcc ttcgtacctt ggacgatgtc  
 120  
 aagcgcactc ctttggcgac cgacgggctc ggccaccagg tcctgctcaa gggctaccag  
 180  
 gccgagggcc acgactacgc acaccccgac tacggcggca acgtctccca ccgtgccggc  
 240  
 gggatgaagg atctcgagaa gctcaccgag tcgggcaggc agtggaaacac cgatttcggc  
 300  
 attcacgtca acctggtgga gtcctatcct gaggcgaatc acttcggcga c  
 351

&lt;210&gt; 184

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 184

Arg Asp Val Thr Met Lys Pro Thr Gly Ser Gly Asp Val Ala Asn Lys  
 1 5 10 15  
 Val Ile Thr His Ile Pro Phe Asn Ile Val Ser Gln Ala Thr His Pro  
 20 25 30  
 Phe Leu Arg Thr Leu Asp Asp Val Lys Arg Ile Ser Leu Ala Thr Asp  
 35 40 45  
 Gly Leu Gly His Gln Val Leu Lys Gly Tyr Gln Ala Glu Gly His  
 50 55 60  
 Asp Tyr Ala His Pro Asp Tyr Gly Gly Asn Val Ser His Arg Ala Gly  
 65 70 75 80  
 Gly Met Lys Asp Leu Glu Lys Leu Thr Glu Ser Gly Arg Gln Trp Asn

```

      85          90          95
Thr Asp Phe Gly Ile His Val Asn Leu Val Glu Ser Tyr Pro Glu Ala
      100          105          110
Asn His Phe Gly Asp
      115

```

<210> 185  
 <211> 396  
 <212> DNA  
 <213> Homo sapiens

```

<400> 185
cgcggtgggtc tcagtaaaga aaatttggtg cttagaggat gcaccattag aaacacagag
60
gctgttggtg gcattgtggt ttatgcaggc catgaaacca aagcaatgct gaacaacagt
120
gggccacggt ataagcgcag caaattagaa agaagagcaa acacagatgt cctctggtgt
180
gtcatgcttc tggtcataat gtgcttaact ggcgcagtag gtcatggaat ctggtgagc
240
aggtatgaaa agatgcattt tttcaatggt cccgagcctg atggacatat catatcacca
300
ctgttggcag gattttatat gttttggacc gtgatcattt tgttacaggt cttgattcct
360
atttctctct atgtttccat cgaaattgtg aagctt
396

```

<210> 186  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

```

<400> 186
Arg Val Gly Leu Ser Lys Glu Asn Leu Leu Leu Arg Gly Cys Thr Ile
1      5      10      15
Arg Asn Thr Glu Ala Val Val Gly Ile Val Val Tyr Ala Gly His Glu
      20      25      30
Thr Lys Ala Met Leu Asn Asn Ser Gly Pro Arg Tyr Lys Arg Ser Lys
      35      40      45
Leu Glu Arg Arg Ala Asn Thr Asp Val Leu Trp Cys Val Met Leu Leu
      50      55      60
Val Ile Met Cys Leu Thr Gly Ala Val Gly His Gly Ile Trp Leu Ser
65      70      75      80
Arg Tyr Glu Lys Met His Phe Phe Asn Val Pro Glu Pro Asp Gly His
      85      90      95
Ile Ile Ser Pro Leu Leu Ala Gly Phe Tyr Met Phe Trp Thr Val Ile
      100      105      110
Ile Leu Leu Gln Val Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu
      115      120      125
Ile Val Lys Leu
      130

```

<210> 187  
 <211> 423

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 187

cgagtgtca ccgcgtcagc cgtcatgcgt cccactgagg ctgttgcttc tcggtcggca  
 60  
 gaacctcgac gagttcagcg gatcctggac cagcgcgagt gggctggcgt cttcgttgct  
 120  
 gatgagcatc gtcgtttgct tggcacggtc ggcgatcaag aggtcatcga ggctgctcgc  
 180  
 cgcgagatc gcagtattgc tgacgcgggtg gaaactaacg gcatactcac ggcgcggaac  
 240  
 gacactccgt tgtccgagct cttcgctccg accagcaacg ccagggtgcc gttggccggt  
 300  
 gtcgacgagg acttccacct catgggtgtc atctctcggg tgaccctgct cgacgcgatg  
 360  
 tcacgagctc gcgacgagggc aggagagggga tctgtcatgt ccttggagaa caccggaaa  
 420  
 ctt  
 423

&lt;210&gt; 188

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 188

Arg	Val	Leu	Thr	Ala	Ser	Ala	Val	Met	Arg	Pro	Thr	Glu	Ala	Val	Val
1				5					10				15		
Ser	Arg	Ser	Ala	Glu	Pro	Arg	Arg	Val	Gln	Arg	Ile	Leu	Asp	Gln	Arg
			20					25				30			
Glu	Trp	Ala	Gly	Val	Phe	Val	Val	Asp	Glu	His	Arg	Arg	Leu	Leu	Gly
		35				40					45				
Thr	Val	Gly	Asp	Gln	Glu	Val	Ile	Glu	Ala	Ala	Arg	Arg	Gly	Asp	Arg
	50				55					60					
Ser	Ile	Ala	Asp	Ala	Val	Glu	Thr	Asn	Gly	Ile	Leu	Thr	Ala	Arg	Thr
65				70					75				80		
Asp	Thr	Pro	Leu	Ser	Glu	Leu	Phe	Ala	Pro	Thr	Ser	Asn	Ala	Arg	Val
			85					90					95		
Pro	Leu	Ala	Val	Val	Asp	Glu	Asp	Phe	His	Leu	Met	Gly	Val	Ile	Ser
		100						105				110			
Arg	Val	Thr	Leu	Leu	Asp	Ala	Met	Ser	Arg	Ala	Arg	Asp	Glu	Ala	Gly
		115				120						125			
Glu	Gly	Ser	Val	Met	Ser	Leu	Glu	Asn	Thr	Gly	Lys	Leu			
	130					135					140				

&lt;210&gt; 189

&lt;211&gt; 429

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 189

ngatggttta ccaacatatg cagggttcga gcggcaatag ctccctcgggg gctggcagtg  
 60



aaatgtttga agatgccggc gtttcgggcc tcaacttggt tcgatgccgt ggttccaccg  
 120  
 atttcgccga tgcggctcat cgcacgggta agaagtttcg tccagataac ccaggacaga  
 180  
 gcaagggtata tcaggctcag aaccaggaaa agcagggcctt taccctcagtg ccccatatag  
 240  
 accgcgctag ctacggcaaa aggcgcgccc agtgggggtcc aggacagcac tttcatggct  
 300  
 gaaggagcgc catcccnagc ttgcctagc cccagagcta acccagcgac cagtggacca  
 360  
 gcgcccatca tcagtaggaa ccctacgata atcagccctt gttttacccc tggaatggag  
 420  
 ctgatttcn  
 429

<210> 190  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 190  
 Met Met Gly Ala Gly Pro Leu Val Ala Gly Leu Ala Leu Gly Leu Gly  
 1 5 10 15  
 Glu Ala Xaa Asp Ala Leu Pro Ser Ala Met Lys Val Leu Ser Trp Thr  
 20 25 30  
 Pro Leu Gly Ala Pro Phe Ala Val Ala Ser Ala Val Tyr Met Gly His  
 35 40 45  
 Trp Gly Lys Ala Leu Leu Phe Leu Val Leu Ser Leu Ile Tyr Leu Ala  
 50 55 60  
 Leu Ser Trp Val Ile Trp Thr Lys Leu Leu Asn Arg Ala Met Ser Arg  
 65 70 75 80  
 Ile Gly Glu Ile Gly Gly Thr Thr Ala Ser Lys Gln Val Glu Ala Gly  
 85 90 95  
 Asn Ala Gly Ile Phe Lys His Phe Thr Ala Ser Pro Arg Gly Ala Ile  
 100 105 110  
 Ala Ala Arg Thr Val His Met Leu Val Asn His  
 115 120

<210> 191  
 <211> 4845  
 <212> DNA  
 <213> Homo sapiens

<400> 191  
 ccgccccggg ccatggcgac actcagcttc gtcttcctgc tgctgggggc agtgtcctgg  
 60  
 cctccggctt ctgcctccgg ccaggagtgc tggcccggaac aatcgcggcg cgatattctg  
 120  
 tcggggggcg cttcccgag acggtatctt ctgtatgacg tcaaccccc ggaaggcttc  
 180  
 aacctgcgca gggatgtcta tatccgaatc gcctctctcc tgaagactct gctgaagacg  
 240  
 gaggagtggg tgcttgctct gcctccatgg ggccgcctct atcactggca gagtctgac  
 300

atccaccagg tccggattcc ctggtctgag ttttttgatc ttccaagtct caataaaaaac  
360  
atccccgtca tcgagtatga gcagttcatc gcagaatctg gtggggccctt tattgaccag  
420  
gtttacgtcc tgcaaagtta cgcagagggg tggaaagaag ggacctggga agagaagggtg  
480  
gacgagcggc cgtgtattga tcagctcctg tactcccagg acaagcacga gtactacaga  
540  
ggatgggtttt ggggttatga ggagaccagg ggtctaaacg tctcctgtct gtccgtccag  
600  
ggctcagcct ccctcgtggc gcccctgctg ctgagaaaca catcagcccg gtccgtgatg  
660  
ttagacagag ccgagaacct acttcacgac cactatggag ggaaagaata ctgggatacc  
720  
cgtcgcagca tgggtgtttgc caggcacctg cgggaggtgg gagacgagtt caggagcaga  
780  
catctcaact ccacggacga cgcagacagg atccccctcc aggaggactg gatgaagatg  
840  
aagggtcaagc tgggtctcgc gctagggggc ccctacctgg gagtccacct gagaagaaaa  
900  
gatttcatct ggggtcacag acaggatgta cccagtctgg aaggggcccgt gaggaagatc  
960  
cgcagcctca tgaagaccca ccggctggac aaggtgtttg tggccacaga tgccgtcaga  
1020  
aaggaatatg aagagctaaa aaagctgtta cccgagatgg tgaggtttga acccactggtg  
1080  
gaggagctgg agctctacaa ggacggaggc gttgcgatta ttgaccagtg gatctgcgca  
1140  
cacgccaggt gcctgcccac gtcactgtcg gccgagagcg ggtcgggtgg ctttcaaagg  
1200  
ttcttctgtc ccaagtactc ggtgtcagag cagatggctg cctgtgttca cagtggctcat  
1260  
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1320  
ggctgaagtt aattgttcat cttgcccctt tagttctcat gcacagaatt cctccatagc  
1380  
aggctgttgg catagctggc ctcgtctcag aacctcttct tgtgtcgcac tttcccatca  
1440  
ttcccggttt ctgcccctgt ctgcccctg ccctgagagt tgcccgtgcc ctggacttgg  
1500  
gcatgtcctt gttgctgtgt tgttgagcat ccgtgagcgt ccccagggcc gggagcgtgg  
1560  
gccctcgtgt gatcattctc gtggggctgc catgagcgtc cccaaggctg ggagcatggg  
1620  
ccctcgtgtg atcgttcttg tggggctgcc gtgagcgtcc ccgaggccgg gagcgtgggc  
1680  
cctcgtgtga tcattctcgt ggggctgccg tgagcgtccc agaggccggg agcgtgggcc  
1740  
ctgcgtgcag tcattctctt ggggttctgt tgggaggtac gcctgggcct ctgttctctc  
1800  
aaagacctgc ctgcccctct gcataggaga tgaaggctgg ggttaggggtg aaacggtttg  
1860  
agttaaattg aaaatgaaag tagagggaaat gatcttcccc gtgggttagca ctgtgcacac  
1920

gcgtgcgtct ctgtgggtta gtctgtctct ctctgccc aggaatgctg agcgccctga  
1980  
gccggtgcct cttcacacat ctgctatttc ctgtgggtgt ctgggcatgg tgtataagac  
2040  
ccacagaggc tccgggtgat gctgtctgct ggggtgtgggt ccccttccct gttaagcaga  
2100  
caggatgcag cgctgacttc ttaggtcagg gcggaggtgt gcaggagccc agtcacgagc  
2160  
tcaccctgc ttctcagggt tggccttggg attttgactg cgaccttggc ggtgctgtct  
2220  
ccgcagccca ggaagcctgc tgtggggagg cttegcactg agctctcagc ctctgccc  
2280  
cagctgcgcg aagcgctcgg ccagctcac tgaagctgcc ctgcctccg gccggcgcg  
2340  
cctgctctgg caggccccct tgtgtgggtt ggtgaggttc tccccaccag tgctgcaccc  
2400  
cgcagcagca tacaggcctg tgtggcctgc tggccctgtg gctctgtgta cagcgctgtg  
2460  
catgttacat ttgctctgga aacatctctg gggtttgctt gttcacgaag ttcataagt  
2520  
gccgctggag agccagagac cagctgcgca ggagccggag gaacgggag gccgctgacc  
2580  
tgaggtctgg agaaaccct ggagaagggt gtccccacca gccatacag cgtgtgtgtg  
2640  
gagggggcct tgacctcgt gatgtctact gtgcctcagg ataaggacc gccatgccct  
2700  
ggctagacag tgtgtggtta gtaggaatct ctattgttc accatgtgac cccaggagg  
2760  
tattcgacct gcactggcgt gcctggcctg ggatttgggt acggagagga gggctcccag  
2820  
ggggacatgc ggtgggacag gagcgtggcg gctgctgact gtggggtgtg gatggggctg  
2880  
cagcaccagg cagagcccct cagggcgccg atgtcgagg cacctgagcg aggggtgcc  
2940  
gcaagggggc ggccggctgg tgggtgctcg ggggacggcc gtgttggttc catgtaactg  
3000  
tggaactcat ttcactcagc tgctcctctc agttctccct gactctggaa cctctgtgac  
3060  
cccagttctc cctgactctg gaacctctgt gatcctttgc aggttttttt attggcacct  
3120  
cagtctcaac attttctttt cggattcatg aggaaagaga aatcctgggg ttggacccca  
3180  
agacgacgta caacaggttc tgcggagacc aagagaaggc gtgtgagcaa cccaccact  
3240  
ggaagatcac ctactgagga ggatcctcca gggccgctcc ccggacccga caggcgcggtg  
3300  
tggtatcagg ttctgtcgcc gtggagtcac cgtctactgc cagccgggag ctgggaggac  
3360  
aggaccgtcc ctgcgagggt ccagggccca gaagaggccc cagcctcta gagctgggct  
3420  
ccgtcctcgg cgttgccagc cgccatggct gatgaagagg ctccgctgct ctggggggcg  
3480  
gcggttgttt tcaggcagcg tctgtgaacc cacagctcgg ttgccagcag tgcccgctg  
3540

gtgaccacaga agcaggagtg tttgtcaggc tcccgctctg gcctttccag ccacctttca  
 3600  
 tgtcttcata ttttaagtgc attgaggata gatgcaggcg ggtgagctgc cctccgtcag  
 3660  
 gtggacccgg gctgacattt ccctgggagc tgggtgcaagg agaagcgtca ttttaaagt  
 3720  
 ctgcagagcg accagggggc tcatgaatct ctccgttgcc ctccgcgcag caggaggctg  
 3780  
 cctgtgtgtt tcctcctggg acgcgtgcaa ggcagacctg gtgctgcaaa ggaaagggcc  
 3840  
 tgaggcctca gggagccccg tggagggatg acagttcagg ccctactgct ggcacgtcag  
 3900  
 agcactggga agtttttcag tgacgtctct ggggcactca gtggattgtc ttaggaaac  
 3960  
 ttgcagctct gtcctcaca ccaggccccg ctggccaccc accctcgccc cactggcca  
 4020  
 cccctccctc gccccgactg ccccgcccca ccctcacccc gactgccccg ccctcgcccc  
 4080  
 gctggccgtc cctgccctcg ccccggtggt caggtgcaca tggggcctcc aggtctgcca  
 4140  
 ttcgctattg agaactagaa atgaggaagg acagttacgc taactccaaa aggtctgcta  
 4200  
 ggatgagctg ctttatcagg gagctccttg taccattttt acagaaatca ttttaggtc  
 4260  
 tttgtgccac caccacgagg ggcattctgca aagagggcaa cgctagacac agaatccgtg  
 4320  
 gaagggtcag cagtgcctca ggggtcctca gggtcaggga gccccctca ccctcttggc  
 4380  
 ccgttaccct ttgtgacttt ccaccatggt gtcgtgtgac cctcagtcag gttggtggg  
 4440  
 gctgagtcct cactgagcag ccactttcca catctgctag aggaacagtg acatggacac  
 4500  
 ctgtgacaga gagaggacag ttagtgagga gggacagaca gctcttcctt tcggagcctg  
 4560  
 gctagtctag gacatcacct tgctgtgtct tctcaagctt ttaaaattga ccctgaacgt  
 4620  
 cctatggtgt tactcaaagc tgtgcagggt aaatgatgac atatatttc 4680  
 tttttccatt tgttctagaa acagtgcctt tttcatcagt tgcattttcc aggtctgagag  
 4740  
 ctgtataaaa cattttggac tgtgaccatg taccttcctt ttttaagaaaa ataaactgct  
 4800  
 ttatggaagt tggtaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa  
 4845

&lt;210&gt; 192

&lt;211&gt; 428

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 192

Pro Pro Gly Ala Met Ala Thr Leu Ser Phe Val Phe Leu Leu Leu Gly  
 1 5 10 15  
 Ala Val Ser Trp Pro Pro Ala Ser Ala Ser Gly Gln Glu Phe Trp Pro  
 20 25 30  
 Gly Gln Ser Ala Ala Asp Ile Leu Ser Gly Ala Ala Ser Arg Arg Arg

35				40				45							
Tyr	Leu	Leu	Tyr	Asp	Val	Asn	Pro	Pro	Glu	Gly	Phe	Asn	Leu	Arg	Arg
50						55					60				
Asp	Val	Tyr	Ile	Arg	Ile	Ala	Ser	Leu	Leu	Lys	Thr	Leu	Leu	Lys	Thr
65					70					75					80
Glu	Glu	Trp	Val	Leu	Val	Leu	Pro	Pro	Trp	Gly	Arg	Leu	Tyr	His	Trp
				85					90					95	
Gln	Ser	Pro	Asp	Ile	His	Gln	Val	Arg	Ile	Pro	Trp	Ser	Glu	Phe	Phe
			100					105					110		
Asp	Leu	Pro	Ser	Leu	Asn	Lys	Asn	Ile	Pro	Val	Ile	Glu	Tyr	Glu	Gln
		115					120				125				
Phe	Ile	Ala	Glu	Ser	Gly	Gly	Pro	Phe	Ile	Asp	Gln	Val	Tyr	Val	Leu
	130					135					140				
Gln	Ser	Tyr	Ala	Glu	Gly	Trp	Lys	Glu	Gly	Thr	Trp	Glu	Glu	Lys	Val
145					150					155					160
Asp	Glu	Arg	Pro	Cys	Ile	Asp	Gln	Leu	Leu	Tyr	Ser	Gln	Asp	Lys	His
				165					170					175	
Glu	Tyr	Tyr	Arg	Gly	Trp	Phe	Trp	Gly	Tyr	Glu	Glu	Thr	Arg	Gly	Leu
			180					185					190		
Asn	Val	Ser	Cys	Leu	Ser	Val	Gln	Gly	Ser	Ala	Ser	Ile	Val	Ala	Pro
		195					200					205			
Leu	Leu	Leu	Arg	Asn	Thr	Ser	Ala	Arg	Ser	Val	Met	Leu	Asp	Arg	Ala
	210					215					220				
Glu	Asn	Leu	Leu	His	Asp	His	Tyr	Gly	Gly	Lys	Glu	Tyr	Trp	Asp	Thr
225					230					235					240
Arg	Arg	Ser	Met	Val	Phe	Ala	Arg	His	Leu	Arg	Glu	Val	Gly	Asp	Glu
				245					250					255	
Phe	Arg	Ser	Arg	His	Leu	Asn	Ser	Thr	Asp	Asp	Ala	Asp	Arg	Ile	Pro
			260					265					270		
Phe	Gln	Glu	Asp	Trp	Met	Lys	Met	Lys	Val	Lys	Leu	Gly	Ser	Ala	Leu
	275						280					285			
Gly	Gly	Pro	Tyr	Leu	Gly	Val	His	Leu	Arg	Arg	Lys	Asp	Phe	Ile	Trp
	290					295					300				
Gly	His	Arg	Gln	Asp	Val	Pro	Ser	Leu	Glu	Gly	Ala	Val	Arg	Lys	Ile
305					310					315					320
Arg	Ser	Leu	Met	Lys	Thr	His	Arg	Leu	Asp	Lys	Val	Phe	Val	Ala	Thr
				325					330					335	
Asp	Ala	Val	Arg	Lys	Glu	Tyr	Glu	Glu	Leu	Lys	Lys	Leu	Leu	Pro	Glu
			340					345					350		
Met	Val	Arg	Phe	Glu	Pro	Thr	Trp	Glu	Glu	Leu	Glu	Leu	Tyr	Lys	Asp
		355					360					365			
Gly	Gly	Val	Ala	Ile	Ile	Asp	Gln	Trp	Ile	Cys	Ala	His	Ala	Arg	Cys
	370					375					380				

<210> 193

<211> 350

<212> DNA

<213> Homo sapiens

&lt;400&gt; 193

gccggcgagc tggactgcgc catcatggcc gagcccttcc ccgacaccgg cctggccacg  
 60  
 gcgcagctgt acgacgagcc cttcgtcgtc gcgctgcggg cgtcgcaccc gctggccgac  
 120  
 cgtgccagca tcagccccga ggaggtcaag ggcgagacca tgttgatgtt gggcacgggc  
 180  
 ccctggtttc cccgggcccg cgggtgggggt ttggcccgga tttggcgctt ttctccagcg  
 240  
 ccgttaaggg catacgccgc agtttcgagg gctcgtcgct ggagaccatc aagcacatcg  
 300  
 tggcttcggg catggcgtga cgggtgtgcc gcagctgtcc gtgccgcgcg  
 350

&lt;210&gt; 194

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

Ala	Gly	Glu	Leu	Asp	Cys	Ala	Ile	Met	Ala	Glu	Pro	Phe	Pro	Asp	Thr
1				5					10					15	
Gly	Leu	Ala	Thr	Ala	Gln	Leu	Tyr	Asp	Glu	Pro	Phe	Val	Val	Ala	Leu
			20					25					30		
Arg	Ala	Ser	His	Pro	Leu	Ala	Asp	Arg	Ala	Ser	Ile	Ser	Pro	Glu	Glu
		35					40					45			
Val	Lys	Gly	Glu	Thr	Met	Leu	Met	Leu	Gly	Thr	Gly	Pro	Trp	Phe	Pro
	50					55					60				
Arg	Ala	Arg	Gly	Gly	Gly	Leu	Ala	Arg	Ile	Trp	Arg	Val	Ser	Pro	Ala
65					70				75					80	
Pro	Leu	Arg	Ala	Tyr	Ala	Ala	Val	Ser	Arg	Ala	Arg	Arg	Trp	Arg	Pro
			85					90					95		
Ser	Ser	Thr	Ser	Trp	Leu	Arg	Ala	Trp	Arg	Asp	Gly	Gly	Ala	Ala	Ala
			100					105					110		
Val	Arg	Ala	Ala												
			115												

&lt;210&gt; 195

&lt;211&gt; 495

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

acgcgtgaac gcgacggctt ggcgatcgga ggcgtcggcc ccgtcggtga gtgggccggt  
 60  
 gaaatgggtc gcttcgacga aagcgagact ctcgaccgcc ttgcatcggg cgtccttgaa  
 120  
 ccagaacttg gcgacgattt ggccgcccgtc ctgctcgatt ctcacgagggt tgctgtcatc  
 180  
 agcgagggat cgaactggct tgcctcgcta cccgtgatcg taggtcgcaa cacggaacag  
 240  
 tttcgcagca taccagacct tgcccgcgac cggatcgaca aactgcacca gttgagccat  
 300

cgcgaaatag cacgaaatcg cgagctcctg cgtgcccgcg ctgcgtcggg gcaggtgcgg  
 360  
 cactgccacg gcgacgcaca cctcggcaac atcgatcatga ttgacggcaa gccggtcctg  
 420  
 ttcgacgcga tcgaatttga tcttgatata gcgacaacgg atgtgctgta cgatttcgcg  
 480  
 ttccctctga tggat  
 495

<210> 196  
 <211> 165  
 <212> PRT  
 <213> Homo sapiens

<400> 196  
 Thr Arg Glu Arg Asp Gly Leu Ala Ile Gly Gly Val Gly Pro Val Val  
 1 5 10 15  
 Glu Trp Ala Val Glu Met Val Arg Phe Asp Glu Ser Glu Thr Leu Asp  
 20 25 30  
 Arg Leu Ala Ser Gly Val Leu Glu Pro Glu Leu Gly Asp Asp Leu Ala  
 35 40 45  
 Ala Val Leu Leu Asp Ser His Arg Val Ala Val Ile Ser Glu Gly Ser  
 50 55 60  
 Asn Trp Leu Ala Ser Leu Pro Val Ile Val Gly Arg Asn Thr Glu Gln  
 65 70 75 80  
 Phe Arg Ser Ile Pro Asp Leu Ala Arg Asp Arg Ile Asp Lys Leu His  
 85 90 95  
 Gln Leu Ser His Arg Glu Ile Ala Arg Asn Arg Glu Leu Leu Arg Ala  
 100 105 110  
 Arg Ala Ala Ser Gly Gln Val Arg His Cys His Gly Asp Ala His Leu  
 115 120 125  
 Gly Asn Ile Val Met Ile Asp Gly Lys Pro Val Leu Phe Asp Ala Ile  
 130 135 140  
 Glu Phe Asp Pro Asp Ile Ala Thr Thr Asp Val Leu Tyr Asp Phe Ala  
 145 150 155 160  
 Phe Pro Leu Met Asp  
 165

<210> 197  
 <211> 402  
 <212> DNA  
 <213> Homo sapiens

<400> 197  
 caagcaatgc ttgacgcagt tgttgaatac ttaccagcac cgactgatata tccagcaatc  
 60  
 aaaggtatca atccagatga aactgaaggt gaacgtcacg caagcgatga tgagccattc  
 120  
 tcttcattag cattcaaaat tgcaactgac ccattcgtag gtaacttaac cttcttccgt  
 180  
 gtgtactcag gtgtaattaa ctctgggtgat acagtattaa actctgtacg tcaaaaacgt  
 240  
 gaacgttttg gtcgtatcgt acagatgcac gctaataaac gtgaagaaat taaagaagtt  
 300

cgtgcgggcg atatcgctgc agcaatcggc ttaaaagatg taactacggg tgaaccatta  
 360  
 tgtgctgtcg atgcaccaat cattcttgag cgtatggaat tc  
 402

<210> 198

<211> 134

<212> PRT

<213> Homo sapiens

<400> 198

Gln Ala Met Leu Asp Ala Val Val Glu Tyr Leu Pro Ala Pro Thr Asp  
 1 5 10 15  
 Ile Pro Ala Ile Lys Gly Ile Asn Pro Asp Glu Thr Glu Gly Glu Arg  
 20 25 30  
 His Ala Ser Asp Asp Glu Pro Phe Ser Ser Leu Ala Phe Lys Ile Ala  
 35 40 45  
 Thr Asp Pro Phe Val Gly Asn Leu Thr Phe Phe Arg Val Tyr Ser Gly  
 50 55 60  
 Val Ile Asn Ser Gly Asp Thr Val Leu Asn Ser Val Arg Gln Lys Arg  
 65 70 75 80  
 Glu Arg Phe Gly Arg Ile Val Gln Met His Ala Asn Lys Arg Glu Glu  
 85 90 95  
 Ile Lys Glu Val Arg Ala Gly Asp Ile Ala Ala Ala Ile Gly Leu Lys  
 100 105 110  
 Asp Val Thr Thr Gly Glu Pro Leu Cys Ala Val Asp Ala Pro Ile Ile  
 115 120 125  
 Leu Glu Arg Met Glu Phe  
 130

<210> 199

<211> 507

<212> DNA

<213> Homo sapiens

<400> 199

acgcgtgaag tcgtgcatag atcgggtgtga catagagaag cctccgaccc aagctgcgta  
 60  
 tctgcacaa agaccaagcg accctggacg ttctagacag aactctgcta cgaggcctga  
 120  
 caatagtga atccccgaga acccagctat ggaagggttt ccagatgctc gaaggcctgt  
 180  
 cataccagag gttagggttaa actgtatgga gactttcgag gtgaaagttg actcgccggg  
 240  
 aaagcctgct cctaaagagg atttagatct gatagatcta tctcagatt caacctcggg  
 300  
 gectgaaaaa cactctatac tctcaacctc cgacagcgac tctcttgat ttgagcctct  
 360  
 tccctctctc agaatagtcg agagtgcga agaagaggag acgatgaacc aaggcgatga  
 420  
 cggccccctc ggtaaaaatg ctgcctcttc tccctccatc cccagccatc cctccgtcct  
 480  
 cagcctgagc acagctccgc ttgtaca  
 507



<210> 200  
 <211> 153  
 <212> PRT  
 <213> Homo sapiens

<400> 200  
 Met Glu Gly Glu Glu Ala Ala Phe Leu Pro Glu Gly Pro Ser Ser Pro  
 1 5 10 15  
 Trp Phe Ile Val Ser Ser Ser Ser Leu Ser Thr Ile Leu Arg Glu  
 20 25 30  
 Gly Arg Gly Ser Asn Thr Arg Glu Ser Leu Ser Glu Val Glu Ser Ile  
 35 40 45  
 Glu Cys Phe Ser Gly Pro Glu Val Glu Ser Glu Asp Arg Ser Ile Arg  
 50 55 60  
 Ser Lys Ser Ser Leu Gly Ala Gly Phe Thr Gly Glu Ser Thr Phe Thr  
 65 70 75 80  
 Ser Lys Val Ser Ile Gln Phe Asn Leu Thr Ser Gly Met Thr Gly Leu  
 85 90 95  
 Arg Ala Ser Gly Asn Pro Ser Ile Ala Gly Phe Ser Gly Ile Ser Leu  
 100 105 110  
 Leu Ser Gly Leu Val Ala Glu Phe Cys Leu Glu Arg Pro Gly Ser Leu  
 115 120 125  
 Gly Leu Cys Ala Ile Tyr Ala Ala Trp Val Gly Gly Phe Ser Met Ser  
 130 135 140  
 His Arg Ser Met His Asp Phe Thr Arg  
 145 150

<210> 201  
 <211> 527  
 <212> DNA  
 <213> Homo sapiens

<400> 201  
 gatgtggcta ttatccctgt ttcccagggt agaaacaggg tcagtgatag agctgggatg  
 60  
 tgtgacctga ggctcaccag ccagtcacct cctcaccaag gatgatgttc tccgtgggtga  
 120  
 gctggtcctt ggtctcctgg aactcgtggc gcacctgggc cagctgcgcc tcgaaggcat  
 180  
 ctttctccat ctctttggct agctgcaagt tctggagctg ctcgttgagg tctgtgatct  
 240  
 catccacctg ctggttgagc gtgcgcttga ggaaggccac aatctccttc ttgttattgg  
 300  
 ccagctgctc aaactcctgg cggaacatct tctcctgcac agccagctca tcccacttcc  
 360  
 gctggtaccg ggctagccgg tctccaggt ctgggatctg gatgtggtag aactccttca  
 420  
 tctccttggc cagaggcggc tccacggcca ccaccggctc cttcttgccc cttttcttct  
 480  
 tgacttcaag ctcttgcct gccttgetca cactcttttt gggaggc  
 527

<210> 202

<211> 70  
 <212> PRT  
 <213> Homo sapiens

<400> 202  
 Gly Arg Pro Gln Ser Pro Ser Cys Tyr Trp Pro Ala Ala Gln Thr Pro  
 1 5 10 15  
 Gly Gly Thr Ser Ser Pro Ala Gln Pro Ala His Pro Thr Ser Ala Gly  
 20 25 30  
 Thr Gly Leu Ala Gly Pro Pro Gly Leu Gly Ser Gly Cys Gly Arg Thr  
 35 40 45  
 Pro Ser Ser Pro Trp Pro Glu Ala Ala Pro Arg Pro Pro Pro Ala Pro  
 50 55 60  
 Ser Cys Pro Leu Ser Ser  
 65 70

<210> 203  
 <211> 304  
 <212> DNA  
 <213> Homo sapiens

<400> 203  
 ngtgcaccgg tggatcatgga caacgccgcc tacgtgggtct acacctcggg atccaccggc  
 60  
 cgacccaagg gagttgtcgt caccacacacc ggactcgaca gcttcgcact cgaccagcag  
 120  
 cgtcgattcc acgcagatca ccactctcga accctgcact tcgccacccc cagcttcgac  
 180  
 ggagccgtct tcgagtacct gcaggcattc ggtgtcggag ccaccatggt gatcgtcccg  
 240  
 accgacatct acggcggcgc cgaactggca agtctcatcc gccgcgaaca cgtcactcac  
 300  
 gcgt  
 304

<210> 204  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 204  
 Xaa Ala Pro Val Val Met Asp Asn Ala Ala Tyr Val Val Tyr Thr Ser  
 1 5 10 15  
 Gly Ser Thr Gly Arg Pro Lys Gly Val Val Val Thr His Thr Gly Leu  
 20 25 30  
 Asp Ser Phe Ala Leu Asp Gln Gln Arg Arg Phe His Ala Asp His His  
 35 40 45  
 Ser Arg Thr Leu His Phe Ala Thr Pro Ser Phe Asp Gly Ala Val Phe  
 50 55 60  
 Glu Tyr Leu Gln Ala Phe Gly Val Gly Ala Thr Met Val Ile Val Pro  
 65 70 75 80  
 Thr Asp Ile Tyr Gly Gly Ala Glu Leu Ala Ser Leu Ile Arg Arg Glu  
 85 90 95  
 His Val Thr His Ala

100

<210> 205  
 <211> 356  
 <212> DNA  
 <213> Homo sapiens

<400> 205  
 nngaattcag caatgataac tggctcaatt gaaggtaaga caacaattga gggaattaat  
 60  
 gcacaattaa atacagtgtt aactttatctt tcaccacaat caaaagataa agatttaatt  
 120  
 atgccagatc aacaagaaga aatagatatt ctgattgcaa ccgactgtat ttcagaagga  
 180  
 cagaacttac aagattgtga ttacttaata aactatgaca ttcattggaa tccagttcgt  
 240  
 atcattcaaa gatttggacg gattgatcga attgggtcga agaataaatg tgtacaatta  
 300  
 gttaactttt ggccagatat tacattagat gaatatattg atctaaaggg acgcgt  
 356

<210> 206  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 206  
 Xaa Asn Ser Ala Met Ile Thr Gly Ser Ile Glu Gly Lys Thr Thr Ile  
 1 5 10 15  
 Glu Gly Ile Asn Ala Gln Leu Asn Thr Val Leu Thr Leu Phe Ser Pro  
 20 25 30  
 Gln Ser Lys Asp Lys Asp Leu Ile Met Pro Asp Gln Gln Glu Glu Ile  
 35 40 45  
 Asp Ile Leu Ile Ala Thr Asp Cys Ile Ser Glu Gly Gln Asn Leu Gln  
 50 55 60  
 Asp Cys Asp Tyr Leu Ile Asn Tyr Asp Ile His Trp Asn Pro Val Arg  
 65 70 75 80  
 Ile Ile Gln Arg Phe Gly Arg Ile Asp Arg Ile Gly Ser Lys Asn Lys  
 85 90 95  
 Cys Val Gln Leu Val Asn Phe Trp Pro Asp Ile Thr Leu Asp Glu Tyr  
 100 105 110  
 Ile Asp Leu Lys Gly Arg  
 115

<210> 207  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

<400> 207  
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg  
 60  
 catggtgtgt gcacgtgtng cactgtgtgt ggatgcatgg taatgtgcac gtgtgcactg  
 120

tgtgtggtgt gtatgcatgg tgtgtgcacg tgtgcactgt gtgtgtgtgt atgcatgtgt  
 180  
 gtgcacatgt gcactgtgtg gtgtgtatgc atggtgtgtg cacgtgtgca ctgtgtatgc  
 240  
 atgngtgtgt gcatgtgtgc actgtgtatg catagtgtgc acgtgtgcac tgtgtggtgt  
 300  
 gtatgcatgg taatgtgcac gtgt  
 324

<210> 208  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 208  
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys  
 1 5 10 15  
 Val Val Cys Met His Gly Val Cys Thr Cys Xaa Thr Val Cys Gly Cys  
 20 25 30  
 Met Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val  
 35 40 45  
 Cys Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Met Cys  
 50 55 60  
 Thr Val Trp Cys Val Cys Met Val Cys Ala Arg Val His Cys Val Cys  
 65 70 75 80  
 Met Xaa Val Cys Met Cys Ala Leu Cys Met His Ser Val His Val Cys  
 85 90 95  
 Thr Val Trp Cys Val Cys Met Val Met Cys Thr Cys  
 100 105

<210> 209  
 <211> 168  
 <212> DNA  
 <213> Homo sapiens

<400> 209  
 nnetccagag gttatgaggt tggaagcccg gtttttttca ggtgcagaaa aggctaccat  
 60  
 attcaagggt ccacgactcg cacctgcctt gccaatataa catggagtgg gatacagacc  
 120  
 gaatgtatac ctcatgcctg cagacagcca gaaaccccg caccgcg  
 168

<210> 210  
 <211> 56  
 <212> PRT  
 <213> Homo sapiens

<400> 210  
 Xaa Ser Arg Gly Tyr Glu Val Gly Ser Pro Val Phe Phe Arg Cys Arg  
 1 5 10 15  
 Lys Gly Tyr His Ile Gln Gly Ser Thr Thr Arg Thr Cys Leu Ala Asn  
 20 25 30  
 Leu Thr Trp Ser Gly Ile Gln Thr Glu Cys Ile Pro His Ala Cys Arg

35                      40                      45  
 Gln Pro Glu Thr Pro Ala His Ala  
 50                      55

<210> 211  
 <211> 354  
 <212> DNA  
 <213> Homo sapiens

<400> 211  
 tacatgggct ttgacacagt ggtggctgaa gctgcactaa ggggtgtttgg aggcaatgtc  
 60  
 cagctggcag ctcagaccct tgcacaccat ggaggaagcc tcccacccga cctgcagttc  
 120  
 tcaggagagg actcctcccc cacaccgtcc acatcccat ctgactctgc agggacctct  
 180  
 agtgcctcga cagatgaaga catggagacg gaggctgtca acgaaatcct ggaggacatt  
 240  
 ccggagcacg aggaggacta cctggactcc acgctggagg atgaagaagt cattattgct  
 300  
 gaatacttgt cctgcgttga aagtataagt tctgcngca aagaacaact gatc  
 354

<210> 212  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 212  
 Tyr Met Gly Phe Asp Thr Val Val Ala Glu Ala Ala Leu Arg Val Phe  
 1                      5                      10                      15  
 Gly Gly Asn Val Gln Leu Ala Ala Gln Thr Leu Ala His His Gly Gly  
 20                      25                      30  
 Ser Leu Pro Pro Asp Leu Gln Phe Ser Gly Glu Asp Ser Ser Pro Thr  
 35                      40                      45  
 Pro Ser Thr Ser Pro Ser Asp Ser Ala Gly Thr Ser Ser Ala Ser Thr  
 50                      55                      60  
 Asp Glu Asp Met Glu Thr Glu Ala Val Asn Glu Ile Leu Glu Asp Ile  
 65                      70                      75                      80  
 Pro Glu His Glu Glu Asp Tyr Leu Asp Ser Thr Leu Glu Asp Glu Glu  
 85                      90                      95  
 Val Ile Ile Ala Glu Tyr Leu Ser Cys Val Glu Ser Ile Ser Ser Ala  
 100                      105                      110  
 Xaa Lys Glu Gln Leu Ile  
 115

<210> 213  
 <211> 669  
 <212> DNA  
 <213> Homo sapiens

<400> 213  
 attgcccaat ctcagagtgt ccaggaaagc ctggagagcc tgttgcagtc tattggggaa  
 60

gttgaacaaa acctggaagg gaaacaggtg tcatcactct catcaggagt catccaggaa  
 120  
 gccttagcca caaatatgaa attgaagcag gacattgctc ggcaaaagag cagcttggag  
 180  
 gccacccgtg agatggtgac ccgattcatg gagacagcag acagtactac agcagcagtg  
 240  
 ctgcagggca aactggcaga ggtgagccag cggttcgaac agctctgtct acagcagcaa  
 300  
 gaaaaggaga gctccctaaa gaagcttcta ccccaggcag agatgtttga acacctctct  
 360  
 ggtaagctgc agcagttcat ggaaaacaaa agtcggatgc tggcctctgg aaatcagcca  
 420  
 gatcaagata ttacacattt cttccaacag atccaggagc tcaatttga aatggaagac  
 480  
 caacaggaga acctagatac tcttgagcac ctggtcactg aactgagctc ttgtggcttt  
 540  
 gcgctggact tgtgccagca tcaggacagg gtacagaatc taagaaaaga cttcacagag  
 600  
 ctacagaaga cagttaaaga gagagagaaa gatgcatcat cttgccagga acagttggat  
 660  
 gaattccgg  
 669

<210> 214

<211> 223

<212> PRT

<213> Homo sapiens

<400> 214

Ile	Ala	Gln	Ser	Gln	Ser	Val	Gln	Glu	Ser	Leu	Glu	Ser	Leu	Leu	Gln
1				5				10					15		
Ser	Ile	Gly	Glu	Val	Glu	Gln	Asn	Leu	Glu	Gly	Lys	Gln	Val	Ser	Ser
		20					25					30			
Leu	Ser	Ser	Gly	Val	Ile	Gln	Glu	Ala	Leu	Ala	Thr	Asn	Met	Lys	Leu
		35				40					45				
Lys	Gln	Asp	Ile	Ala	Arg	Gln	Lys	Ser	Ser	Leu	Glu	Ala	Thr	Arg	Glu
	50				55			60							
Met	Val	Thr	Arg	Phe	Met	Glu	Thr	Ala	Asp	Ser	Thr	Thr	Ala	Ala	Val
65				70				75						80	
Leu	Gln	Gly	Lys	Leu	Ala	Glu	Val	Ser	Gln	Arg	Phe	Glu	Gln	Leu	Cys
			85					90						95	
Leu	Gln	Gln	Gln	Glu	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Leu	Leu	Pro	Gln
		100					105					110			
Ala	Glu	Met	Phe	Glu	His	Leu	Ser	Gly	Lys	Leu	Gln	Gln	Phe	Met	Glu
		115				120					125				
Asn	Lys	Ser	Arg	Met	Leu	Ala	Ser	Gly	Asn	Gln	Pro	Asp	Gln	Asp	Ile
	130				135			140							
Thr	His	Phe	Phe	Gln	Gln	Ile	Gln	Glu	Leu	Asn	Leu	Glu	Met	Glu	Asp
145				150				155						160	
Gln	Gln	Glu	Asn	Leu	Asp	Thr	Leu	Glu	His	Leu	Val	Thr	Glu	Leu	Ser
			165				170						175		
Ser	Cys	Gly	Phe	Ala	Leu	Asp	Leu	Cys	Gln	His	Gln	Asp	Arg	Val	Gln
		180					185					190			
Asn	Leu	Arg	Lys	Asp	Phe	Thr	Glu	Leu	Gln	Lys	Thr	Val	Lys	Glu	Arg

	195		200		205									
Glu	Lys	Asp	Ala	Ser	Ser	Cys	Gln	Glu	Gln	Leu	Asp	Glu	Phe	Arg
	210					215					220			

<210> 215  
 <211> 814  
 <212> DNA  
 <213> Homo sapiens

<400> 215  
 aaatttcgta cccgctccgg cacagtacga gcccttgacg atgtgagcct ggctattaag  
 60  
 agagggttcca tctcagccgt tatcgggcac tccggagccg gcaaatccac cctgggttcg  
 120  
 ctcatcaacg gattagagac tcccacgcgt ggccgcgtct tggtagacgg caccgacgtc  
 180  
 tcgcagctct cggacaaagc gatgcgcccc ctacgcgcag acatcgggat gatcttccaa  
 240  
 cagttcaacc tattcggctc aaggaccatc tacgacaacg ttgcctatcc actcaagctg  
 300  
 gtcattgga agaaagcaga cgagaagaag cgcgtcaccg aattgctgag cttcgtcggg  
 360  
 ttgacgagca aagcctggga ccatccagac cagctctcgg gcggacagaa acagcgggtt  
 420  
 ggtattgccc gagcgctagc aactaaacca tcgattttgt tggctgacga gtccacctcg  
 480  
 gcgctggatc cagaaacgac agctgatgtc ctatccctgc tcaagcgggt caatgcggaa  
 540  
 ctaggggtga cggtcgtcgt catcaccac gagatggagg tcgtccgctc gattgcccag  
 600  
 caggtctcgg tactagcagc tggccatctc gtcgagtctg gaagcggccg ccaggtcttc  
 660  
 gctcatccac agtcagagac caccacgcgt ttccctggcga cgattatcgg ccagcaccg  
 720  
 agtggggagg aacaggcacg gttgcagtcg gaaaaccag atgcacgact cgtcgcgctc  
 780  
 agttcgggtg ccagtcactc gttcgggtgac gcgt  
 814

<210> 216  
 <211> 271  
 <212> PRT  
 <213> Homo sapiens

<400> 216  
 Lys Phe Arg Thr Arg Ser Gly Thr Val Arg Ala Leu Asp Asp Val Ser  
 1 5 10 15  
 Leu Ala Ile Lys Arg Gly Ser Ile Ser Ala Val Ile Gly His Ser Gly  
 20 25 30  
 Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Glu Thr Pro  
 35 40 45  
 Thr Arg Gly Arg Val Leu Val Asp Gly Thr Asp Val Ser Gln Leu Ser  
 50 55 60  
 Asp Lys Ala Met Arg Pro Leu Arg Ala Asp Ile Gly Met Ile Phe Gln

```

65          70          75          80
Gln Phe Asn Leu Phe Gly Ser Arg Thr Ile Tyr Asp Asn Val Ala Tyr
          85          90          95
Pro Leu Lys Leu Ala His Trp Lys Lys Ala Asp Glu Lys Lys Arg Val
          100          105          110
Thr Glu Leu Leu Ser Phe Val Gly Leu Thr Ser Lys Ala Trp Asp His
          115          120          125
Pro Asp Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg
          130          135          140
Ala Leu Ala Thr Lys Pro Ser Ile Leu Leu Ala Asp Glu Ser Thr Ser
145          150          155          160
Ala Leu Asp Pro Glu Thr Thr Ala Asp Val Leu Ser Leu Leu Lys Arg
          165          170          175
Val Asn Ala Glu Leu Gly Val Thr Val Val Val Ile Thr His Glu Met
          180          185          190
Glu Val Val Arg Ser Ile Ala Gln Gln Val Ser Val Leu Ala Ala Gly
          195          200          205
His Leu Val Glu Ser Gly Ser Ala Arg Gln Val Phe Ala His Pro Gln
          210          215          220
Ser Glu Thr Thr Gln Arg Phe Leu Ala Thr Ile Ile Gly Gln His Pro
225          230          235          240
Ser Gly Glu Glu Gln Ala Arg Leu Gln Ser Glu Asn Pro Asp Ala Arg
          245          250          255
Leu Val Asp Val Ser Ser Val Ala Ser His Ser Phe Gly Asp Ala
          260          265          270

```

&lt;210&gt; 217

&lt;211&gt; 500

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 217

```

nnacgcgtcg cgatgaaaga ggcgctgaaa ggtgccatcc agattccaac agtgactttt
60
agctctgaga agtccaatac tacagccctg gctgagttcg gaaaatacat tcataaagtc
120
tttcctacag tggtcagcac cagctttatc cagcatgaag tcgtggaaga gtatagccac
180
ctgttcacta tccaaggctc ggaccccgagc ttgcagccct acctgctgat ggctcacttt
240
gatgtggtgc ctgcccctga agaaggctgg gaggtgcccc cattctctgg gttggagcgt
300
gatggcgtca tctatggttg gggcacactg gacgacaaga actctgtgat ggcattactg
360
caggccttgg agctcctgct gatcaggaag tacatcccc gaagatcttt cttcatttct
420
ctggggccatg atgaggagtc atcagggaca ggggctcaga ggatctcagc cctgctacag
480
tcaaggggagc tccagctagc
500

```

&lt;210&gt; 218

&lt;211&gt; 166

&lt;212&gt; PRT



<213> Homo sapiens

<400> 218

```

Xaa Arg Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro
 1           5           10           15
Thr Val Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu
          20           25           30
Phe Gly Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser
          35           40           45
Phe Ile Gln His Glu Val Val Glu Glu Tyr Ser His Leu Phe Thr Ile
          50           55           60
Gln Gly Ser Asp Pro Ser Leu Gln Pro Tyr Leu Leu Met Ala His Phe
65           70           75           80
Asp Val Val Pro Ala Pro Glu Glu Gly Trp Glu Val Pro Pro Phe Ser
          85           90           95
Gly Leu Glu Arg Asp Gly Val Ile Tyr Gly Trp Gly Thr Leu Asp Asp
          100          105          110
Lys Asn Ser Val Met Ala Leu Leu Gln Ala Leu Glu Leu Leu Leu Ile
          115          120          125
Arg Lys Tyr Ile Pro Arg Arg Ser Phe Phe Ile Ser Leu Gly His Asp
          130          135          140
Glu Glu Ser Ser Gly Thr Gly Ala Gln Arg Ile Ser Ala Leu Leu Gln
145          150          155          160
Ser Arg Gly Val Gln Leu
          165

```

<210> 219

<211> 361

<212> DNA

<213> Homo sapiens

<400> 219

```

acgcgttgaa acgggtatat tggggatgac gccgctgtgc aatatgcgca aggccataca
60
caagggtccgc acgctcccat gtccctcggtt ttcgacagtt cttttgcgcc gcattatggc
120
gaagccgtcg agattgcgcc tgatatcaag cgcacacagg tcaacaaccc cagccccttc
180
acttttttgc gcaccaacag ttatctgata ggccgcgata cgctggcatt gatcgatccc
240
ggtcgcgttg acgaggccca tcacgcggcg ctgctgcgtg ccattgccgg cgggccggtc
300
agccatatct ttgtcagcca cacacaccgg gaccactcgc cagtcgagac ggttttgaaa
360
g
361

```

<210> 220

<211> 102

<212> PRT

<213> Homo sapiens

<400> 220

```

Met Ala Asp Arg Pro Ala Gly Asn Gly Thr Gln Gln Arg Arg Val Met

```

```

      1           5           10           15
Gly Leu Val Lys Arg Thr Gly Ile Asp Gln Cys Gln Arg Ile Ala Ala
      20           25           30
Asp Gln Ile Thr Val Gly Ala Glu Lys Ser Glu Gly Ala Gly Val Val
      35           40           45
Asp Arg Asp Ala Leu Asp Ile Arg Arg Asn Leu Asp Gly Phe Ala Ile
      50           55           60
Met Arg Arg Lys Arg Thr Val Glu Asn Glu Gly His Gly Ser Val Arg
      65           70           75           80
Thr Leu Cys Met Ala Leu Arg Ile Leu His Ser Gly Val Ile Pro Asn
      85           90           95
Ile Pro Val Ser Thr Arg
      100

```

&lt;210&gt; 221

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 221

```

agatctctgt gtcgtcggt gcaaagagga tgagcccaga tgcatatcag gggctcctc
60
ccacatccca cctgctcggg cagcccacgg cagccccaca ctgctgcagc acacctcgct
120
gcagctctgg ttctctctca gaaatatccc tgccaccctg ctaagccttg gccaacactg
180
caccctgtcc caatgagggt ccagtgaacca cacccccagg gcataccctc ctacagagca
240
ttccccaaaa aggctagagt agacaccagc ctgctccgta gggggcctcc accccattct
300
ccaaggcctc caccagggga cgcctggtga accagcatcc aggcctggcc cacctccctg
360
ctcagagtcc atgttctgtg acaaggggtg caactgggat t
401

```

&lt;210&gt; 222

&lt;211&gt; 124

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 222

```

Met Asp Ser Glu Gln Gly Gly Gly Pro Gly Leu Asp Ala Gly Ser Pro
      1           5           10           15
Gly Val Pro Gly Trp Arg Pro Trp Arg Met Gly Trp Arg Pro Pro Thr
      20           25           30
Glu Gln Ala Gly Val Tyr Ser Ser Leu Phe Trp Glu Cys Ser Val Gly
      35           40           45
Gly Tyr Ala Leu Gly Val Trp Ser Leu Glu Pro His Trp Asp Arg Val
      50           55           60
Gln Cys Trp Pro Arg Leu Ser Arg Val Ala Gly Ile Phe Leu Arg Arg
      65           70           75           80
Asn Gln Ser Cys Ser Glu Val Cys Cys Ser Ser Val Gly Leu Pro Trp
      85           90           95
Ala Ala Arg Ala Gly Gly Met Trp Glu Gly Ala Pro Asp Met His Leu

```

100 105 110  
 Gly Ser Ser Ser Leu Gln Pro Thr Thr Gln Arg Ser  
 115 120

<210> 223  
 <211> 331  
 <212> DNA  
 <213> Homo sapiens

<400> 223  
 tcatgaaatc tgtgggcagt gaccaggag ggtatgggca ggcccaacca ggttggtgtg  
 60  
 cccttgaagc cccacagacc tgccagggca gcagggcagt tgggagccgg agaacctgag  
 120  
 aaccaagcca ggctgcatgc aggaggctgg cacgtgaacg ctgcaggtgt tgccggcagc  
 180  
 cgtggtgcct ggcagatagt gttcgacccc cnaggacctt cttgctgggc agcccagtc  
 240  
 aaaagctggt cccgcttaag ccacccccac cgccttggcc acacctggca catgggtgaa  
 300  
 gcaagggcac ttcccggggc ttcctgttcc c  
 331

<210> 224  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 224  
 Met Pro Leu Leu His Pro Cys Ala Arg Cys Gly Gln Gly Gly Gly Gly  
 1 5 10 15  
 Gly Leu Ser Gly Asn Ser Phe Trp Thr Gly Leu Pro Ser Lys Lys Val  
 20 25 30  
 Leu Gly Gly Arg Thr Leu Ser Ala Arg His His Gly Cys Arg Gln His  
 35 40 45  
 Leu Gln Arg Ser Arg Ala Ser Leu Leu His Ala Ala Trp Leu Gly Ser  
 50 55 60  
 Gln Val Leu Arg Leu Pro Thr Ala Leu Leu Pro Trp Gln Val Cys Gly  
 65 70 75 80  
 Ala Ser Arg Ala His Gln Pro Gly Trp Ala Cys Pro Tyr Pro Pro Gly  
 85 90 95  
 Ser Leu Pro Thr Asp Phe Met  
 100

<210> 225  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

<400> 225  
 tgatcacggg cgtgagccac cagcccagca tcccttgctt ttcattcgca cctccacctc  
 60  
 cagaatgacc ctcatccct cctgcacaga cggtgacagc agtaactcct acaaacacca  
 120

ccagactgat cttcaagagc agaggaactc ccaatcacga ttccaccccc gccgggctct  
 180  
 caaatcctcc agggctgcct gctatggggg agggaggcac actttgcttg gctctcaagg  
 240  
 cctcagccag ccgggtccaa accaactccc agcctggcct caccatccca ccgccaaacc  
 300  
 tttgctcaca ctggcccctc ttcctggaac atgggcctn  
 339

<210> 226

<211> 91

<212> PRT

<213> Homo sapiens

<400> 226

Met	Thr	Leu	Ile	Pro	Ser	Cys	Thr	Asp	Gly	Asp	Ser	Ser	Asn	Ser	Tyr
1				5					10				15		
Lys	His	His	Gln	Thr	Asp	Leu	Gln	Glu	Gln	Arg	Asn	Ser	Gln	Ser	Arg
			20					25				30			
Phe	His	Pro	Arg	Arg	Ala	Leu	Lys	Ser	Ser	Arg	Ala	Ala	Cys	Tyr	Gly
		35					40					45			
Gly	Gly	Arg	His	Thr	Leu	Leu	Gly	Ser	Gln	Gly	Leu	Ser	Gln	Pro	Gly
	50					55				60					
Pro	Asn	Gln	Leu	Pro	Ala	Trp	Pro	His	His	Pro	Thr	Ala	Lys	Pro	Leu
65					70				75					80	
Leu	Thr	Leu	Ala	Pro	Leu	Pro	Gly	Thr	Trp	Ala					
				85					90						

<210> 227

<211> 353

<212> DNA

<213> Homo sapiens

<400> 227

gtcgacccct tcgattgtgg cgaactccat ggctgctgcg ggctgctgta ggctctcgag  
 60  
 tagctcgacg tcgggttcgc gagggctcgc agcgtggcca tgetgcttct tggatggttc  
 120  
 gggcaactcc tcgggggatt cgagcagttc ttggcgcacc tgctctggcg tcatcccgga  
 180  
 ggccaggccg acaagtgtg cctcctgcca cccgctgagc gacgctgcca tgttgagtac  
 240  
 ggcgtcttca ctggtcaggg cgagcgcggt atcgaccagg ttggcgtcca ggccgagaga  
 300  
 cagcatgtct gctcagtcgc ggtgatgact ggagtggcgg tctcctgcac ggg  
 353

<210> 228

<211> 102

<212> PRT

<213> Homo sapiens

<400> 228

Met Leu Ser Leu Gly Leu Asp Ala Asn Leu Val Asp Thr Ala Leu Ala

1	5	10	15
Leu Thr Ser Glu Asp	Ala Val Leu Asn Met	Ala Ala Ser Leu Ser Gly	
20	25	30	
Trp Gln Glu Ala Ala	Leu Val Gly Leu Ala Ser Gly Met Thr Pro Glu		
35	40	45	
Gln Val Arg Gln Glu Leu Leu Glu Ser Pro Glu Glu Leu Pro Glu Pro			
50	55	60	
Ser Lys Lys Gln His Gly His Ala Ala Ser Pro Arg Glu Pro Asp Val			
65	70	75	80
Glu Leu Leu Glu Ser Leu Arg Arg Pro Ala Ala Met Glu Phe Ala			
85	90	95	
Thr Ile Glu Gly Val Asp			
100			

<210> 229  
 <211> 743  
 <212> DNA  
 <213> Homo sapiens

<400> 229  
 nnggctaggg acacggcctc ctcctcaaca ggcagtgctc gtgcaggctc aggggcatca  
 60  
 tcaaagataa cacagggctg gtcaggggct gctggctgct cctgccccag gactggctcc  
 120  
 aggatgggca aggctgcctc cctggtagcc agggggagag gggaaggag caccagggag  
 180  
 tgggccagca ggtgtggcat cggccaggag gagatggagg ccagcagcag ccaagaccag  
 240  
 agtaaagtgt ctgccccagg ggtgctcaca gcccaggacc gggtagttgg aaagccagcc  
 300  
 cagcttgcca ctcagcggag ccaggaggca gatgttcagg actgggagtt cagaaagagg  
 360  
 gattcccagg gcacttactc cagccgggat gcagaactcc aggaccagga attcggaaag  
 420  
 agagattcac tgggtaccta cagtagtcga gatgtaagcc ttggggactg ggaatttggg  
 480  
 aagagagatt ctctgggtgc ttatgccagc caagatgcc aagagcaggg ccaagatttg  
 540  
 gggaagaggg accaccatgg taggtacagc agccaggatg ccgatgagca ggactgggag  
 600  
 ttccagaaga gagatgtgtc actcggcacc tatggcagcc gggctgcgga gccacaggaa  
 660  
 caggagtttg ggaagagcgc ttggataagg gactacagca gtggtggcag ctccaggacc  
 720  
 cttgacgcc aggacagaag ctt  
 743

<210> 230  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

<400> 230  
 Xaa Ala Arg Asp Thr Ala Ser Ser Ser Thr Gly Ser Ala Cys Ala Gly

```
<210> 231
<211> 431
<212> DNA
<213> Homo sapiens
```

```
<400> 231
acgcgttggc caccgagagg ctggcgaggg tgtgcagcac ggcgcagtgt ggagggtcc
60
cagggtgcag cctgcgcagc agctcctcca tcaccttgct gatgaactgt cttcccacgg
120
ccaccaggac gccactcgcc gcctgctgcc agtcccagac caggtccttc gtcttggtca
180
tctcgctgga ggccaggagg atgatgggtgc tggctgtgtc cttgtccagc tcaactggcg
240
gactgctcag gacctctctc atggccctca ggaccgctgc tcggtatggg tgtgccagct
300
tgtcatgctg ccgcagatac tcctcgcagg cacggagcgt ctccaccctg ctggacgcc
360
tcaccgataa ggacccctg gtgcaggagc aggtctgcag tgccctgtgc tcctcgggg
420
aggtgcggcc g
431
```

<210> 232  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 232  
 Met Ala Ser Ser Arg Val Glu Thr Leu Arg Ala Cys Glu Glu Tyr Leu  
 1 5 10 15  
 Arg Gln His Asp Lys Leu Ala His Pro Tyr Arg Ala Ala Val Leu Arg  
 20 25 30  
 Ala Met Glu Arg Val Leu Ser Ser Arg Ala Ser Glu Leu Asp Lys Asp  
 35 40 45  
 Thr Ala Ser Thr Ile Ile Leu Leu Ala Ser Ser Glu Met Thr Lys Thr  
 50 55 60  
 Lys Asp Leu Val Trp Asp Trp Gln Gln Ala Ala Ser Gly Val Leu Val  
 65 70 75 80  
 Ala Val Gly Arg Gln Phe Ile Ser Lys Val Met Glu Glu Leu Leu Arg  
 85 90 95  
 Arg Leu His Pro Gly Thr Leu Pro His Cys Ala Val Leu His Thr Leu  
 100 105 110  
 Ala Ser Leu Ser Val Ala Asn Ala  
 115 120

<210> 233  
 <211> 606  
 <212> DNA  
 <213> Homo sapiens

<400> 233  
 acgcgttcag ggatgccaga aatctaactg ggtaataaaa agctgggaga acattccaga  
 60  
 aagggtgggca cccttagcat tccccaaaag caccagccct cctcatcctt cccagcttct  
 120  
 gtgctggaat gcaccccat cggaagggt cgaaaactca ggacacatta ggatcacctg  
 180  
 gaaagcattt gtcaaaacgc atctccctgc gggtcagggt ccaagttaaa atcaaaacttc  
 240  
 aggtgatgct gactcagggt gctccagaaa cacctgggga agcagcactt tggaggctgc  
 300  
 ctctcacatc caccacacag caagtgggca gggagctagg taaatctcct tcccagttga  
 360  
 gaaggggctc ggagcaggca cagagaagag atacccttag aatgcaagtt gttcagctgc  
 420  
 gaaagtccag cctgcaggct tcctgggcaa gctagtgggc tgaagtatgc cacagcaaca  
 480  
 ggcttctaga gccggctgcc cagctcctac tctgcctctg ccactcactg actgtgtggt  
 540  
 cttgagcagg tcacctgtct gacttggtga gagctgacag gcacacactg ttagaggctt  
 600  
 acgcgt  
 606

<210> 234

<211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 234  
 Met His Pro His Arg Lys Gly Ser Lys Thr Gln Asp Thr Leu Gly Ser  
 1 5 10 15  
 Pro Gly Lys His Leu Ser Lys Arg Ile Ser Leu Arg Val Arg Val Gln  
 20 25 30  
 Val Lys Ile Lys Leu Gln Val Met Leu Thr Gln Val Ala Pro Glu Thr  
 35 40 45  
 Pro Gly Glu Ala Ala Leu Trp Arg Leu Pro Leu Thr Ser Thr Pro Gln  
 50 55 60  
 Gln Val Gly Arg Glu Leu Gly Lys Ser Pro Ser Gln Leu Arg Arg Gly  
 65 70 75 80  
 Ser Glu Gln Ala Gln Arg Arg Asp Thr Leu Arg Met Gln Val Val Gln  
 85 90 95  
 Leu Arg Lys Ser Ser Leu Gln Ala Ser Trp Ala Ser  
 100 105

<210> 235  
 <211> 328  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
 cgaccgttga ctattctcta caaaccacaa agacaatgat tgattttaact gaatttagaa  
 60  
 atagcaaaca cttaaacag cagcagtaca gagctgaaaa ccagattctt ttgaaagaga  
 120  
 ttgaaagtct agaggaagaa cgacttgatc tgaaaaaaaa aattcgccaa atgggtcaag  
 180  
 aaagaggaaa aagaaggga acttcaggat taaccactgg ggacctgaac ctaactgaaa  
 240  
 acatttctca aggagataga ataagtga gaaaattgga tttattgagc ctcaaaaata  
 300  
 tgagtgaagc acaatcaaag aatgaatt  
 328

<210> 236  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
 Met Ile Asp Leu Thr Glu Phe Arg Asn Ser Lys His Leu Lys Gln Gln  
 1 5 10 15  
 Gln Tyr Arg Ala Glu Asn Gln Ile Leu Leu Lys Glu Ile Glu Ser Leu  
 20 25 30  
 Glu Glu Glu Arg Leu Asp Leu Lys Lys Ile Arg Gln Met Ala Gln  
 35 40 45  
 Glu Arg Gly Lys Arg Arg Ala Thr Ser Gly Leu Thr Thr Gly Asp Leu  
 50 55 60  
 Asn Leu Thr Glu Asn Ile Ser Gln Gly Asp Arg Ile Ser Glu Arg Lys



65                                      70                                      75                                      80  
 Leu Asp Leu Leu Ser Leu Lys Asn Met Ser Glu Ala Gln Ser Lys Asn  
    85                                      90                                      95  
 Glu

<210> 237

<211> 2059

<212> DNA

<213> Homo sapiens

<400> 237

ggccataagg gcacgacgca ttcctagccg atgcaccaac acgggcatga agcctgccga  
 60  
 gagcacgaag ccggcggtcca tagctacggc ccatacggtc atgtctgcca tggctccggt  
 120  
 gatgtcagac tgcacatgaa atcggttacg gtaccccagg atcatcgcta ccgagtacac  
 180  
 cccgaacagc acccgctggg cgccgatcag cgtgaggag tgccccacca gtggcacttt  
 240  
 tcttagatag cggaacccat ccaccacatc ccagtcacc gttctcatcg tccgggaacg  
 300  
 atccaccagt ggcgcccaa gctcccgacg tgaaaactgc agcccctagg cgaccgagac  
 360  
 tgcaagagg gctgcggaga tgcagaaaat gatcgtgtcg gctgggtgca caggaatatg  
 420  
 gcgtccggca atcatgcgca ctgctgcagc aacaaccgca ccgatcatga gccctagcgg  
 480  
 ccaatcgttg gcatgattga cgatgccgtc aggtagtcgc gcttgctgat ggtgtattcc  
 540  
 aaccagcgca ccaaggcggg gagcaaaaac cggttcaggc tcatcgcgat gagcaaccca  
 600  
 atgagcaagg ccagggtggga gggcttatcg cgcgcaccac ccagaccaa gatccccagc  
 660  
 ccgaccagg tgacggcacg cattcatctg cgtattgtcc cgactacacc gtgagggcgc  
 720  
 tctctgatct gcagctcatc aaggttacgc gactgcagta cctcaatgca ctctggcta  
 780  
 ccgagccca gaacctgcca cagtccctg agaacaccga cctgcagggt attccaggca  
 840  
 gccagaccag gctccttggg gagaagacca ccacagcggc agctttccca gtagcccttt  
 900  
 ccctctttgg cacagttgga acctccagtt gataaatgac tgtggactag cgcgcgtttt  
 960  
 ttgttttcag agcacacgta aggggtccagc cacagcaggc ccggcgctccc ggtggaaggc  
 1020  
 agccctgggc ggaaccagg cgtttaacgg ctactaggc agccccagat ctggggaagg  
 1080  
 agatgagcac gtggggagct ggagtgagct gagcagaagt tttgtgccc cctgccccca  
 1140  
 tcccctccag gccacgtttt agatggccct ttagttgctg ggtcctgggt gtcctcagaa  
 1200  
 ctagacatca atgcctggat ccttcagccg gccctgccct cctttaggag acaggagtca  
 1260

ccagggcaca gccctccagg cccgcctcag gaaggaatga aaggaatgcc atcatctcta  
 1320  
 gttcccaggg ccacagccttc cccttctccc ccggggcagg gacagtgcgg catattcaga  
 1380  
 ttcagacctc tttgggctga gccaccttgt gagtgcagtt actgcctttg tgtggccgtg  
 1440  
 acctctatatt gtttgctttt aatttgccaa cctatcgctg ctggcagcac tttttgagca  
 1500  
 agccgagagc acccattttg gctgggggatt cagatcgatg gccttgtcca tgttgtcctt  
 1560  
 tctggcttcc ctgatgggtg catgtttcag cgcagtcgcc ccagcctttc ccatgtgcca  
 1620  
 aaccagaagc tccactgccc gtaggctgtc cctgtagccc tgctccctcc ctggaggctg  
 1680  
 ctcttctgat tctgagagct ggcctagtgg tgctgagggc ccctttctgc ttctctgccc  
 1740  
 acctgctgag ttgccactcg cagtgttgct agttcccgtg ttctgagaag aggtcatgcc  
 1800  
 tgggaggaag ggatcgctcat gctgcatcga atcctctctc cgccgtgtgg ccccaggag  
 1860  
 agtagctgcc tgttgacact gtcacacacc tccccacagc ctccctgcag gtgctgtgtg  
 1920  
 gccgtgatgt gcagagagca gtgagggagg gttcatgaac caggtggatc ctctttaaaa  
 1980  
 aaaaaaaaaaag tttttgttat atctctaaaa tcccatagct aggaacagaa aaaaaggaaa  
 2040  
 agacttgaaa tgttctaga  
 2059

&lt;210&gt; 238

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 238

Ala	Glu	Gln	Lys	Phe	Cys	Ala	Arg	Leu	Pro	Pro	Ser	Pro	Pro	Gly	His
1				5				10						15	
Val	Leu	Asp	Gly	Pro	Cys	Ser	Cys	Gly	Ser	Trp	Val	Ser	Ser	Glu	Leu
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Asp	Ile	Asn	Ala	Trp	Ile	Leu	Gln	Pro	Ala	Leu	Pro	Ser	Phe	Arg	Arg
		35				40						45			
Gln	Glu	Ser	Pro	Gly	His	Ser	Pro	Pro	Gly	Pro	Pro	Gln	Glu	Gly	Met
	50				55				60						
Lys	Gly	Met	Pro	Ser	Ser	Leu	Val	Pro	Arg	Ala	Gln	Pro	Ser	Pro	Ser
65					70				75					80	
Pro	Pro	Gly	Gln	Gly	Gln	Cys	Gly	Ile	Phe	Arg	Phe	Arg	Pro	Leu	Trp
			85					90					95		
Ala	Glu	Pro	Pro	Cys	Glu	Cys	Ser	Tyr	Cys	Leu	Cys	Val	Ala	Val	Thr
		100					105					110			
Ser	Ile	Cys	Leu	Leu	Leu	Ile	Cys	Gln	Pro	Ile	Ala	Ala	Gly	Ser	Thr
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Phe															

<210> 239  
 <211> 388  
 <212> DNA  
 <213> Homo sapiens

<400> 239  
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 ggtcagctgc ccctcctcca cttctgcttc tcggcggttac cccataccgt attggccgcg  
 180  
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 240  
 atgccgacct cagcatcggc atctgcagtg atgagtgcgt atcgcgccac acgaaacgcc  
 300  
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 ggtcgtgtat ataaagcaaa ggaacttn  
 388

<210> 240  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 240  
 Met Val Asp Trp Met Ser Gln Val Leu Val Val Ala Ala Ala Val Gly  
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 Gln Leu Pro Leu Leu His Phe Cys Phe Ser Ala Leu Pro His Thr Val  
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 Leu Ala Ala Cys Ser Pro Leu Asn Ala Ala Met Ser Ser Ser Pro Tyr  
 35 40 45  
 Arg Asn Asp Val Pro Ser Lys Met Pro Thr Ser Ala Ser Ala Ser Ala  
 50 55 60  
 Val Met Ser Ala Tyr Arg Ala Thr Arg Asn Ala Gln Arg Asn Arg Val  
 65 70 75 80  
 Leu Ala Arg Tyr Glu Val Leu Gly Tyr Leu Ser Ser Gly Thr Tyr Gly  
 85 90 95  
 Arg Val Tyr Lys Ala Lys Glu Leu  
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<210> 241  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

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 120  
 tcccatctgg gggcccttag cacagtcctt gggacccac atgctgcctt tcaggctgat  
 180

gtgggcaaac tcggcagccc agcctactcc cgggccatgg gccaccatct cagcttcctt  
 240  
 ggggctaage cgtgtgctct gaatcaaaag cagtagtggc atcggcggca ctggcgccat  
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 gggaaacggg ttgacttgca caaccagcac  
 330

<210> 242  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 242  
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 Arg Leu Ser Pro Arg Glu Ala Glu Met Val Ala His Gly Pro Gly Val  
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 35 40 45  
 Gly Pro Arg Asp Cys Ala Lys Gly Pro Gln Met Gly Arg Ala Lys Gly  
 50 55 60  
 Ala Trp Glu Gly Arg Cys Phe Pro Gln Ala Arg Pro Gly Ser Ser Ile  
 65 70 75 80  
 Pro Arg Ser Glu Ala Ser Ser Thr Ala Ser Val Pro Ala Ala Phe Asn  
 85 90 95  
 Ser Ala Pro Arg  
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<210> 243  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

<400> 243  
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 120  
 cccgtactgc tacacatgct agatattctc ccctccttgc ggactacagt ggtgatggtg  
 180  
 caggcagaag tagccgatcg attggctgcc acaccaggca gccgcattta cggtgtcccc  
 240  
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 330

<210> 244  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 244  
 Xaa Pro Ser Leu Arg Val Ile Thr Lys Asp Ala Met His Val Thr Ala

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Glu Glu Ile Leu His Thr Gly His Pro Ala Pro Thr Ala Leu Val Ala
      20           25           30
Asn Leu Pro Tyr Asn Val Ala Val Pro Val Leu Leu His Met Leu Asp
      35           40           45
Ile Leu Pro Ser Leu Arg Thr Thr Val Val Met Val Gln Ala Glu Val
      50           55           60
Ala Asp Arg Leu Ala Ala Thr Pro Gly Ser Arg Ile Tyr Gly Val Pro
      65           70           75           80
Ser Val Lys Val Asn Phe Tyr Gly Thr Val Ser Arg Ala Gly Ala Ile
      85           90           95
Gly Arg Asn Val Phe Trp Pro Ala Pro Asn Val Asp Ser Gly
      100           105           110

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<210> 245  
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 <212> DNA  
 <213> Homo sapiens

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120
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240
ganttggaac ccacagcatc gaatttgccc agaaggaagt ggtcgttggt gagggatttg
300
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355

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<210> 246  
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 <212> PRT  
 <213> Homo sapiens

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<400> 246
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      1           5           10           15
Trp Thr Asn Ser Met Leu Trp Leu Pro Xaa Pro Pro Thr Ala Trp Thr
      20           25           30
Gly Lys Ile Phe Val Val Asn Ser Arg Trp Met Pro Arg Asp Ala Ser
      35           40           45
Ile Arg Ser Glu Cys Arg Leu Pro Pro Thr Val Asn Phe Cys Phe Cys
      50           55           60
Asn Thr Leu His Ser Thr Phe Pro Arg Trp Val Trp Leu Pro Ser Ser
      65           70           75           80
Ile Arg Ala Arg His Cys Phe Gln Val Thr Pro Ala Glu Val Asn Pro
      85           90           95
Lys Leu Gly Gly Gly
      100

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<210> 247  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

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 gcctgggaca ccagcgctcg gtccgagatc aagatgggag acagggtacga gacggtcagg  
 120  
 ttctttccact gctacaagcg cggagtggac cgcgtgttcg ttgaccaccc actgttcctg  
 180  
 gagagggttt ggggaaagac cgaggagaag atctacgggc ctgacgctgg aacggactac  
 240  
 agggaacaacc agctgcgggt cagcctgcta tgccaggcag cacttgaagc tccaaggatc  
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 ctgagcctca acaacaaccc atacttctcc gga  
 333

<210> 248  
 <211> 111  
 <212> PRT  
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<400> 248  
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 20 25 30  
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 35 40 45  
 Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg Val Trp  
 50 55 60  
 Gly Lys Thr Glu Glu Lys Ile Tyr Gly Pro Asp Ala Gly Thr Asp Tyr  
 65 70 75 80  
 Arg Asp Asn Gln Leu Arg Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu  
 85 90 95  
 Ala Pro Arg Ile Leu Ser Leu Asn Asn Pro Tyr Phe Ser Gly  
 100 105 110

<210> 249  
 <211> 5503  
 <212> DNA  
 <213> Homo sapiens

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 120  
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 180  
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 240

cagaagttcg tcatgttcta cgacagcgag tatgatatcc gtgggcttca aagctttctg  
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<210> 250

<211> 927

<212> PRT

<213> Homo sapiens

<400> 250

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			20					25					30		
Phe	Val	Gln	Arg	Asn	Pro	Gly	Gly	Ser	Pro	Arg	Thr	Ala	Cys	His	Leu
		35					40					45			
Asn	Pro	Ser	Pro	Asp	Gly	Glu	Ala	Tyr	Thr	Leu	Ala	Ser	Arg	Pro	Pro
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Val	Arg	Leu	Asn	Asp	Val	Met	Leu	Arg	Leu	Val	Thr	Glu	Leu	Arg	Trp
65				70					75					80	
Gln	Lys	Phe	Val	Met	Phe	Tyr	Asp	Ser	Glu	Tyr	Asp	Ile	Arg	Gly	Leu
			85					90						95	
Gln	Ser	Phe	Leu	Asp	Gln	Ala	Ser	Arg	Leu	Gly	Leu	Asp	Val	Ser	Leu
			100					105					110		
Gln	Lys	Val	Asp	Lys	Asn	Ile	Ser	His	Val	Phe	Thr	Ser	Leu	Phe	Thr
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Thr	Met	Lys	Thr	Glu	Glu	Leu	Asn	Arg	Tyr	Arg	Asp	Thr	Leu	Arg	Arg
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Ala	Ile	Leu	Leu	Leu	Ser	Pro	Gln	Gly	Ala	His	Ser	Phe	Ile	Asn	Glu
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Ala	Val	Glu	Thr	Asn	Leu	Ala	Ser	Lys	Asp	Ser	His	Trp	Val	Phe	Val
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Asn	Glu	Glu	Ile	Ser	Asp	Pro	Glu	Ile	Leu	Asp	Leu	Val	His	Ser	Ala
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Leu	Gly	Arg	Met	Thr	Val	Val	Arg	Gln	Ile	Phe	Pro	Ser	Ala	Lys	Asp
	195					200						205			
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225			230					235						240	
Leu	Tyr	Asp	Ser	Val	Leu	Met	Leu	Ala	Asn	Ala	Phe	His	Arg	Lys	Leu
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Glu	Asp	Arg	Lys	Trp	His	Ser	Met	Ala	Ser	Leu	Asn	Cys	Ile	Arg	Lys

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Lys	Gly	His	Ile	Thr	Gly	Leu	Thr	Gly	Val	Met	Glu	Phe	Arg	Glu	Asp	
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Ser	Ser	Asn	Pro	Tyr	Val	Gln	Phe	Glu	Ile	Leu	Gly	Thr	Thr	Tyr	Ser	
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Glu	Thr	Phe	Gly	Lys	Asp	Met	Arg	Lys	Leu	Ala	Thr	Trp	Asp	Ser	Glu	
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Lys	Gly	Leu	Asn	Gly	Ser	Leu	Gln	Glu	Arg	Pro	Met	Gly	Ser	Arg	Leu	
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Gln	Gly	Leu	Thr	Leu	Lys	Val	Val	Thr	Val	Leu	Glu	Glu	Pro	Phe	Val	
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Met	Val	Ala	Glu	Asn	Ile	Leu	Gly	Gln	Pro	Lys	Arg	Tyr	Lys	Gly	Phe	
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Ser	Ile	Asp	Val	Leu	Asp	Ala	Leu	Ala	Lys	Ala	Leu	Gly	Phe	Lys	Tyr	
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Glu	Ile	Tyr	Gln	Ala	Pro	Asp	Gly	Arg	Tyr	Gly	His	Gln	Leu	His	Asn	
			405						410					415		
Thr	Ser	Trp	Asn	Gly	Met	Ile	Gly	Glu	Leu	Ile	Ser	Lys	Arg	Ala	Asp	
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Leu	Ala	Ile	Ser	Ala	Ile	Thr	Ile	Thr	Pro	Glu	Arg	Glu	Ser	Val	Val	
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Asp	Phe	Ser	Lys	Arg	Tyr	Met	Asp	Tyr	Ser	Val	Gly	Ile	Leu	Ile	Lys	
	450					455				460						
Lys	Pro	Glu	Glu	Lys	Ile	Ser	Ile	Phe	Ser	Leu	Phe	Ala	Pro	Phe	Asp	
465					470					475					480	
Phe	Ala	Val	Trp	Ala	Cys	Ile	Ala	Ala	Ala	Ile	Pro	Val	Val	Gly	Val	
			485						490					495		
Leu	Ile	Phe	Val	Leu	Asn	Arg	Ile	Gln	Ala	Val	Arg	Ala	Gln	Ser	Ala	
		500						505					510			
Ala	Gln	Pro	Arg	Pro	Ser	Ala	Ser	Ala	Thr	Leu	His	Ser	Ala	Ile	Trp	
	515						520					525				
Ile	Val	Tyr	Gly	Ala	Phe	Val	Gln	Gln	Gly	Gly	Glu	Ser	Ser	Val	Asn	
	530					535					540					
Ser	Met	Ala	Met	Arg	Ile	Val	Met	Gly	Ser	Trp	Trp	Leu	Phe	Thr	Leu	
545					550					555					560	
Ile	Val	Cys	Ser	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Thr	Val	
			565						570					575		
Ser	Arg	Met	Asp	Asn	Pro	Ile	Arg	Thr	Phe	Gln	Asp	Leu	Ser	Lys	Gln	
		580						585					590			
Val	Glu	Met	Ser	Tyr	Gly	Thr	Val	Arg	Asp	Ser	Ala	Val	Tyr	Glu	Tyr	
	595						600	</								

690	695	700
Arg Ile Leu Glu Leu Gln Asp Thr Gly Asp Leu Asp Val Leu Lys Gln		
705	710	715
Lys Trp Trp Pro His Met Gly Arg Cys Asp Leu Thr Ser His Ala Ser		720
	725	730
Ala Gln Ala Asp Gly Lys Ser Leu Lys Leu His Ser Phe Ala Gly Val		735
	740	745
Phe Cys Ile Leu Ala Ile Gly Leu Leu Leu Ala Cys Leu Val Ala Ala		750
	755	760
Leu Glu Leu Trp Trp Asn Ser Asn Arg Cys His Gln Glu Thr Pro Lys		765
	770	775
Glu Asp Lys Glu Val Asn Leu Glu Gln Val His Arg Arg Met Asn Ser		780
785	790	795
Leu Met Asp Glu Asp Ile Ala His Lys Gln Ile Ser Pro Ala Ser Ile		800
	805	810
Glu Leu Ser Ala Leu Glu Met Gly Gly Leu Ala Pro Thr Gln Thr Leu		815
	820	825
Glu Pro Thr Arg Glu Tyr Gln Asn Thr Gln Leu Ser Val Ser Thr Phe		830
	835	840
Leu Pro Glu Gln Ser Ser His Gly Thr Ser Arg Thr Leu Ser Ser Gly		845
	850	855
Pro Ser Ser Asn Leu Pro Leu Pro Leu Ser Ser Ser Ala Thr Met Pro		860
865	870	875
Ser Met Gln Cys Lys His Arg Ser Pro Asn Gly Gly Leu Phe Arg Gln		880
	885	890
Ser Pro Val Lys Thr Pro Ile Pro Met Ser Phe Gln Pro Val Pro Gly		895
	900	905
Gly Val Leu Pro Glu Ala Leu Asp Thr Ser His Gly Thr Ser Ile		910
	915	920
		925

<210> 251  
 <211> 291  
 <212> DNA  
 <213> Homo sapiens

<400> 251  
 nngatcagcc gcggggtccg cgccctcgat tcggcgggtgg agaccgagag tctgcgtgag  
 60  
 gacgtcaacg cgctcgaacg gctgcgggtg gccgtgcgcg ccagcgtggt catcctcatc  
 120  
 gattaccacc attcgggtgac cctgctgctg cgggtgcgcg ggaactcacc tctggaacga  
 180  
 gaggccctcg aggccgcgcg ccgtatcgat gcgaagggttc ccgctctcgt cgagagcgcc  
 240  
 atcgccgagg gtggtctgcg ctccgatttc actcccgggc tcatcacgcg t  
 291

<210> 252  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 252  
 Xaa Ile Ser Arg Gly Val Arg Ala Leu Asp Ser Ala Val Glu Thr Glu

```

      1             5             10             15
Ser Leu Arg Glu Asp Val Asn Ala Leu Glu Arg Leu Arg Leu Ala Val
      20             25             30
Arg Ala Ser Val Val Ile Leu Ile Glu Tyr His His Ser Val Thr Leu
      35             40             45
Leu Leu Arg Val Arg Gly Asn Ser Pro Leu Glu Arg Glu Ala Leu Glu
      50             55             60
Ala Arg Arg Arg Ile Asp Ala Lys Val Pro Ala Leu Val Glu Ser Ala
      65             70             75             80
Ile Ala Glu Gly Gly Leu Arg Ser Asp Phe Thr Pro Gly Leu Ile Thr
      85             90             95
Arg

```

<210> 253  
 <211> 327  
 <212> DNA  
 <213> Homo sapiens

```

<400> 253
gtgcacggat gggagcgcgc gcgcgcgtgc tggcgccttc acagcccggc gagcggcgtg
60
cgctcacggc cctgtaccga ccgatctcgc aaccttcgcg agaccgatcc accaaccgcg
120
cccacatgtc ggcagtgatg gcgggcacct tgcgggagaa ggccgggaag gtcgagcgag
180
ccaatgaccg tcgcacgggc ggcacgctcc acgagcggga cgagaagctc gcggcaggac
240
gtcactcgt cgcggtgtcc tccgcggtct ccataccgt ccctgcgaca tggaacgccc
300
acgacttcgg acggcgactc gacgcgt
327

```

<210> 254  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

```

<400> 254
Met Gly Ala Leu Ala Arg Val Leu Val Pro Ser Gln Pro Gly Glu Arg
1             5             10             15
Arg Ala Leu Thr Val Leu Tyr Arg Pro Ile Ser Gln Pro Ser Ala Asp
      20             25             30
Arg Ser Thr Asn Arg Ala His Met Ser Ala Val Met Ala Gly Thr Leu
      35             40             45
Arg Glu Lys Ala Gly Lys Val Glu Arg Ala Asn Asp Arg Arg Thr Val
      50             55             60
Gly Thr Leu His Glu Arg Asp Glu Lys Leu Ala Ala Gly Arg Ser Leu
      65             70             75             80
Val Ala Val Ser Ser Ala Val Ser Ile Thr Val Pro Ala Thr Trp Asn
      85             90             95
Ala His Asp Phe Gly Arg Arg Leu Asp Ala
      100             105

```

<210> 255  
 <211> 372  
 <212> DNA  
 <213> Homo sapiens

<400> 255  
 ctagaaatgg ctggctacga atacatggaa gctgaaaata gccacaagc ccacgaaatt  
 60  
 atcgtggacc atagacctga cttaatctta tgtgattgga tgatgccagg agggagtggc  
 120  
 atcgagctaa ctcgctgctt aaagaaagac agcacgacag cagaaatccc tggtatttta  
 180  
 ctaacggcca aaagtgaaga agacaataaa attcaaggct tagaagtcgg tgcagatgac  
 240  
 tacatcacta aacctttctc tcctcgtgaa ctagtagcac gcctcaaggc ggtattacgc  
 300  
 cgagcgactc cacaaggtat tgatgatcct attgaaattg atggtttaac gcttgatccc  
 360  
 attagccaac gc  
 372

<210> 256  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 256  
 Leu Glu Met Ala Gly Tyr Glu Tyr Met Glu Ala Glu Asn Ser Gln Gln  
 1 5 10 15  
 Ala His Glu Ile Ile Val Asp His Arg Pro Asp Leu Ile Leu Cys Asp  
 20 25 30  
 Trp Met Met Pro Gly Gly Ser Gly Ile Glu Leu Thr Arg Arg Leu Lys  
 35 40 45  
 Lys Asp Ser Thr Thr Ala Glu Ile Pro Val Ile Leu Thr Ala Lys  
 50 55 60  
 Ser Glu Glu Asp Asn Lys Ile Gln Gly Leu Glu Val Gly Ala Asp Asp  
 65 70 75 80  
 Tyr Ile Thr Lys Pro Phe Ser Pro Arg Glu Leu Val Ala Arg Leu Lys  
 85 90 95  
 Ala Val Leu Arg Arg Ala Thr Pro Gln Gly Ile Asp Asp Pro Ile Glu  
 100 105 110  
 Ile Asp Gly Leu Thr Leu Asp Pro Ile Ser Gln Arg  
 115 120

<210> 257  
 <211> 639  
 <212> DNA  
 <213> Homo sapiens

<400> 257  
 nnacgcgtag cggctcgaggt tgccgacacc atgcccgaa cggcctgct cgccatcgag  
 60  
 gcacccatgg gacacggcaa gaccgaggcc gccctcatgt gcgcacaggt gctcgccgaa  
 120

cggttcgggc tcggcggcat cttcttcggt ctaccgacga tggccacgtc caatcccatg  
 180  
 ttcggtcgag ttcgggaatg gctggacgct gtgccagcca aggacccgtc aagcatttcc  
 240  
 ctggctcact cgaaagctgg actcaacgag gagtaccagc agtcatgcc gtggaacgcc  
 300  
 accatggccg tctacgacga aggtgccggc acgcagcgtg aagcttcggc gatcgccat  
 360  
 gagtggttct tgggccgcaa gcgcgcgac ctggccgacc acgtcgtcgg gaccatcgac  
 420  
 caggcactgt tcaccggtct caaagccaag catgtggtgt tacgccacct cggctcggcg  
 480  
 agcaaggctg tcatcattga tgaggtccac gccgccgacg tctatatgcg cgaatacctc  
 540  
 aaggtcgtcc tcgaatggct cggcgcctac cgcacgccag tcatcctcat gtccgcgacg  
 600  
 ctgccaccgg cccaacgtca tgaactcgcg ctagcgtac  
 639

<210> 258  
 <211> 213  
 <212> PRT  
 <213> Homo sapiens

<400> 258  
 Xaa Arg Val Ala Val Glu Val Ala Asp Thr Met Pro Glu Pro Gly Leu  
 1 5 10 15  
 Leu Ala Ile Glu Ala Pro Met Gly His Gly Lys Thr Glu Ala Ala Leu  
 20 25 30  
 Met Cys Ala Gln Val Leu Ala Glu Arg Phe Gly Leu Gly Gly Ile Phe  
 35 40 45  
 Phe Gly Leu Pro Thr Met Ala Thr Ser Asn Pro Met Phe Gly Arg Val  
 50 55 60  
 Arg Glu Trp Leu Asp Ala Val Pro Ala Lys Asp Pro Ser Ser Ile Ser  
 65 70 75 80  
 Leu Ala His Ser Lys Ala Gly Leu Asn Glu Glu Tyr Gln Gln Leu Met  
 85 90 95  
 Pro Trp Asn Ala Thr Met Ala Val Tyr Asp Glu Gly Ala Gly Thr Gln  
 100 105 110  
 Arg Glu Ala Ser Ala Ile Val His Glu Trp Phe Leu Gly Arg Lys Arg  
 115 120 125  
 Ala Ile Leu Ala Asp His Val Val Gly Thr Ile Asp Gln Ala Leu Phe  
 130 135 140  
 Thr Gly Leu Lys Ala Lys His Val Val Leu Arg His Leu Gly Leu Ala  
 145 150 155 160  
 Ser Lys Val Val Ile Ile Asp Glu Val His Ala Ala Asp Val Tyr Met  
 165 170 175  
 Arg Glu Tyr Leu Lys Val Val Leu Glu Trp Leu Gly Ala Tyr Arg Thr  
 180 185 190  
 Pro Val Ile Leu Met Ser Ala Thr Leu Pro Pro Ala Gln Arg His Glu  
 195 200 205  
 Leu Ala Leu Ala Tyr  
 210

<210> 259  
 <211> 252  
 <212> DNA  
 <213> Homo sapiens

<400> 259  
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg  
 60  
 ncatgggtgtg tgcacgtgtg cnactgtgtg tgcacgtgtg tgcacgtgtg tgcacgtgtg  
 120  
 tgtnggtgtg tatgcatgng tgtgtgcacg tgtgcactgn agtgtggggg gtatgcatgg  
 180  
 tgtgtgcaca tgagcactgt gtggtgtgtg tgcacgtgtg ggtgcacgtg tgcactgtgt  
 240  
 atgcaatggt gt  
 252

<210> 260  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens

<400> 260  
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys  
 1 5 10 15  
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met  
 20 25 30  
 Val Met Cys Thr Cys Ala Xaa Val Cys Xaa Cys Val Cys Met Xaa Val  
 35 40 45  
 Cys Thr Cys Ala Leu Xaa Cys Gly Val Tyr Ala Trp Cys Val His Met  
 50 55 60  
 Ser Thr Val Trp Cys Val Cys Met Val Xaa Cys Thr Cys Ala Leu Cys  
 65 70 75 80  
 Met Gln Trp Cys

<210> 261  
 <211> 1202  
 <212> DNA  
 <213> Homo sapiens

<400> 261  
 gctagcccg tgcggttcgt cgtcgatttg ctggcggcag tccccctgat cgtcttcggt  
 60  
 ctgtggggcg gcatcgtctt cggatcgtcg ggaatcatca acggttacgc gggggcctta  
 120  
 ttcaaagcgc tcggctggat tccgatcttt tccgaagatc cgtcgtgggc ctcggctact  
 180  
 ggcacgggtc accttgccag tctcgtcctg gccatcatga tctgccaat tatcactgct  
 240  
 gttagccgcg acgtcatgcc ccgaacgccc catgatcaag tcgaggccgc gctcgcctc  
 300  
 ggatcgacgc gctgggaggt catcaagctt gcagtgttcc cccactcgcg gtccggcatc  
 360



atttccggat ccatgttggg tctaggacgc gccctcggcg agaccctggc tgtcaccctc  
 420  
 atcctgcaga cgatgagccc catggcgctc aaacagaacc tcaacctgtc gatcttcgtc  
 480  
 ggtggtgaga cattcgcgtc gaagattgcc ggtaacttct ccgaggccat tagcgatccc  
 540  
 acctcgctgg gtgccctcgt ggcgtcggcc ctggccctgt tcgtcattac cttcgtggtc  
 600  
 aacgcgactg cccggttgat tgcggcgaag ggggttaagc gatgagcgcc accaccctg  
 660  
 accacatcac ccaccatggc gacaacacgc ccggacagct agatctctcc cgcccgtctg  
 720  
 gtaaaccggac tatcaagagc ggctgcgctt caacattcat gatcgtggcc accgtactgg  
 780  
 ctgttatccc actggcctgg ctgctcttcg cggccgtccg gcgcggcatc ggatcactat  
 840  
 tccacgcgtc gtggtggacc cactcgatgg atccctcctt cgacttggcc gagcagggcg  
 900  
 ccattccacgc tatcgtcgga acccttgaaa ttggccttat tacatcgatt atctcggtac  
 960  
 cgatcgctct gatgaccgcy atcttcctag tcgagtacgc ccgcggaact aagatcgcca  
 1020  
 aggtcattag cttcgccgtc gacgtgctaa ccggtgtacc ttcaatcgtc gcggccctct  
 1080  
 tcgtcttcgc cgtagtcggt accaccttcg gtggcaccca atccgcgtgg gcctcctcgt  
 1140  
 tggccctcat gatcctcatg gttccgacgg tgctgcgac aaccgaggaa atgctcaagc  
 1200  
 tt  
 1202

&lt;210&gt; 262

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 262

Ala	Ser	Pro	Val	Ala	Phe	Val	Val	Asp	Leu	Leu	Ala	Ala	Val	Pro	Ser
1				5				10						15	
Ile	Val	Phe	Gly	Leu	Trp	Gly	Gly	Ile	Val	Phe	Gly	Ser	Ser	Gly	Ile
		20					25					30			
Ile	Asn	Gly	Tyr	Ala	Gly	Ala	Leu	Phe	Lys	Ala	Leu	Gly	Trp	Ile	Pro
	35					40					45				
Ile	Phe	Ser	Glu	Asp	Pro	Ser	Trp	Ser	Ser	Ala	Thr	Gly	Thr	Val	Tyr
	50				55					60					
Leu	Ala	Ser	Leu	Val	Leu	Ala	Ile	Met	Ile	Leu	Pro	Ile	Ile	Thr	Ala
65				70				75						80	
Val	Ser	Arg	Asp	Val	Met	Pro	Arg	Thr	Pro	His	Asp	Gln	Val	Glu	Ala
		85				90					95				
Ala	Leu	Ala	Leu	Gly	Ser	Thr	Arg	Trp	Glu	Val	Ile	Lys	Leu	Ala	Val
	100						105				110				
Phe	Pro	His	Ser	Arg	Ser	Gly	Ile	Ile	Ser	Gly	Ser	Met	Leu	Gly	Leu
	115					120					125				
Gly	Arg	Ala	Leu	Gly	Glu	Thr	Leu	Ala	Val	Thr	Leu	Ile	Leu	Gln	Thr

```

      130              135              140
Met Ser Pro Met Ala Leu Lys Gln Asn Leu Asn Leu Ser Ile Phe Val
145              150              155              160
Gly Gly Glu Thr Phe Ala Ser Lys Ile Ala Gly Asn Phe Ser Glu Ala
      165              170              175
Ile Ser Asp Pro Thr Ser Leu Gly Ala Leu Val Ala Ser Ala Leu Ala
      180              185              190
Leu Phe Val Ile Thr Phe Val Val Asn Ala Thr Ala Arg Leu Ile Ala
      195              200              205
Ala Lys Gly Val Lys Arg
      210

```

&lt;210&gt; 263

&lt;211&gt; 424

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 263

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acgcgtgagt gctctgcgct ggaaacaacg gtgatagagc ccatccgccg tgaactttcc
60
gacgtggtgc tcgtgaacaa gctcgaaaag tatgtacgcg aacgtacctc ggaagacgtt
120
gcgcacatgg aagaggatgc ggaccagacg ggcaacgaca tcctcacgac gatcctgctg
180
tcgaactggg atccactatt ggatatgacg acgcaggatc atgtgctggc catgcaaaag
240
gcttatatgg cctcgccatt ccgtgccaat ttggacctgg catacccatc ttcgacgcca
300
caggcccagt cccagccggc gatgccgccg tgggagacag ggacctcagc cagtagcatg
360
gcggatgctc gtgaatttgc gctgctgaag ctgtacctgc gtagcttgct gcagaagcac
420
gann
424

```

&lt;210&gt; 264

&lt;211&gt; 99

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 264

```

Met Glu Glu Asp Ala Asp Gln Thr Gly Asn Asp Ile Leu Thr Thr Ile
1      5      10      15
Leu Leu Ser Asn Trp Asp Pro Leu Leu Asp Met Thr Thr Gln Asp His
      20      25      30
Val Leu Ala Met Gln Lys Ala Tyr Met Ala Ser Pro Phe Arg Ala Asn
      35      40      45
Leu Asp Leu Ala Tyr Pro Ser Ser Thr Pro Gln Ala Gln Ser Gln Pro
      50      55      60
Ala Met Pro Pro Trp Glu Thr Gly Thr Ser Ala Ser Ser Met Ala Asp
      65      70      75      80
Ala Arg Glu Phe Ala Leu Leu Lys Leu Tyr Leu Arg Ser Leu Leu Gln
      85      90      95
Lys His Xaa

```

<210> 265  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 265  
 ncgtacggcc ctggcgctccg catggacgag ggataccatt ccggcatgac ggtgccgggt  
 60  
 gccttcgact ccctcatcgg caagctcatc atcactgggt atagccgtga gcaagccctg  
 120  
 gtcgagctg cccgcgccct cgacgaaatc gtcacgacg gcatgccgac ggtcattccc  
 180  
 tttcaccagg cgggtggttca cgacccgggt ttcactgccg ccgacgggtg cttcggcgtc  
 240  
 ttaccgact ggatcgaaac cgagttcgac aacaagatcg agccatacac cgggtctctg  
 300  
 ggcgagtctg ccaattccga gcctcctcgt gaggtcgtcg tcgaggtcaa cggtaaacgc  
 360

<210> 266  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 266  
 Xaa Tyr Gly Pro Gly Val Arg Met Asp Glu Gly Tyr His Ser Gly Met  
 1 5 10 15  
 Thr Val Pro Gly Ala Phe Asp Ser Leu Ile Gly Lys Leu Ile Ile Thr  
 20 25 30  
 Gly Asp Ser Arg Glu Gln Ala Leu Ala Arg Ala Arg Ala Leu Asp  
 35 40 45  
 Glu Ile Val Ile Asp Gly Met Pro Thr Val Ile Pro Phe His Gln Ala  
 50 55 60  
 Val Val His Asp Pro Ala Phe Thr Ala Ala Asp Gly Cys Phe Gly Val  
 65 70 75 80  
 Phe Thr Asp Trp Ile Glu Thr Glu Phe Asp Asn Lys Ile Glu Pro Tyr  
 85 90 95  
 Thr Gly Ser Leu Gly Glu Ser Ala Asn Ser Glu Pro Pro Arg Glu Val  
 100 105 110  
 Val Val Glu Val Asn Gly Lys Arg  
 115 120

<210> 267  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

<400> 267  
 natcctcaac gtgtgttcag ttccacgcga aagatcatgt tcgtcatcgg atcgatgccg  
 60  
 ttaacgcac ctagtcaatc caccgatggc gaccctggca aaaaatacga ggtgacttgg  
 120

ctagatctcg ggcaccttca ccctagtcgg cggggactcg tcaactatcac cacaactgtc  
 180  
 gatgatgacg tcatcacctc ttcccaggta aatgtcggca acctccaccg cggggatgaa  
 240  
 aaacttttctg aagctcgcga ttaccgccag attccgatgc ttgcatcacg tcatggctgg  
 300  
 acagctccat tcattggtga gaccggcgca gcccatgcc a tcgaggatgc gatgggcatt  
 360  
 accatcccaa ctgcgctggc atggatacga accctgctcg ctgagttcag cagaatcacc  
 420  
 tcacacttca catttttctc atgggtaggc catcactgtg atgatgccgg c  
 471

<210> 268

<211> 157

<212> PRT

<213> Homo sapiens

<400> 268

Xaa	Pro	Gln	Arg	Val	Phe	Ser	Ser	Thr	Arg	Lys	Ile	Met	Phe	Val	Ile
1				5					10					15	
Gly	Ser	Met	Pro	Leu	Thr	His	Pro	Ser	Gln	Ser	Thr	Asp	Gly	Asp	Pro
			20					25					30		
Gly	Lys	Lys	Tyr	Glu	Val	Thr	Trp	Leu	Asp	Leu	Gly	His	Leu	His	Pro
	35						40					45			
Ser	Arg	Pro	Gly	Leu	Val	Thr	Ile	Thr	Thr	Thr	Val	Asp	Asp	Asp	Val
	50					55					60				
Ile	Thr	Ser	Ser	Gln	Val	Asn	Val	Gly	Asn	Leu	His	Arg	Gly	Asp	Glu
65					70				75					80	
Lys	Leu	Phe	Glu	Ala	Arg	Asp	Tyr	Arg	Gln	Ile	Pro	Met	Leu	Ala	Ser
				85					90					95	
Arg	His	Gly	Trp	Thr	Ala	Pro	Phe	Ile	Gly	Glu	Thr	Gly	Ala	Ala	His
				100					105				110		
Ala	Ile	Glu	Asp	Ala	Met	Gly	Ile	Thr	Ile	Pro	Thr	Arg	Val	Ala	Trp
		115					120					125			
Ile	Arg	Thr	Leu	Leu	Ala	Glu	Phe	Ser	Arg	Ile	Thr	Ser	His	Phe	Thr
	130						135					140			
Phe	Leu	Ser	Trp	Val	Gly	His	His	Cys	Asp	Asp	Ala	Gly			
145					150					155					

<210> 269

<211> 387

<212> DNA

<213> Homo sapiens

<400> 269

acgcgtgtcg tgtttccaga aaaaaccaat aaattagagt ttatggtaga agtgattgct  
 60  
 gatatgacgg taatcaatcc atttgatttc tttgtggaaa gctacgcaga agactacca  
 120  
 tttgcttatg acaaagctct taaaaaagag ttagaacctt atttacaggt ttctgaacct  
 180  
 tgttcgttac tcgacaaatg gctgtctggt gttgatcgtg aaaaaacacc gatcaatgat  
 240

tttctagtcg caataaacag tcgccttgcc ggtgatattg gctatgggtat tcgcttagaa  
 300  
 ccgggcggttc agtcacctga agaaacgctc acattaatga aaggctcttg tcgcgatacc  
 360  
 tcgggggttat tggttcaaact actacgc  
 387

<210> 270  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

<400> 270  
 Thr Arg Val Val Phe Pro Glu Lys Thr Asn Lys Leu Glu Phe Met Val  
 1 5 10 15  
 Glu Val Ile Ala Asp Met Thr Val Ile Asn Pro Phe Asp Phe Phe Val  
 20 25 30  
 Glu Ser Tyr Ala Glu Asp Tyr Pro Phe Ala Tyr Asp Lys Ala Leu Lys  
 35 40 45  
 Lys Glu Leu Glu Pro Tyr Leu Gln Val Ser Glu Pro Cys Ser Leu Leu  
 50 55 60  
 Asp Lys Trp Leu Ser Gly Val Asp Arg Glu Lys Thr Pro Ile Asn Asp  
 65 70 75 80  
 Phe Leu Val Ala Ile Asn Ser Arg Leu Ala Gly Asp Ile Gly Tyr Gly  
 85 90 95  
 Ile Arg Leu Glu Pro Gly Val Gln Ser Pro Glu Glu Thr Leu Thr Leu  
 100 105 110  
 Met Lys Gly Ser Cys Arg Asp Thr Ser Gly Leu Leu Val Gln Ile Leu  
 115 120 125  
 Arg

<210> 271  
 <211> 443  
 <212> DNA  
 <213> Homo sapiens

<400> 271  
 gccggcacca acggaaagtc ctctaccgcg cgcgatggtcg attcgctttt gcgtgccttc  
 60  
 caccgccgag tgggtttggt aaccagccca cacctgcagc gcgttactga gcgcacggc  
 120  
 attgatggcc agcccattca cccgcgcgat tatgtacgca tctggcacga gattaagcca  
 180  
 tttgtggaat tggctgatgc cgaatcggac gtgcctatgt ctaagttcga ggtcttcgtg  
 240  
 ggctgtcct atgctgcgtt tgccgacgcc cccggggacg tcgctgtcgt cgaagtcggc  
 300  
 cttggcggac gttgggacgc taccaatgtg gtcaacgcgg atgtctctgt cattaccccg  
 360  
 gtgggcatgg accacacgga ttacctgggg gagacgatca ctgaaatcgc aggcgagaaa  
 420  
 gctggcatta ttaagccacg cgt  
 443

<210> 272  
 <211> 147  
 <212> PRT  
 <213> Homo sapiens

<400> 272  
 Ala Gly Thr Asn Gly Lys Ser Ser Thr Ala Arg Met Val Asp Ser Leu  
 1 5 10 15  
 Leu Arg Ala Phe His Arg Arg Val Gly Leu Val Thr Ser Pro His Leu  
 20 25 30  
 Gln Arg Val Thr Glu Arg Ile Gly Ile Asp Gly Gln Pro Ile His Pro  
 35 40 45  
 Arg Asp Tyr Val Arg Ile Trp His Glu Ile Lys Pro Phe Val Glu Met  
 50 55 60  
 Val Asp Ala Glu Ser Asp Val Pro Met Ser Lys Phe Glu Val Phe Val  
 65 70 75 80  
 Gly Leu Ser Tyr Ala Ala Phe Ala Asp Ala Pro Gly Asp Val Ala Val  
 85 90 95  
 Val Glu Val Gly Leu Gly Gly Arg Trp Asp Ala Thr Asn Val Val Asn  
 100 105 110  
 Ala Asp Val Ser Val Ile Thr Pro Val Gly Met Asp His Thr Asp Tyr  
 115 120 125  
 Leu Gly Glu Thr Ile Thr Glu Ile Ala Gly Glu Lys Ala Gly Ile Ile  
 130 135 140  
 Lys Pro Arg  
 145

<210> 273  
 <211> 864  
 <212> DNA  
 <213> Homo sapiens

<400> 273  
 caaagtaaga ctgcttcaaa ttttgtgttc tgctctgcag ctgctcccc cctgctgtcg  
 60  
 aagagaagcc aaagcccccc cccccacct caaaggctcg gaagtctggc atccctactt  
 120  
 ccgagcctgg atcccagtaa ggatcttgcc ctccctgcaa caccgagtgc cttagacagc  
 180  
 tgctgcctga gaactggcct ccagccggtg tcctcattcc atggggctcc ctgctgactg  
 240  
 catttctga tctgggatga tgtttaccag cccaaaacca gtcattgttct tccaaaagct  
 300  
 tctctttgat agaattttga ggccatgcc cctcccttcc agtcacatg gaattccaga  
 360  
 atcagtcaca gcctctgatt ttttccaaga agagattgcc ttcaccattg ttaaattgtc  
 420  
 gcctgtacgg cagagacatg gtggtctgca caagcctgga caagttcttc catattgatg  
 480  
 gtgggagcaa cccctgtaat ctactccttg gaaggatttt ttgctttgct tatgaaaagc  
 540  
 tgtgcttgag acttaggtac ttttctcacg tggacacact gatcccatcc catattgcat  
 600

ctttgaagag atggatatca agtacacttt ggtagctgaa ataatcatat ctttctgatg  
 660  
 tctattgtat ctcctttgag gaaaagaaca cacattttta atggagattg gctgctttca  
 720  
 ggtatgtgtg tctatcattg aaagagcatg gactcaaaca tcagccctga gttcttgagt  
 780  
 ccacccaact cccatcttct tgtggcacag gaaagctgcc ctctccctct cccaccacac  
 840  
 tcctgactaa tgcccttcac gcgt  
 864

<210> 274  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 274  
 Met Trp Thr Gly Arg Glu Val Ala Trp Pro Gln Asn Ser Ile Lys Glu  
 1 5 10 15  
 Lys Leu Leu Glu His Asp Trp Phe Trp Ala Gly Lys His His Pro  
 20 25 30  
 Arg Ser Gly Asn Ala Val Ser Arg Glu Pro His Gly Met Arg Thr Pro  
 35 40 45  
 Ala Gly Gly Gln Phe Ser Gly Ser Ser Cys Leu Arg His Ser Val Leu  
 50 55 60  
 Gln Gly Gly Gln Asp Pro Tyr Trp Asp Pro Gly Ser Glu Val Gly Met  
 65 70 75 80  
 Pro Asp Phe Arg Ala Phe Glu Val Gly Gly Gly Phe Gly Phe Ser  
 85 90 95  
 Ser Thr Ala Gly Ser Glu Leu Gln Ser Arg Thr Gln Asn Leu Lys  
 100 105 110  
 Gln Ser Tyr Phe  
 115

<210> 275  
 <211> 911  
 <212> DNA  
 <213> Homo sapiens

<400> 275  
 naaatttaaa ggaacctccc ttctataacg gagagtattt attgcagctt tcctttctgt  
 60  
 ttattttcag gaatgaaagg aattacccag cttctgctt ttatacctac agctgaaagt  
 120  
 aattcctttc agcctcaggt gaagactttg ccattctcaa ttgatgctaa acagcagttg  
 180  
 caacggaaaa tccagaagaa gcagcaagaa cagaaactac aatccccttt gccaggagaa  
 240  
 tctgcagcaa aaaagtcaga aagtgtaca agcaatggag tgactaatct tcctaattga  
 300  
 aatccttcaa tcctttctcc tcaacctatt ggtatcgttg tggcagctgt ccctagtccc  
 360  
 attccggtcc agcggactag gcaattggta acttcaccga gtccaatgag ttcttctnga  
 420

cggcaaagtt cttccctca atgtacaggt ggtcactcag cacatgcagt ctgtgaaaca  
 480  
 ggcaccaaag actccccaga acgttcacgc agtcctggtg ggaatcggtc tgcccgccac  
 540  
 cgttaccctc agatcttacc caaaccagcg aacaccagtg cactcaccat tcgctctcca  
 600  
 actactgtcc tctttactag tagtcccatc aaaactgctg ttgtaccgcg ttcacacatg  
 660  
 agttctctaa atgtggtgaa aatgacaaca atatccctca caccagcaa cagtaacacc  
 720  
 cctcttaaac attctgcctc agtcagcagt gctacaggaa caacagaaga atcaaggagt  
 780  
 gttccacaga tcaagaatgg ttctgtcgtg tcgcttcagt ctctggggtc caggagcagc  
 840  
 agtgccggggg gaacatctgc tgtggaagtc aaagtggaac ccgaaacatc atcagatgag  
 900  
 catcctgtac a  
 911

<210> 276

<211> 279

<212> PRT

<213> Homo sapiens

<400> 276

Met	Lys	Gly	Ile	Thr	Gln	Pro	Ser	Ala	Phe	Ile	Pro	Thr	Ala	Glu	Ser
1			5						10				15		
Asn	Ser	Phe	Gln	Pro	Gln	Val	Lys	Thr	Leu	Pro	Ser	Pro	Ile	Asp	Ala
			20					25					30		
Lys	Gln	Gln	Leu	Gln	Arg	Lys	Ile	Gln	Lys	Lys	Gln	Gln	Glu	Gln	Lys
			35				40						45		
Leu	Gln	Ser	Pro	Leu	Pro	Gly	Glu	Ser	Ala	Ala	Lys	Lys	Ser	Glu	Ser
			50				55					60			
Ala	Thr	Ser	Asn	Gly	Val	Thr	Asn	Leu	Pro	Asn	Gly	Asn	Pro	Ser	Ile
65					70					75				80	
Leu	Ser	Pro	Gln	Pro	Ile	Gly	Ile	Val	Val	Ala	Ala	Val	Pro	Ser	Pro
				85					90					95	
Ile	Pro	Val	Gln	Arg	Thr	Arg	Gln	Leu	Val	Thr	Ser	Pro	Ser	Pro	Met
			100					105					110		
Ser	Ser	Ser	Xaa	Arg	Gln	Ser	Ser	Ser	Pro	Gln	Cys	Thr	Gly	Gly	His
			115				120					125			
Ser	Ala	His	Ala	Val	Cys	Glu	Thr	Gly	Thr	Lys	Asp	Ser	Pro	Glu	Arg
			130				135				140				
Ser	Ser	Ser	Pro	Gly	Gly	Asn	Arg	Ser	Ala	Arg	His	Arg	Tyr	Pro	Gln
145					150					155				160	
Ile	Leu	Pro	Lys	Pro	Ala	Asn	Thr	Ser	Ala	Leu	Thr	Ile	Arg	Ser	Pro
				165					170					175	
Thr	Thr	Val	Leu	Phe	Thr	Ser	Ser	Pro	Ile	Lys	Thr	Ala	Val	Val	Pro
			180					185					190		
Ala	Ser	His	Met	Ser	Ser	Leu	Asn	Val	Val	Lys	Met	Thr	Thr	Ile	Ser
			195				200					205			
Leu	Thr	Pro	Ser	Asn	Ser	Asn	Thr	Pro	Leu	Lys	His	Ser	Ala	Ser	Val
			210			215					220				
Ser	Ser	Ala	Thr	Gly	Thr	Thr	Glu	Glu	Ser	Arg	Ser	Val	Pro	Gln	Ile



225                      230                      235                      240  
 Lys Asn Gly Ser Val Val Ser Leu Gln Ser Pro Gly Ser Arg Ser Ser  
                                  245                      250                      255  
 Ser Ala Gly Gly Thr Ser Ala Val Glu Val Lys Val Glu Pro Glu Thr  
                                  260                      265                      270  
 Ser Ser Asp Glu His Pro Val  
                                  275

<210> 277  
 <211> 652  
 <212> DNA  
 <213> Homo sapiens

<400> 277  
 nnaccggtgg ggactctcgc tgaggctcctt aatggccctt ctcgtgtccc ggacggcacc  
 60  
 atgaaccttg ttggtgggct gcgtcaggca atggccacca ctggttactc ggaggtcaaa  
 120  
 gagttccagc gcatcgagct gacgattcgc taaccgttcc accacgcaga atggtgttcc  
 180  
 ggtgagcggg tggatagcta gccttcggcc atgagtgaag tgcccgatga attggtcgtg  
 240  
 ttgcgtggcg cgattgacaa catggacgcc gccctcatcc atctgcttgc cgaaagggtc  
 300  
 cggattactc gcgaggtagg ccgcctcaag gcggagtgcg gtttacctcc ggccgacccc  
 360  
 gcccgtgagg ctgagcagat cgcgcggttg cggcagttag cggtcgagtc gaacctcgac  
 420  
 ccgaattcg cgcagaaggt catcacgttc atcgtggccg aggtggtgcg tcaccacgaa  
 480  
 gctattgctg acgattctgg cgacgactct ggagtggcgg atacggggga ggcggatgtc  
 540  
 cctgggtcgg gcagctgagt tacagatcag gcgatgacgt cgccctggtg caccttcgac  
 600  
 gggattccga cgacgactgt gccgggggcg acatccttga cgaccaacgc gt  
 652

<210> 278  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 278  
 Met Ser Glu Val Pro Asp Glu Leu Val Val Leu Arg Gly Ala Ile Asp  
 1                      5                      10                      15  
 Asn Met Asp Ala Ala Leu Ile His Leu Leu Ala Glu Arg Phe Arg Ile  
                                  20                      25                      30  
 Thr Arg Glu Val Gly Arg Leu Lys Ala Glu Cys Gly Leu Pro Pro Ala  
                                  35                      40                      45  
 Asp Pro Ala Arg Glu Ala Glu Gln Ile Ala Arg Leu Arg Gln Leu Ala  
                                  50                      55                      60  
 Val Glu Ser Asn Leu Asp Pro Glu Phe Ala Gln Lys Val Ile Thr Phe  
 65                      70                      75                      80  
 Ile Val Ala Glu Val Val Arg His His Glu Ala Ile Ala Asp Asp Ser

	85		90		95
Gly Asp Asp Ser Gly Val Ala Asp Thr Gly Glu Ala Asp Val Pro Gly					
	100		105		110
Ser Gly Ser					
	115				

<210> 279  
 <211> 348  
 <212> DNA  
 <213> Homo sapiens

<400> 279  
 cgggagggtca cacaagcatt caaacatag cagatggtaa atgttatgtt atgtgtattt  
 60  
 taccacaatc cttaaaaaga aaagaaagaa aggcataatg aaccctagt tacctctcat  
 120  
 ccagcttcaa aattgtcagt gcatgggtcaa tcttgtctta tctgcccctc acccaccctt  
 180  
 ttccagaaag aagaccaga ggattccaca tctgcctgga aaccacgacc agtctcgact  
 240  
 ggaagtgtgt gttaatgttg catgtattca taaaacctct aggcatttct agtgtccctc  
 300  
 agaatttttc caaattcagg caaacacaga aattacttcc aaaaattt  
 348

<210> 280  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 280  
 Met Cys Ile Leu Pro Gln Ser Leu Lys Arg Lys Glu Arg Lys Ala Tyr  
 1 5 10 15  
 Gly Thr Pro Ser Tyr Leu Ser Ser Ser Phe Lys Ile Val Ser Ala Trp  
 20 25 30  
 Ser Ile Leu Ser Tyr Leu Pro Leu Thr His Pro Phe Pro Glu Arg Arg  
 35 40 45  
 Pro Arg Gly Phe His Ile Cys Leu Glu Thr Thr Thr Ser Leu Asp Trp  
 50 55 60  
 Lys Leu Leu Leu Met Leu His Val Phe Ile Lys Pro Leu Gly Ile Ser  
 65 70 75 80  
 Ser Val Pro Gln Asn Phe Ser Lys Phe Arg Gln Thr Gln Lys Leu Leu  
 85 90 95  
 Pro Lys Ile

<210> 281  
 <211> 384  
 <212> DNA  
 <213> Homo sapiens

<400> 281  
 agatctgcgc agatcgataa tggattaaag actcttgacg ctggagtcac cgagatgaac  
 60

aacaaggtgt tgggggcaac gaaggctgtc ggtgattcca ccactaccgt caaccaggtg  
120  
aattctgcgt taggaantgc cgactcagcg gcagagaaga cgtcgagcgc cgttactcag  
180  
acgcgcgtgg gtgcccaggc gattaccggc gctgctcaaa atgtcatggc tgattcccaa  
240  
gctgtcaact cagccatggg tccgcttatt aataacgtga caaagaatct tcctaccttg  
300  
caaaaacagg ccaggaatct cgtgtcagtg aacggtaccc tgcagaaccc caacggtgat  
360  
tctgtcatta agattcaaca gacc  
384

<210> 282  
<211> 110  
<212> PRT  
<213> Homo sapiens

<400> 282  
Met Asn Asn Lys Val Leu Gly Ala Thr Lys Ala Val Gly Asp Ser Thr  
1 5 10 15  
Thr Thr Val Asn Gln Val Asn Ser Ala Leu Gly Xaa Ala Asp Ser Ala  
20 25 30  
Ala Glu Lys Thr Ser Ser Ala Val Thr Gln Thr Arg Val Gly Ala Gln  
35 40 45  
Ala Ile Thr Gly Ala Ala Gln Asn Val Met Ala Asp Ser Gln Ala Val  
50 55 60  
Asn Ser Ala Met Val Pro Leu Ile Asn Asn Val Thr Lys Asn Leu Pro  
65 70 75 80  
Thr Leu Gln Lys Gln Ala Arg Asn Leu Val Ser Val Asn Gly Thr Leu  
85 90 95  
Gln Asn Pro Asn Gly Asp Ser Val Ile Lys Ile Gln Gln Thr  
100 105 110

<210> 283  
<211> 426  
<212> DNA  
<213> Homo sapiens

<400> 283  
cgcgtagacc aatgtgagac ggccgtcacc aagggtcatgc gcgacaagtc gggttgtagc  
60  
ggaccggata ttgtgcgtcg cgagctgcgc catgtcgtga cgagcggcac gattgtcgat  
120  
ggaagcgtac tggctgacga attgagcagc tactgcatga gtatcaagga gcacgtccgc  
180  
tctgatggcc tatccgagtt tggcatctgc accctcgacg ccgccaccgc cgagttccga  
240  
tacatgacat tcgtcgacga tgccgtgctg tcacaactcg agacattgct gcgttctcta  
300  
cgcatcaagg aagtcttgca tgaaaaaggg gtcattgtgc cttccacgct gcgcttgatc  
360  
cgcaacgcgg tgcccaccac ctgcaaatt accatgctca agcctgatac cgaattgtcg  
420

gagaga

426

&lt;210&gt; 284

&lt;211&gt; 142

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 284

```

Arg Val Asp Gln Cys Glu Thr Ala Val Thr Lys Gly Met Arg Asp Lys
 1             5             10             15
Ser Val Gly Ser Gly Pro Asp Ile Val Arg Arg Glu Leu Arg His Val
      20             25             30
Val Thr Ser Gly Thr Ile Val Asp Gly Ser Val Leu Ala Asp Glu Leu
      35             40             45
Ser Ser Tyr Cys Met Ser Ile Lys Glu His Val Arg Ser Asp Gly Leu
      50             55             60
Ser Glu Phe Gly Ile Cys Thr Leu Asp Ala Ala Thr Ala Glu Phe Arg
      65             70             75             80
Tyr Met Thr Phe Val Asp Asp Ala Val Leu Ser Gln Leu Glu Thr Leu
      85             90             95
Leu Arg Ser Leu Arg Ile Lys Glu Val Leu His Glu Lys Gly Val Met
      100            105            110
Leu Pro Ser Thr Leu Arg Leu Ile Arg Asn Ala Val Pro Thr Thr Cys
      115            120            125
Gln Ile Thr Met Leu Lys Pro Asp Thr Glu Leu Ser Glu Arg
      130            135            140

```

&lt;210&gt; 285

&lt;211&gt; 345

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 285

```

acgcgtgcag tcccttaccg acatgctggc agatgagctc gacggcagcc gcttcaccgg
60
cgatttctca gaaatctaca aacgtcagaa ctcgatcttc ggcgatgtaa ggaataactt
120
ttacaaaaaa ggataaccga tcatcaacgt agcgaatggg gtattgcgca agatttcact
180
ggtaagcgca ggcaatgcag acaatgtgaa aggtcaggcc ctgttcttcc gcggtgtggc
240
gcatttcgaa ctcgtcggtt tgtttgcaca accctggggg tatacttcgg acaattcaca
300
ctacggcatc ccgctccgca atgaaatcgt aattgggttct attcn
345

```

&lt;210&gt; 286

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 286

```

Met Leu Ala Asp Glu Leu Asp Gly Ser Arg Phe Thr Gly Asp Phe Ser

```

```

      1           5           10           15
Glu Ile Tyr Lys Arg Gln Asn Ser Ile Phe Gly Asp Val Arg Asn Asn
      20           25           30
Phe Tyr Lys Lys Gly Tyr Arg Ile Ile Asn Val Ala Asn Gly Val Leu
      35           40           45
Arg Lys Ile Ser Leu Val Ser Ala Gly Asn Ala Asp Asn Val Lys Gly
      50           55           60
Gln Ala Leu Phe Phe Arg Gly Val Ala His Phe Glu Leu Val Arg Leu
65           70           75           80
Phe Ala Gln Pro Trp Gly Tyr Thr Ser Asp Asn Ser His Tyr Gly Ile
      85           90           95
Pro Leu Arg Asn Glu Ile Val Ile Gly Ser Ile
      100           105

```

<210> 287  
 <211> 1379  
 <212> DNA  
 <213> Homo sapiens

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<400> 287
nnttaactgc ccctttgcag tctttattct gggacattag cactgtctgg ttatcttgc
60
tcagttgagg gattcgggac aatagcagtg ctgatggtta tgttggcgat ttccctgttt
120
gttttgcagg tcacggccag gggctttggg ccgctgttac agtttgccta cactgccaag
180
ctgttactca gcagagaaaa catccgcgag gtcacccgct gtgctgagtt cctgcgcatg
240
cacaacctgg aggactcctg cttcagcttc ctgcagaccc agctcctgaa cagtgaggat
300
ggcctgtttg tgtgccggaa ggatgctgcg tgccagcgcc cacacgagga ctgcgagaac
360
tctgcaggag aggaggagga tgaagaggag gagacgatgg attcagagac ggccaagatg
420
gcttgcccca gggaccagat gcttcagag cccatcagct ttgaggccgc cgccatcccc
480
gtagcagaga aggaagaagc cctgctgccc gagcctgacg tgcccacaga caccaaggag
540
agctcagaaa aggacgcgtt aacgcagtac ccagataca agaaatacca gcttgcatgt
600
accaagaatg tctataatgc atcatcacac agtacctcag gttttgcaag cacattccgg
660
gaagataact ctagcaacag cctcaagccg gggcttgcca gggggcagat taaaagtgg
720
ccgcccagtg aagagaatga ggaagagagc atcacgctct gcctgtctgg agatgagcct
780
gacgccaagg acagagcggg ggatgtcgag atggaccgga aacagcccag ccctgcccct
840
acccccacgg cccagctgg ggccgcctgc ctggagagat ccaggagcgt ggctcgccc
900
tcttgcttaa ggtctctgtt cagcataacg aaaagtgtgg agctgtctgg cctgcccagt
960
acatctcagc agcactttgc caggagtcca gcctgccctt ttgacaaggg gatcactcag
1020

```

ggtgacctta aaactgacta cacccttttc acaggaatt atggacagcc ccacgtgggc  
 1080  
 cagaaggagg tgtccaactt caccatgggg tcgcccctca gggggcctgg gttggaggct  
 1140  
 ctctgtaaag aggagggaga gctggaccgg aggagcgtga tcttctctc cagcgtttgt  
 1200  
 gaccaagtga gcacctcggt gcattcttat tctgggggtga gcagtttgga caaagacctc  
 1260  
 tctgagccgg tgccaaaggg tctgtgggtg ggagccggcc agtccctccc cagctcgag  
 1320  
 gcctactccc acggtgggct gatggccgac cacttgccag gaaggatgag gcccaacac  
 1379

<210> 288

<211> 428

<212> PRT

<213> Homo sapiens

<400> 288

Met	Val	Met	Leu	Ala	Ile	Ser	Leu	Phe	Val	Leu	Gln	Val	Thr	Ala	Arg
1				5					10					15	
Gly	Phe	Gly	Pro	Leu	Leu	Gln	Phe	Ala	Tyr	Thr	Ala	Lys	Leu	Leu	Leu
			20					25					30		
Ser	Arg	Glu	Asn	Ile	Arg	Glu	Val	Ile	Arg	Cys	Ala	Glu	Phe	Leu	Arg
		35					40					45			
Met	His	Asn	Leu	Glu	Asp	Ser	Cys	Phe	Ser	Phe	Leu	Gln	Thr	Gln	Leu
	50					55					60				
Leu	Asn	Ser	Glu	Asp	Gly	Leu	Phe	Val	Cys	Arg	Lys	Asp	Ala	Ala	Cys
65					70				75					80	
Gln	Arg	Pro	His	Glu	Asp	Cys	Glu	Asn	Ser	Ala	Gly	Glu	Glu	Glu	Asp
				85					90					95	
Glu	Glu	Glu	Glu	Thr	Met	Asp	Ser	Glu	Thr	Ala	Lys	Met	Ala	Cys	Pro
			100					105					110		
Arg	Asp	Gln	Met	Leu	Pro	Glu	Pro	Ile	Ser	Phe	Glu	Ala	Ala	Ala	Ile
		115					120					125			
Pro	Val	Ala	Glu	Lys	Glu	Glu	Ala	Leu	Leu	Pro	Glu	Pro	Asp	Val	Pro
		130				135					140				
Thr	Asp	Thr	Lys	Glu	Ser	Ser	Glu	Lys	Asp	Ala	Leu	Thr	Gln	Tyr	Pro
145					150					155				160	
Arg	Tyr	Lys	Lys	Tyr	Gln	Leu	Ala	Cys	Thr	Lys	Asn	Val	Tyr	Asn	Ala
				165					170					175	
Ser	Ser	His	Ser	Thr	Ser	Gly	Phe	Ala	Ser	Thr	Phe	Arg	Glu	Asp	Asn
		180					185						190		
Ser	Ser	Asn	Ser	Leu	Lys	Pro	Gly	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Ser
		195				200						205			
Glu	Pro	Pro	Ser	Glu	Glu	Asn	Glu	Glu	Ser	Ile	Thr	Leu	Cys	Leu	
	210					215					220				
Ser	Gly	Asp	Glu	Pro	Asp	Ala	Lys	Asp	Arg	Ala	Gly	Asp	Val	Glu	Met
225					230				235					240	
Asp	Arg	Lys	Gln	Pro	Ser	Pro	Ala	Pro	Thr	Pro	Thr	Ala	Pro	Ala	Gly
				245					250					255	
Ala	Ala	Cys	Leu	Glu	Arg	Ser	Arg	Ser	Val	Ala	Ser	Pro	Ser	Cys	Leu
			260						265				270		
Arg	Ser	Leu	Phe	Ser	Ile	Thr	Lys	Ser	Val	Glu	Leu	Ser	Gly	Leu	Pro

275	280	285
Ser Thr Ser Gln Gln His Phe Ala Arg Ser Pro Ala Cys Pro Phe Asp		
290	295	300
Lys Gly Ile Thr Gln Gly Asp Leu Lys Thr Asp Tyr Thr Pro Phe Thr		
305	310	315
Gly Asn Tyr Gly Gln Pro His Val Gly Gln Lys Glu Val Ser Asn Phe		
325	330	335
Thr Met Gly Ser Pro Leu Arg Gly Pro Gly Leu Glu Ala Leu Cys Lys		
340	345	350
Gln Glu Gly Glu Leu Asp Arg Arg Ser Val Ile Phe Ser Ser Ser Ala		
355	360	365
Cys Asp Gln Val Ser Thr Ser Val His Ser Tyr Ser Gly Val Ser Ser		
370	375	380
Leu Asp Lys Asp Leu Ser Glu Pro Val Pro Lys Gly Leu Trp Val Gly		
385	390	395
Ala Gly Gln Ser Leu Pro Ser Ser Gln Ala Tyr Ser His Gly Gly Leu		
405	410	415
Met Ala Asp His Leu Pro Gly Arg Met Arg Pro Asn		
420	425	

&lt;210&gt; 289

&lt;211&gt; 822

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 289

ngcattaccg ggctgaagac ggggtgctcat gacctcaacg atataggcta ttgctagaac  
 60  
 cacgccggcc caccgcgcgc aaagcgcaga caccgcacca ggaggggtca catggctgat  
 120  
 agcaagtcga aggcgaagga cgagcgcact gccgatgaga tcaggcggga tattgcagcg  
 180  
 acccgtgctt gcctggcagc cgggggtggag aacctcgtgg aggaggtgca tccggcaacc  
 240  
 ctcaagcgtg aagcatctga tcgtgcccgt gattttgtgc aggggtgagtt tgatcaggtc  
 300  
 aagagccagg tcaaagatga gaaatggtgg cgcgtgcagc ggatcgcgat ggccgcagga  
 360  
 gtgctcgctg ccggcgtcgt cagcattatt gtgctgcgcg cgatagtcgg tcgcgcaacg  
 420  
 ggcgctaccg ctgctcgcaa gcttgagaag ctgcagcttt ctcaggcgaa gcgggttcga  
 480  
 aaagatgcc aagcagcgtag taaggaagat gaaaaggcag ccaagaaaaa tgccaagctc  
 540  
 ggcaagaaga acgctaagaa gtacggcaag ctcgataccg atgactcgtc ggtaagcaac  
 600  
 cttgccgaga aaatgctcaa acaggccgcc gtgctgcgtg cacaggcggc tgccggggcg  
 660  
 tgagaacagt gccgcctagc aaacagcggc cacagcgcaa aacaggtttg gctccgaccc  
 720  
 atggtggacc ggagccaaac tgtgttaccg catcatttga taccgccagc agccaggcct  
 780  
 gcgacaatgc gacgctggaa taccagcacc atgatgacta gt  
 822

<210> 290  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 290  
 Met Ala Asp Ser Lys Ser Lys Ala Lys Asp Glu Arg Thr Ala Asp Glu  
 1 5 10 15  
 Ile Arg Arg Asp Ile Ala Ala Thr Arg Ala Cys Leu Ala Ala Gly Val  
 20 25 30  
 Glu Asn Leu Val Glu Glu Val His Pro Ala Thr Leu Lys Arg Glu Ala  
 35 40 45  
 Ser Asp Arg Ala Arg Asp Phe Val Gln Gly Glu Phe Asp Gln Val Lys  
 50 55 60  
 Ser Gln Val Lys Asp Glu Lys Trp Trp Arg Val Gln Arg Ile Ala Met  
 65 70 75 80  
 Ala Ala Gly Val Leu Ala Ala Gly Val Val Ser Ile Ile Val Leu Arg  
 85 90 95  
 Ala Ile Val Gly Arg Ala Thr Gly Ala Thr Ala Arg Arg Lys Leu Glu  
 100 105 110  
 Lys Leu Gln Leu Ser Gln Ala Lys Arg Val Arg Lys Asp Ala Lys Gln  
 115 120 125  
 Arg Ser Lys Glu Asp Glu Lys Ala Ala Lys Lys Asn Ala Lys Leu Gly  
 130 135 140  
 Lys Lys Asn Ala Lys Lys Tyr Gly Lys Leu Asp Thr Asp Asp Ser Ser  
 145 150 155 160  
 Val Ser Asn Leu Ala Glu Lys Met Leu Lys Gln Ala Ala Val Leu Arg  
 165 170 175  
 Ala Gln Ala Ala Ala Gly Ala  
 180

<210> 291  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
 ctccacgccg acaagactta cgacgggcgt cgctgccggg ctgagtgcgg ggcccgtcc  
 60  
 atcaccccc gcacgctcg ccgcggcgtg gagaccagcg agcgcttggg ccggtatcgc  
 120  
 tgggtcgctg agcgacctt cgctggctc aaccgcttcc ggcgctcgc catccgctac  
 180  
 gacgggcgtg ctgacatcca cgaagccttc gtgacccctg gctgcgcct catctgcctc  
 240  
 aaccagatca gacggttttg ttagtgctg taaagggaga atggctgcag ctgggctatc  
 300  
 tgctccctcg tcaaccagaa acaggctgct catcctcact caacaacgcg t  
 351

<210> 292  
 <211> 87  
 <212> PRT



<213> Homo sapiens

<400> 292

```

Leu His Ala Asp Lys Thr Tyr Asp Gly Arg Arg Cys Arg Ala Glu Cys
 1           5           10           15
Arg Ala Arg Ser Ile Thr Pro Arg Ile Ala Arg Arg Gly Val Glu Thr
          20           25           30
Ser Glu Arg Leu Gly Arg Tyr Arg Trp Val Val Glu Arg Thr Phe Ala
          35           40           45
Trp Leu Asn Arg Phe Arg Arg Leu Ala Ile Arg Tyr Glu Arg Arg Ala
          50           55           60
Asp Ile His Glu Ala Phe Val Ile Leu Gly Cys Ala Leu Ile Cys Leu
65           70           75           80
Asn Gln Ile Arg Arg Phe Cys
          85

```

<210> 293

<211> 716

<212> DNA

<213> Homo sapiens

<400> 293

```

nncttcacca caccggccat caacgcacct cctcgtgata acttgacctt ctgccgaacc
60
ggttaatcag tttagtggcg aggcattgaca cgttgacgag tcagctgtgg tacatgtgcg
120
gaacactcac aatgccacgg cggcatgttg ctgtcggtea cgacccttat ggtgatcgct
180
gtgagaaccc gaacggcaga tgcgattctg gcggcactgg atctgaacag gtttaaggtt
240
gcgaagactt tcgatgttcc agtgtgctgc atagctgggtg ccgggacagg taaaactcgt
300
gctgtcactc atcgcattgc ctacgggtgca gcgacaggca agcttgatcc gcgtcgtacc
360
ctcgcggtea cttttacgac taaggcagct ggcacgatga gaggtcgact cgccgatctg
420
gggggttggt gtgtgcaggc tcgcactatt cattctgcgg cgttgcgga gatcaagttt
480
ttctggcctc gtgcatataa ctgtgagttg ccaccgggtga gtgattctcg tttctcgatg
540
gtggcggaga cgacccatcg cattggtctg ggcaatgaca aggcgctgct gcgcgacttg
600
tccgccgaga tctcgtgggc gaaggctctca aatgtgccga ctgatcaata cgcacccctg
660
gctagggcgg aaggctcgggt ggtggcgga gtttcggcaa ctgacgtagg acgcgt
716

```

<210> 294

<211> 190

<212> PRT

<213> Homo sapiens

<400> 294

```

Met Leu Leu Ser Val Thr Thr Leu Met Val Ile Ala Val Arg Thr Arg

```

```

      1           5           10           15
Thr Ala Asp Ala Ile Leu Ala Ala Leu Asp Leu Asn Arg Phe Lys Val
      20           25           30
Ala Lys Thr Phe Asp Val Pro Val Cys Val Ile Ala Gly Ala Gly Thr
      35           40           45
Gly Lys Thr Arg Ala Val Thr His Arg Ile Ala Tyr Gly Ala Ala Thr
      50           55           60
Gly Lys Leu Asp Pro Arg Arg Thr Leu Ala Val Thr Phe Thr Thr Lys
      65           70           75           80
Ala Ala Gly Thr Met Arg Gly Arg Leu Ala Asp Leu Gly Val Val Gly
      85           90           95
Val Gln Ala Arg Thr Ile His Ser Ala Ala Leu Arg Gln Ile Lys Phe
      100          105          110
Phe Trp Pro Arg Ala Tyr Asn Cys Glu Leu Pro Pro Val Ser Asp Ser
      115          120          125
Arg Phe Ser Met Val Ala Glu Thr Thr His Arg Ile Gly Leu Gly Asn
      130          135          140
Asp Lys Ala Leu Leu Arg Asp Leu Ser Ala Glu Ile Ser Trp Ala Lys
      145          150          155          160
Val Ser Asn Val Pro Thr Asp Gln Tyr Ala Ser Leu Ala Arg Ala Glu
      165          170          175
Gly Arg Val Val Ala Gly Val Ser Ala Thr Asp Val Gly Arg
      180          185          190

```

&lt;210&gt; 295

&lt;211&gt; 417

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 295

```

ttcatatcag gcagtagccg agtccatgag atcaacaacg tcagcgtatc tttcacccat
60
tctggagtgac accttctcat gggagaaagc ggatcaggaa aaagcaccct catcaatctc
120
ctagctgggtc tggatacccc agattcgggg tccgtctacg cagaaggcgt caccgtatct
180
gattcagagcg aggcgagcag agcccaattt cgattacgcc acatcgccgt catcttccag
240
gacgacaacc tcattcgtga gttgaccaat accgagaata ttgcgctacc cctgtgggag
300
cagggcacat cgaagtccga tgccactgaa atcgccacg aagccatgag aaaactagga
360
atcgagtcac tgggcagacg ctaccccgag gaggtctcgg gtggccaacg gcaacgc
417

```

&lt;210&gt; 296

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 296

```

Phe Ile Ser Gly Ser Thr Arg Val His Ala Ile Asn Asn Val Ser Val
      1           5           10           15
Ser Phe Thr His Ser Gly Val His Leu Leu Met Gly Glu Ser Gly Ser

```

```

      20      25      30
Gly Lys Ser Thr Leu Ile Asn Leu Leu Ala Gly Leu Asp Thr Pro Asp
      35      40      45
Ser Gly Ser Val Tyr Ala Glu Gly Val Thr Val Ser Asp Gln Ser Glu
      50      55      60
Ala Ser Arg Ala Gln Phe Arg Leu Arg His Ile Ala Val Ile Phe Gln
65      70      75      80
Asp Asp Asn Leu Ile Ala Glu Leu Thr Asn Thr Glu Asn Ile Ala Leu
      85      90      95
Pro Leu Trp Ala Gln Gly Thr Ser Lys Ser Asp Ala Thr Glu Ile Ala
      100      105      110
His Glu Ala Met Arg Lys Leu Gly Ile Glu Ser Leu Gly Arg Arg Tyr
      115      120      125
Pro Gly Glu Val Ser Gly Gly Gln Arg Gln Arg
      130      135

```

&lt;210&gt; 297

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 297

```

tacaccatcg gtgaccagat tgtcgaagct ctgcagggtgc actcgaagat gtccgacaag
60
gacgcttggg gcgctgccat cgagctgctc gacttggtgg ggattccgaa tcccagggtg
120
cgtgccaaag cttttccgca cgagttttcc ggtggcatga ggcaacgagt cgtcatcgcc
180
atggccatcg cgaacgaccc tgacctcatc atcgccgacg agccgacgac ggccttcgac
240
gtgaccatcc aggcccagat tctcgatttg ctgcgcgtag cccagcgtga aacccatgcg
300
ggcgtcggtta tgatcaccca cgacctcggt gtggttagctg gtctggctga cagggttgcc
360
gtgatgtatg ccggacgc
378

```

&lt;210&gt; 298

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 298

```

Tyr Thr Ile Gly Asp Gln Ile Val Glu Ala Leu Gln Val His Ser Lys
1      5      10      15
Met Ser Asp Lys Asp Ala Trp Ala Arg Ala Ile Glu Leu Leu Asp Leu
      20      25      30
Val Gly Ile Pro Asn Pro Glu Val Arg Ala Lys Ala Phe Pro His Glu
      35      40      45
Phe Ser Gly Gly Met Arg Gln Arg Val Val Ile Ala Met Ala Ile Ala
      50      55      60
Asn Asp Pro Asp Leu Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp
65      70      75      80
Val Thr Ile Gln Ala Gln Ile Leu Asp Leu Arg Val Ala Gln Arg

```

					85					90						95			
Glu	Thr	His	Ala	Gly	Val	Val	Met	Ile	Thr	His	Asp	Leu	Gly	Val	Val				
			100					105					110						
Ala	Gly	Leu	Ala	Asp	Arg	Val	Ala	Val	Met	Tyr	Ala	Gly	Arg						
		115					120						125						

<210> 299  
 <211> 368  
 <212> DNA  
 <213> Homo sapiens

gtg	cac	ggtt	tcg	tgg	cat	gcg	caat	gac	cgg	gaga	aact	tgc	gtttt	tga	tcc	gag	actt		
60																			
ccag	cccaat	ggac	gtcgat	caa	acacc	ac	atg	ctcattg	gcg	actctca	cat	gctcg	tt						
120																			
ttc	ctggaac	gtg	acg	ccat	tac	gttccag	att	ctgtc	gg	gccat	gaccg	cg	acgtg	aca					
180																			
gtg	cgc	gggtg	ag	ctctacca	catt	gggggtt	gag	ccggtga	ggg	tgc	ggtt	gt	ccgat	cag					
240																			
ggg	ccgttgc	gtc	ctagc	ct	gcg	cg	ttacc	cat	ccgat	ct	cgg	ggttgcg	t	cgag	ctgac				
300																			
ggt	tctctta	t	actgc	aga	agt	tcccg	gc	agcattg	ctg	ag	acgattg	g	gt	cttctccg					
360																			
at	ctcgac																		
368																			

<210> 300  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

Val	His	Gly	Phe	Val	Gly	Met	Arg	Asn	Asp	Arg	Glu	Asn	Leu	Arg	Phe				
1				5					10					15					
Asp	Pro	Arg	Leu	Pro	Ala	Gln	Trp	Thr	Ser	Ile	Lys	His	His	Met	Leu				
			20					25					30						
Ile	Gly	Asp	Ser	His	Met	Leu	Val	Phe	Leu	Glu	Arg	Asp	Ala	Ile	Thr				
		35				40						45							
Phe	Gln	Ile	Leu	Ser	Gly	His	Asp	Arg	Asp	Val	Thr	Val	Arg	Gly	Glu				
	50					55						60							
Leu	Tyr	His	Ile	Gly	Val	Glu	Pro	Val	Arg	Val	Pro	Leu	Ser	Asp	Gln				
65					70					75					80				
Gly	Pro	Leu	Arg	Pro	Ser	Leu	Arg	Val	Thr	His	Pro	Ile	Ser	Gly	Leu				
			85					90						95					
Arg	Arg	Ala	Asp	Gly	Ser	Leu	Ile	Thr	Ala	Glu	Val	Pro	Gly	Ser	Ile				
		100						105						110					
Ala	Glu	Thr	Ile	Gly	Ser	Ser	Pro	Ile	Ser										
		115				</													

&lt;400&gt; 301

ggccggggtta ttgcccgcc gtttgtcggg gaaacccggc agaccttcga gcgcaccggc  
 60  
 aaccggcgcg actattecgt accgccgcc gaaccgacct tgctcgacag gcttacggac  
 120  
 gcgggcccga cggatgacgc aatcggaag attggtgata tctacgcga caaaggcgtg  
 180  
 tctcagggtgc gtaaggcaat ggcaatattg gccttggtcg atgaaacact cattgccatg  
 240  
 gacgacgcgc aggacggcga tctggtcttc accaacttcg tggatttcga catgctctac  
 300  
 gggcatcgca gggatgtgcc cggctatgcc gccgcgctcg aggctttcga ccggaggcgtg  
 360  
 ccggaagcca tggcgaaatt gcggacgggc gatcttctga tcttgacagc cgatcatggc  
 420  
 tgcgaccgca ccctcaaggg aaccgaccac acgcgt  
 456

&lt;210&gt; 302

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 302

Gly	Arg	Val	Ile	Ala	Arg	Pro	Phe	Val	Gly	Glu	Thr	Arg	Gln	Thr	Phe
1				5					10					15	
Glu	Arg	Thr	Gly	Asn	Arg	Arg	Asp	Tyr	Ser	Val	Pro	Pro	Pro	Glu	Pro
			20					25					30		
Thr	Leu	Leu	Asp	Arg	Leu	Thr	Asp	Ala	Gly	Arg	Thr	Val	Ile	Ala	Ile
		35					40					45			
Gly	Lys	Ile	Gly	Asp	Ile	Tyr	Ala	His	Lys	Gly	Val	Ser	Gln	Val	Arg
	50				55					60					
Lys	Ala	Met	Ala	Ile	Leu	Ala	Leu	Phe	Asp	Glu	Thr	Leu	Ile	Ala	Met
65				70					75					80	
Asp	Asp	Ala	Gln	Asp	Gly	Asp	Leu	Val	Phe	Thr	Asn	Phe	Val	Asp	Phe
			85					90					95		
Asp	Met	Leu	Tyr	Gly	His	Arg	Arg	Asp	Val	Pro	Gly	Tyr	Ala	Ala	Ala
			100				105					110			
Leu	Glu	Ala	Phe	Asp	Arg	Arg	Leu	Pro	Glu	Ala	Met	Ala	Lys	Leu	Arg
	115						120				125				
Thr	Gly	Asp	Leu	Leu	Ile	Leu	Thr	Ala	Asp	His	Gly	Cys	Asp	Pro	Thr
	130				135						140				
Leu	Lys	Gly	Thr	Asp	His	Thr	Arg								
145					150										

&lt;210&gt; 303

&lt;211&gt; 402

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 303

nncgtgggca tcgaggagtt cctcgacatg aagtatcacg cgacgccgat tcacgtcgc  
 60

tgacagcgggt tttccggaac acatcagcgt tcagacagga gcgaggagac catgtacctg  
 120  
 ggtgctcagc tgttcagtga cagcgagtac gagcagcgcc tgagacgtgt ccgtagagctc  
 180  
 atggaccgtc aggggtctgtc ggcgatcatc gtcaccgatc cggccaacat cttctatctg  
 240  
 atcggttaca acgcctggtc gttctacacc cgcagatgc tgttcgtgcc gatcgacgga  
 300  
 gagatgggtcc tctacgctcg cgagatggat cgcattggcg acatcngcac gacgtcgttg  
 360  
 cccgccgatc agatcgctcg ttaccgggag agttatgtgc ac  
 402

<210> 304

<211> 97

<212> PRT

<213> Homo sapiens

<400> 304

Met	Tyr	Leu	Gly	Ala	Gln	Leu	Phe	Ser	Asp	Ser	Glu	Tyr	Glu	Gln	Arg
1				5					10					15	
Leu	Arg	Arg	Val	Arg	Glu	Leu	Met	Asp	Arg	Gln	Gly	Leu	Ser	Ala	Ile
			20					25					30		
Ile	Val	Thr	Asp	Pro	Ala	Asn	Ile	Phe	Tyr	Leu	Ile	Gly	Tyr	Asn	Ala
		35					40					45			
Trp	Ser	Phe	Tyr	Thr	Pro	Gln	Met	Leu	Phe	Val	Pro	Ile	Asp	Gly	Glu
	50					55					60				
Met	Val	Leu	Tyr	Ala	Arg	Glu	Met	Asp	Arg	Met	Ala	His	Ile	Xaa	Thr
65					70					75				80	
Thr	Ser	Leu	Pro	Ala	Asp	Gln	Ile	Val	Gly	Tyr	Pro	Glu	Ser	Tyr	Val
			85					90						95	

His

<210> 305

<211> 375

<212> DNA

<213> Homo sapiens

<400> 305

nnacgcgtcg gttccgcacg gagcgaccgg atcgcatcga cgagcacgct gcaccagtgc  
 60  
 gtgtcgtcct ggcgaatatg ggcgatcagc cggtagagtt cgggatcgtc gctcacctcg  
 120  
 gccgccattt cggatgcgac acgcgcgcct gcgcgctcgg cctccagcaa ctcgtcgagc  
 180  
 gtcgccacca gcgcggcgcg atcttcatgc ggagtcagat cggcgcgggc gtcaggccccg  
 240  
 tcgccatgcg tcggaatcga catgcagcac cctcctgccg ggatcgatgg cgtaatacgt  
 300  
 gcgacggtag acggcgcggt ttgcacgaac gtgcaaatca gcgcgtgcct cgtgccatat  
 360  
 acgtcacatc atatg  
 375

<210> 306  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 306  
 Xaa Arg Val Gly Ser Ala Ser Ser Asp Arg Ile Ala Ser Thr Ser Thr  
 1 5 10 15  
 Leu His Gln Cys Val Ser Ser Trp Arg Ile Trp Ala Ile Ser Arg Tyr  
 20 25 30  
 Ser Ser Gly Ser Ser Leu Thr Ser Ala Ala Ile Ser Asp Ala Thr Arg  
 35 40 45  
 Ala Pro Ala Arg Ser Ala Ser Ser Asn Ser Ser Ser Val Ala Thr Ser  
 50 55 60  
 Ala Ala Arg Ser Ser Cys Gly Val Arg Ser Ala Arg Ala Ser Gly Pro  
 65 70 75 80  
 Ser Pro Cys Val Gly Ile Asp Met Gln His Pro Pro Ala Arg Ile Asp  
 85 90 95  
 Gly Val Ile Arg Ala Thr Val His Gly Ala Cys Cys Thr Asn Val Gln  
 100 105 110  
 Ile Ser Ala Cys Leu Val Pro Tyr Thr Ser His His Met  
 115 120 125

<210> 307  
 <211> 685  
 <212> DNA  
 <213> Homo sapiens

<400> 307  
 actagttctg gccgctcccc tggggctttg ggtaacaatt gtcagcccca cccatcctag  
 60  
 ggtaggaag gctattctct ttggccactc tcatacctaag acctatttgg agaacctctg  
 120  
 gggtttgagt ctttttttca gcagaatgag gcttgatccc gcattatagc acctgcaca  
 180  
 tttgatgtct cttcttctca cccactcacc ccacctggg ggtggggca aaaaagtggc  
 240  
 tcaaagctgc gggtcagagt tccttgtaaa caaggctcct ccctcactgt cctcacctg  
 300  
 ctccagcaga gggagcagcg gaaggaccac tctgctgcag ccatgcttgt ttctaaccga  
 360  
 gcagaactgg acataatggg aacagggtct gaagacaatc aatccagggc tgcagtgggt  
 420  
 gctgagtctg gggaagcctc cacctggagg ggcagctggg cagtggcagc tcccttgaa  
 480  
 tggctcagcc tctggacatc accccaccca accagagccc tggtctctgc tggatgtcca  
 540  
 cagatgagtg cctgggattg gtctcagcca ctatgggggg gatgtgcagg gagaggtgat  
 600  
 gagggagtga gcaggactgt ctatgtgcct ctgtcctcat cctgaggctt gggctctgaa  
 660  
 ttggtgctgc agcactggca cgcgt  
 685

<210> 308  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 308  
 Met Leu Val Ser Asn Pro Ala Glu Leu Asp Ile Met Gly Thr Gly Ser  
 1 5 10 15  
 Glu Asp Asn Gln Ser Arg Ala Ala Val Gly Ala Glu Ser Gly Glu Ala  
 20 25 30  
 Ser Thr Trp Arg Gly Ser Trp Ala Val Ala Ala Pro Leu Glu Trp Leu  
 35 40 45  
 Ser Leu Trp Thr Ser Pro His Pro Thr Arg Ala Leu Ala Leu Ala Gly  
 50 55 60  
 Cys Pro Gln Met Ser Ala Trp Asp Trp Ser Gln Pro Leu Trp Gly Gly  
 65 70 75 80  
 Cys Ala Gly Arg Gly Asp Glu Gly Val Ser Arg Thr Val Tyr Val Pro  
 85 90 95  
 Leu Ser Ser Ser  
 100

<210> 309  
 <211> 432  
 <212> DNA  
 <213> Homo sapiens

<400> 309  
 caggctcgta ctattcgtat ccctgtgcat atggctcgagg tcatcaataa gctggctcgc  
 60  
 gtccagcgtc agatgctcca ggacctaggt cgtgagccca ccccggaaga gcttgccaac  
 120  
 gaactcgata tgaccgcaga gaaggtcatt gaggtgcaga aatacggtcg cgagccgac  
 180  
 tcgctgcata cccactggg tgaggatggc gattctgagt tcggtgacct tattgaggat  
 240  
 tccgaggcca tcgtgccagc agacgccgtc aacttcaccc tgttcagga gcagctgcat  
 300  
 gatgtcctcg ataccttgtc cgagcgagag gccggtgtcg tgtcgatgcg attcggcttg  
 360  
 accgacggac agcccaagac cctggatgag atcggcaaag tctacggtgt tactcgggag  
 420  
 cgcacccgcc ag  
 432

<210> 310  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 310  
 Gln Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn  
 1 5 10 15  
 Lys Leu Ala Arg Val Gln Arg Gln Met Leu Gln Asp Leu Gly Arg Glu



```

      20      25      30
Pro Thr Pro Glu Glu Leu Ala Asn Glu Leu Asp Met Thr Ala Glu Lys
      35      40      45
Val Ile Glu Val Gln Lys Tyr Gly Arg Glu Pro Ile Ser Leu His Thr
      50      55      60
Pro Leu Gly Glu Asp Gly Asp Ser Glu Phe Gly Asp Leu Ile Glu Asp
65      70      75      80
Ser Glu Ala Ile Val Pro Ala Asp Ala Val Asn Phe Thr Leu Leu Gln
      85      90      95
Glu Gln Leu His Asp Val Leu Asp Thr Leu Ser Glu Arg Glu Ala Gly
      100      105      110
Val Val Ser Met Arg Phe Gly Leu Thr Asp Gly Gln Pro Lys Thr Leu
      115      120      125
Asp Glu Ile Gly Lys Val Tyr Gly Val Thr Arg Glu Arg Ile Arg Gln
      130      135      140

```

<210> 311  
 <211> 358  
 <212> DNA  
 <213> Homo sapiens

```

<400> 311
acgcgtatcg aaaatatccc tcccattatt accgctcgcc ctgaactgat ggctcatgaa
60
ctgacgccag aatctcttga tgcgagcctg gagtggggccg atgtgggtggt cattggtcct
120
ggactgggac aacaagcgtg gggcaaaaaa gcgctacaaa aggtcgagaa ttgtcgtaaa
180
ccgatgctgt gggatgccga cgcgcttaac cttctggcaa tcaatcctga taaacgtcac
240
aatcgcatcc tgacgccaca ccccggcgag gccgcgcggc tgcttagctg cagcgctcgca
300
gaaattgaaa acgatcgctt acttntctgc gcacgtctgg taaaacggta acccgagt
358

```

<210> 312  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

```

<400> 312
Thr Arg Ile Glu Asn Ile Pro Pro Ile Ile Thr Ala Arg Pro Glu Leu
1      5      10      15
Met Ala His Glu Leu Thr Pro Glu Ser Leu Asp Ala Ser Leu Glu Trp
      20      25      30
Ala Asp Val Val Val Ile Gly Pro Gly Leu Gly Gln Gln Ala Trp Gly
      35      40      45
Lys Lys Ala Leu Gln Lys Val Glu Asn Cys Arg Lys Pro Met Leu Trp
      50      55      60
Asp Ala Asp Ala Leu Asn Leu Leu Ala Ile Asn Pro Asp Lys Arg His
65      70      75      80
Asn Arg Ile Leu Thr Pro His Pro Gly Glu Ala Ala Arg Leu Leu Ser
      85      90      95
Cys Ser Val Ala Glu Ile Glu Asn Asp Arg Leu Leu Xaa Cys Ala Arg

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100 105 110  
 Leu Val Lys Arg  
 115

<210> 313  
 <211> 347  
 <212> DNA  
 <213> Homo sapiens

<400> 313  
 ncaactgaaa gcattgagat gagcgacgtg ctgtccccct tccacccac caaggccaac  
 60  
 acccctgggtg gcgaaccgcg caccatccgc acctcgaacg cgcacatcat tgccgtcacc  
 120  
 agtggcaaag gcggcgtggg caagaccttt gtctccgcca acctggccgc cgcgctgacc  
 180  
 cgcctgggac tgcgctgct ggtactggac gccgacctgg gcctggccaa cttggacgtg  
 240  
 gtgctgaacc tctaccccaa ggtgacgctg cacgatgtgt tcaccggcaa ggctcgtgct  
 300  
 caagacgcgg tggtcacggc ccccggcggc ttccatgtgc tgetagc  
 347

<210> 314  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 314  
 Xaa Thr Glu Ser Ile Glu Met Ser Asp Val Leu Ser Pro Phe His Pro  
 1 5 10 15  
 Thr Lys Ala Asn Thr Pro Gly Gly Glu Pro Arg Thr Ile Arg Thr Ser  
 20 25 30  
 Asn Ala His Ile Ile Ala Val Thr Ser Gly Lys Gly Gly Val Gly Lys  
 35 40 45  
 Thr Phe Val Ser Ala Asn Leu Ala Ala Leu Thr Arg Leu Gly Leu  
 50 55 60  
 Arg Val Leu Val Leu Asp Ala Asp Leu Gly Leu Ala Asn Leu Asp Val  
 65 70 75 80  
 Val Leu Asn Leu Tyr Pro Lys Val Thr Leu His Asp Val Phe Thr Gly  
 85 90 95  
 Lys Ala Ser Leu Gln Asp Ala Val Val Thr Ala Pro Gly Gly Phe His  
 100 105 110  
 Val Leu Leu  
 115

<210> 315  
 <211> 544  
 <212> DNA  
 <213> Homo sapiens

<400> 315  
 nnacgcgttc gtcaacagga aaacaacaac ggcttctcgc tggaggggaac catgcttgcc  
 60

gaagatatct acgcgatcat gctgttttca tcgctcatcc tggctgtccc gggggccatcc  
 120  
 aacaccttgc tgctcagcgc ccgtttccat ttccggtcgc tgcgggcggc gcccttcac  
 180  
 ctgcttgagg cggtgggcta ctcgctatcc atttcggcat ggggctgggt attggcgcgc  
 240  
 ctgtccgaga gcaatccatg gatcatcagt ctgaccaagg cactctgcgc gctatatgtg  
 300  
 gcgcttctgg cgggtgaagac ctggaatgcc ntcgatccgc agtgcggggc cggtaaactc  
 360  
 cgccatgggc ccttgcccct gttcgtggca accctgtcga acccgaaggc gctgatcttc  
 420  
 gccagcgtga tctttcccg caaggcgttc ctcgacttct ggaacaacta cacgatctcg  
 480  
 ctgctggcct tcttggttgt gctggcgccc atcgggatgc tttgggtcgg gctgggggcc  
 540  
 ggta  
 544

<210> 316  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 316  
 Ile Tyr Ala Ile Met Leu Phe Ser Ser Leu Ile Leu Val Val Pro Gly  
 1 5 10 15  
 Pro Ser Asn Thr Leu Leu Leu Ser Ala Arg Phe His Phe Gly Ser Leu  
 20 25 30  
 Arg Ala Ala Pro Phe Ile Leu Leu Glu Ala Leu Gly Tyr Ser Leu Ser  
 35 40 45  
 Ile Ser Ala Trp Gly Trp Val Leu Ala Arg Leu Ser Glu Ser Asn Pro  
 50 55 60  
 Trp Ile Ile Ser Leu Thr Lys Ala Leu Cys Ala Leu Tyr Val Ala Leu  
 65 70 75 80  
 Leu Ala Val Lys Thr Trp Asn Ala Xaa Asp Pro Gln Cys Gly Ala Gly  
 85 90 95  
 Asn Phe Arg His Gly Pro Leu Pro Leu Phe Val Ala Thr Leu Ser Asn  
 100 105 110  
 Pro Lys Ala Leu Ile Phe Ala Ser Val Ile Phe Pro Gly Lys Ala Phe  
 115 120 125  
 Leu Asp Phe Trp Asn Asn Tyr Thr Ile Ser Leu Leu Ala Phe Leu Val  
 130 135 140  
 Val Leu Ala Pro Ile Gly Met Leu Trp Val Gly Leu Gly Ala Gly  
 145 150 155

<210> 317  
 <211> 343  
 <212> DNA  
 <213> Homo sapiens

<400> 317  
 nggtcagcct ctcgcccagg caattctctt aagatacatg agctgctatg agtaccaaag  
 60

ccagagggttt gtccactgag agaagcacat tggaaagggg ggcgtggggc tgggactgtg  
 120  
 tggcacttta tgcacggggg gggcctaagg gggnggtcc accaaccatg cactgnnggt  
 180  
 ggggtgtggg taacatgccg tgcattttgg ggggtgtgcca tgagtggcac accatggggg  
 240  
 tggcatgtgg ggcatgtatg catgtggtgt tggcgcagca aactcagctc ttacctggct  
 300  
 ggggccagcc tctaaaactt ctcacattgg gctcccttct gac  
 343

<210> 318

<211> 98

<212> PRT

<213> Homo sapiens

<400> 318

Met	Ser	Thr	Lys	Ala	Arg	Gly	Leu	Ser	Thr	Glu	Arg	Ser	Thr	Leu	Glu
1				5					10					15	
Arg	Gly	Ala	Trp	Ala	Trp	Asp	Cys	Val	Ala	Leu	Tyr	Ala	Arg	Gly	Gly
			20				25					30			
Pro	Lys	Gly	Gly	Gly	Pro	Pro	Thr	Met	His	Xaa	Gly	Trp	Gly	Val	Gly
		35					40					45			
Asn	Met	Pro	Cys	Ile	Leu	Gly	Val	Cys	His	Glu	Trp	His	Thr	Met	Gly
	50					55					60				
Val	Ala	Cys	Gly	Ala	Cys	Met	His	Val	Val	Leu	Ala	Gln	Gln	Thr	Gln
65					70					75					80
Leu	Leu	Pro	Gly	Trp	Gly	Gln	Pro	Leu	Lys	Leu	Leu	Thr	Leu	Gly	Ser
			85						90					95	

Leu Leu

<210> 319

<211> 429

<212> DNA

<213> Homo sapiens

<400> 319

gaattctcga tgtaccccct cccggcagtc ctattctcga gctgagcggg cacagtggcc  
 60  
 ccgttaacag tgtggcttgg ggtccacca gccagagcac gttgcgaaat ggacctagta  
 120  
 agggcatgat atgtacagga ggcgacgatg ctcagtgcct cgtatatgat ctgactagct  
 180  
 caactcttcg aacagcatct gctcaaggac ggcgctctcg aaacagtcca tataaaca  
 240  
 gccattcacc gggaatagac ggatggcgtg tcggcgcaga agtgccggtg ctcgcttata  
 300  
 cggccccgtc tatggccaac aatgctagct ggctcggcat gcctgcgcca tcaaacgca  
 360  
 catcgctaca gagcaaacac cgcagccttt accgcagctt actcagttag tggactgagt  
 420  
 atacgtccn  
 429

<210> 320  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 320  
 Met Ile Cys Thr Gly Gly Asp Asp Ala Gln Cys Leu Val Tyr Asp Leu  
 1 5 10 15  
 Thr Ser Ser Thr Leu Arg Thr Ala Ser Ala Gln Gly Arg Arg Ser Arg  
 20 25 30  
 Asn Ser Pro Tyr Lys Gln Ser His Ser Pro Gly Ile Asp Gly Trp Arg  
 35 40 45  
 Val Gly Ala Glu Val Pro Val Leu Ala Tyr Thr Ala Pro Ser Met Val  
 50 55 60  
 Asn Asn Ala Ser Trp Leu Gly Met Pro Ala Pro Ser Lys Arg Thr Ser  
 65 70 75 80  
 Leu Gln Ser Lys His Arg Ser Leu Tyr Arg Ser Leu Leu Ser Glu Trp  
 85 90 95  
 Thr Glu Tyr Thr Ser  
 100

<210> 321  
 <211> 530  
 <212> DNA  
 <213> Homo sapiens

<400> 321  
 ngtgcacgac gtgctcgcca agtccctcgg gtcctctaata gcgatcaacg tggttcacgc  
 60  
 caccgtcgat gcgttgacgc agctcgagga gcccgagag gtcgcccgtc gccgcggcaa  
 120  
 gtccgttgag gagatcgccc cagcagccat gctgcgtgcg cgcaaggagg ccgacgaggg  
 180  
 cgccgctgct gcccgcatgg aggaaaaggc ggggggtaac tgatgagcaa gctgaagatc  
 240  
 acccagatca agtctggcat cgctaccaag ccaaatacatc gtgagaccct gcgcagcctc  
 300  
 ggactgaagc gtattggtga caccgtcatc aaggaggacc gcccgaggtt ccgcggcatg  
 360  
 gtccggaccg ttcgtcacct cgtcaccatg gaagaggtgg actgacatgg ctattgagct  
 420  
 ccatgacctc aagccccgtc ctgggtgccc caaggccaag acccgcggtg gtcgtggtga  
 480  
 gggttccaag ggtaagaccg ctgggtcgcg taccaagggc accggtgcac  
 530

<210> 322  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens

<400> 322  
 Met Ser Lys Leu Lys Ile Thr Gln Ile Lys Ser Gly Ile Ala Thr Lys

1	5	10	15
Pro Asn His Arg Glu Thr Leu Arg Ser Leu Gly Leu Lys Arg Ile Gly			
	20	25	30
Asp Thr Val Ile Lys Glu Asp Arg Pro Glu Phe Arg Gly Met Val Arg			
	35	40	45
Thr Val Arg His Leu Val Thr Met Glu Glu Val Asp			
50	55	60	

&lt;210&gt; 323

&lt;211&gt; 468

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 323

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ntccggaccc gctgtggcca cgtattctgc cgttcctgta ttgctaccag tctaaagaac
60
aacaagtgga cctgtcctta ttgccgggca tatcttcctt cagaaggagt tccagcaact
120
gatgtagcca aaagaatgaa atcagagtat aagaactgcg ctgagtgtga caccctgggt
180
tgccctcagt aaatgagggc acatattcgg acttgtcaga agtacataga taagtatgga
240
ccactacaag aacttgagga gacagcagca aggtgtgtat gtcccttttg tcagagggaa
300
ctgtatgaag acagcttgct ggatcattgt attactcatc acagatcgga acggaggcct
360
gtgttctgtc cactttgcca tttaataccc gatgagaatc caagcagctt cagtggcagt
420
ttaataagac atctgcaagt tagtcacact ttggtttatg atgatttc
468

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&lt;210&gt; 324

&lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 324

Xaa Arg Thr Arg Cys Gly His Val Phe Cys Arg Ser Cys Ile Ala Thr			
1	5	10	15
Ser Leu Lys Asn Asn Lys Trp Thr Cys Pro Tyr Cys Arg Ala Tyr Leu			
	20	25	30
Pro Ser Glu Gly Val Pro Ala Thr Asp Val Ala Lys Arg Met Lys Ser			
	35	40	45
Glu Tyr Lys Asn Cys Ala Glu Cys Asp Thr Leu Val Cys Leu Ser Glu			
	50	55	60
Met Arg Ala His Ile Arg Thr Cys Gln Lys Tyr Ile Asp Lys Tyr Gly			
65	70	75	80
Pro Leu Gln Glu Leu Glu Glu Thr Ala Ala Arg Cys Val Cys Pro Phe			
	85	90	95
Cys Gln Arg Glu Leu Tyr Glu Asp Ser Leu Leu Asp His Cys Ile Thr			
	100	105	110
His His Arg Ser Glu Arg Arg Pro Val Phe Cys Pro Leu Cys His Leu			
	115	120	125
Ile Pro Asp Glu Asn Pro Ser Ser Phe Ser Gly Ser Leu Ile Arg His			

130 135 140  
 Leu Gln Val Ser His Thr Leu Val Tyr Asp Asp Phe  
 145 150 155

<210> 325  
 <211> 374  
 <212> DNA  
 <213> Homo sapiens

<400> 325  
 acgctgaag ggaggacgag gaagtaacgg gaagcacaag gccgctgctg gggagatggc  
 60  
 actggagccc cctaggaagc atctcacagg ctgtggccct tggcacgggg atctggggcc  
 120  
 aggtcgagcg caggtctggg tatcatgcga gtgcgggctc gctggggcgg gaaagagttt  
 180  
 ggagctctgc tcccaggga tccccactcc cgcagatgac ttgcccgaga gagttctgct  
 240  
 ggtggatttt gatggaaatt ctatttgatc gcacccactt ggttcactgt gtgcttcggg  
 300  
 gtccccaggt tttaggtgct tcatgccctg ctgggaacga gacacgctcc tgcctcagt  
 360  
 gaatcttcag tcta  
 374

<210> 326  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 326  
 Met Lys His Leu Lys Pro Gly Asp Pro Glu Ala His Ser Glu Pro Ser  
 1 5 10 15  
 Gly Cys Asp Gln Ile Glu Phe Pro Ser Lys Ser Thr Ser Arg Thr Leu  
 20 25 30  
 Ser Gly Lys Ser Ser Ala Gly Val Gly Ile Pro Trp Glu Gln Ser Ser  
 35 40 45  
 Lys Leu Phe Pro Ala Pro Ala Ser Pro His Ser His Asp Thr Gln Thr  
 50 55 60  
 Cys Ala Arg Pro Gly Pro Arg Ser Pro Cys Gln Gly Pro Gln Pro Val  
 65 70 75 80  
 Arg Cys Phe Leu Gly Gly Ser Ser Ala Ile Ser Pro Ala Ala Ala Leu  
 85 90 95  
 Cys Phe Pro Leu Leu Pro Arg Pro Pro Phe Thr Arg  
 100 105

<210> 327  
 <211> 538  
 <212> DNA  
 <213> Homo sapiens

<400> 327  
 cactataaaa tccagtttgg ggcccgtgtt ctttcctatt ggtctgtcag gtgaaaaact  
 60

ccggctgggg gaaaagcgtc cgggtggttg ttggtaaaga gggcgctga tgggctctgg  
 120  
 ggaatggagg atggcgcacc ggctgtgggt ggactgtgga aacggggggg ggagtgccg  
 180  
 gggtagttgt cctgctggtc tggttttggg atcctgggct ggagaaatgc gatccaaaag  
 240  
 agctcgggat gggctcagag cgacccacga aaataccagg ggccaagtaa aatgaaccca  
 300  
 ccctttaaca gtgcacaaaag cgctggcaca cgggtccacgt ctggtgacgc aggctgcccg  
 360  
 aagcgctcca accattttgc aaacctggga gagcaagagg ggctctgcag gtctagccgc  
 420  
 cgccccctgc ccactctggc cagccggagt ttttcaccta cagaccaata ggaaagaaca  
 480  
 cgggccccaa actggatttt atagtctgag ctctcagcat ctaaggaatg atatgccc  
 538

<210> 328

<211> 125

<212> PRT

<213> Homo sapiens

<400> 328

Met	Val	Gly	Ala	Leu	Arg	Ala	Ala	Cys	Val	Thr	Arg	Arg	Gly	Pro	Cys
1				5					10					15	
Ala	Ser	Ala	Leu	Cys	Thr	Val	Lys	Gly	Trp	Val	His	Phe	Thr	Trp	Pro
			20					25					30		
Leu	Val	Phe	Ser	Trp	Val	Ala	Leu	Ser	Pro	Ser	Arg	Ala	Leu	Leu	Asp
		35					40					45			
Arg	Ile	Ser	Pro	Ala	Gln	Asp	Pro	Lys	Thr	Arg	Pro	Ala	Gly	Gln	Leu
	50					55					60				
Pro	Arg	His	Cys	His	Pro	Pro	Phe	Pro	Gln	Ser	Thr	His	Ser	Arg	Cys
	65				70				75					80	
Ala	Ile	Leu	His	Ser	Pro	Glu	Pro	Ile	Thr	His	Pro	Leu	Tyr	Gln	Gln
			85					90					95		
Thr	Thr	Gly	Arg	Phe	Ser	Pro	Ser	Arg	Ser	Phe	Ser	Pro	Asp	Arg	Pro
		100						105					110		
Ile	Gly	Lys	Asn	Thr	Gly	Pro	Lys	Leu	Asp	Phe	Ile	Val			
		115					120					125			

<210> 329

<211> 407

<212> DNA

<213> Homo sapiens

<400> 329

tccggagagt tccctcccca ggaattcctt ctaagaatcc atgtggaaat agagcctgaa  
 60  
 gctcttcagt cttctctgctc cactgagcag tgttttcttg atacccttgg taccctgcca  
 120  
 gcagcctcgt tatgactcct aactccattg ccctccatgg cccctgggag ctctctctct  
 180  
 cttctctctcc aggtagtaga gcaactgcttc tggtctcttg tgcacagaag gggtttccac  
 240



agctgagagc tgggctccta ctgacatagt tatttccttt atatcctgcc ccaccttctt  
 300  
 ctggtagcac acagcaacct tgcatagttag ctggtatcat taccttccca atcaacagge  
 360  
 cttgatttct tataggactt tttctctcag atttacattg cttcttt  
 407

<210> 330  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 330  
 Met Ile Pro Ala Thr Met Gln Gly Cys Cys Val Leu Pro Glu Glu Gly  
 1 5 10 15  
 Gly Ala Gly Tyr Lys Gly Asn Asn Tyr Val Ser Arg Ser Pro Ala Leu  
 20 25 30  
 Ser Cys Gly Lys Pro Phe Cys Ala Gln Glu Ala Arg Ser Ser Ala Leu  
 35 40 45  
 Leu Pro Gly Glu Lys Glu Arg Glu Ser Ala Gln Gly Pro Trp Arg Ala  
 50 55 60  
 Met Glu Leu Gly Val Ile Thr Arg Leu Leu Ala Gly Tyr Gln Gly Tyr  
 65 70 75 80  
 Gln Glu Asn Thr Ala Gln Trp Ser Arg Lys Thr Glu Glu Leu Gln Ala  
 85 90 95  
 Leu Phe Pro His Gly Phe Leu Glu Gly Ile Pro Gly Glu Gly Thr Leu  
 100 105 110  
 Arg

<210> 331  
 <211> 523  
 <212> DNA  
 <213> Homo sapiens

<400> 331  
 tgtaccgaac ctgctgggtct cgagggectt gctgggctcg tcgtacgcac agctgacgaa  
 60  
 tccaccggcc cccatcccgg cgccactttc gctgaggcca tggagtcgat cggagccagc  
 120  
 tacgacggat cggccgggtt ggccggaagt cacgtcggcg tcgatgtgcc cgtgacaagg  
 180  
 ttgcagcgag cggtgaact ctctgtcgaa ttgttgaaca ccacgagcct ggttgaagag  
 240  
 gacatgcgcc gtcagatcga cgcggcgcga gcctccctgg ccagaccag ccagcgcgga  
 300  
 tcggccctag ccgagatggc agcagcacgt gcgctatggc cagtggggtc acggtcgtcc  
 360  
 ctgcccacga tcggtaccct ctctgtcggg gaaaagctca acgccgcagc cgcacgagaa  
 420  
 ttctgggccg cgcaactggac gatctccgat gccgtgctgg tggttgccgg agagggagtc  
 480  
 gaggacctcg acttgtcaat attcaaggag tggacgacca gct  
 523

<210> 332  
 <211> 174  
 <212> PRT  
 <213> Homo sapiens

<400> 332  
 Cys Thr Glu Pro Ala Gly Leu Glu Gly Leu Ala Gly Leu Val Val Arg  
 1 5 10 15  
 Thr Ala Asp Glu Ser Thr Gly Pro His Pro Gly Ala Thr Phe Ala Glu  
 20 25 30  
 Ala Met Glu Ser Ile Gly Ala Ser Tyr Asp Gly Ser Ala Gly Leu Ala  
 35 40 45  
 Gly Ser His Val Gly Val Asp Val Pro Val Thr Arg Phe Asp Ala Ala  
 50 55 60  
 Ala Glu Leu Phe Val Glu Leu Leu Asn Thr Thr Ser Leu Val Glu Glu  
 65 70 75 80  
 Asp Ile Ala Arg Gln Ile Asp Ala Ala Arg Ala Ser Leu Ala Gln Thr  
 85 90 95  
 Ser Gln Arg Gly Ser Ala Leu Ala Glu Met Ala Ala Ala Arg Ala Leu  
 100 105 110  
 Trp Pro Val Gly Ser Arg Ser Ser Leu Pro Thr Ile Gly Thr Leu Ser  
 115 120 125  
 Ser Val Glu Lys Leu Asn Ala Ala Ala Arg Glu Phe Trp Ala Ala  
 130 135 140  
 His Trp Thr Ile Ser Asp Ala Val Leu Val Val Ala Gly Glu Gly Val  
 145 150 155 160  
 Glu Asp Leu Asp Leu Ser Ile Phe Lys Glu Trp Thr Thr Ser  
 165 170

<210> 333  
 <211> 372  
 <212> DNA  
 <213> Homo sapiens

<400> 333  
 nntgttcgtc gtgtcgaccc ggaactcaag gcccgagcga tgacggtgaa ggtgcccaacc  
 60  
 gatcccatc accgcccggg agttccattg aagtctgcga aggaccgtat ggacatcatt  
 120  
 tctgcttacc gagaactcgg aagctatcgc gccgcagccg aggtgtgctg caccacccac  
 180  
 aagaccgtca agcgggtggt cgatcggttt gaagccggcg atccacccac cggtggcaag  
 240  
 gaacgggccc gcaactacga tgcgggtggc cagctcgtcg cgcagcgagt cgcgcgggtca  
 300  
 cacggccgga tcaactgcaa acggctgcta ccggtagcgc gagcggcagg atatgagggg  
 360  
 tcggcgcgga at  
 372

<210> 334  
 <211> 88  
 <212> PRT

<213> Homo sapiens

<400> 334

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Met Asp Ile Ile Ser Ala Tyr Arg Glu Leu Gly Ser Tyr Arg Ala Ala
 1           5           10           15
Ala Glu Val Cys Gly Thr Thr His Lys Thr Val Lys Arg Val Val Asp
      20           25           30
Arg Phe Glu Ala Gly Asp Pro Pro Thr Gly Gly Lys Glu Arg Ala Arg
      35           40           45
Asn Tyr Asp Ala Val Ala Gln Leu Val Ala Gln Arg Val Ala Arg Ser
      50           55           60
His Gly Arg Ile Thr Ala Lys Arg Leu Leu Pro Val Ala Arg Ala Ala
65           70           75           80
Gly Tyr Glu Gly Ser Ala Arg Asn
                        85

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<210> 335

<211> 356

<212> DNA

<213> Homo sapiens

<400> 335

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gtgcacgcct tgctgggcga gggcgatgcg cctgcgcgca ccttcgtgga cggtaccttt
60
ggcaggggag ggcattcgcg gctcatcctg cagcgggttg ggccgcaagg ccgcctgggtg
120
gcgttcgaca aggacaccga agccattcaa gcagcggcgc gcatcacgga tgcgcgcttt
180
tccatcnggc accaggggtt cagccatctc ggggaactgc ccgccccag cgtgtccggt
240
gtgctgctgg acctgggcgt gagctccccg cagatcgacg acccccagcg cgggttcagt
300
tttcgtttcg atggtccgct ggacatgcgc atggacacca ctccgatgca tggatg
356

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<210> 336

<211> 118

<212> PRT

<213> Homo sapiens

<400> 336

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Val His Ala Leu Leu Gly Glu Gly Asp Ala Pro Ala Arg Thr Phe Val
 1           5           10           15
Asp Gly Thr Phe Gly Arg Gly Gly His Ser Arg Leu Ile Leu Gln Arg
      20           25           30
Leu Gly Pro Gln Gly Arg Leu Val Ala Phe Asp Lys Asp Thr Glu Ala
      35           40           45
Ile Gln Ala Ala Ala Arg Ile Thr Asp Ala Arg Phe Ser Ile Xaa His
      50           55           60
Gln Gly Phe Ser His Leu Gly Glu Leu Pro Ala Ala Ser Val Ser Gly
65           70           75           80
Val Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Ile Asp Asp Pro Gln
      85           90           95
Arg Gly Phe Ser Phe Arg Phe Asp Gly Pro Leu Asp Met Arg Met Asp

```

100  
Thr Thr Pro Met His Gly  
115

105

110

<210> 337  
<211> 447  
<212> DNA  
<213> Homo sapiens

<400> 337  
cagcctctct ccgaccgcgc cgggtgtgaag cacgggcatg ccgggtgtgca agtggcacca  
60  
cagccaaaac agcgagctca cacttcaaac tccttcaaag accccaggcc tctgtaagaa  
120  
ccgctcatct ctgtgccac agtcccccg cttccatgtg acccagaaat ggaaccacgc  
180  
agcagaggcg gggatcacag gtgaagcagc tgtgaacatt tgcttcaggc ttctgtgcaa  
240  
acaggcgcca tcatgtcagc cggtgagcag gagcaacgtg cgtgggtcag ggggtggcca  
300  
cacgtccaac ttataagaa atgacagatt ccctgatggc catagggatc tgcagggcca  
360  
gcagcaggca taggacttcc ggtggccctg cgtcttcac aacactgagt attgtcaggg  
420  
tttctgtact gtttttacag ccaattg  
447

<210> 338  
<211> 111  
<212> PRT  
<213> Homo sapiens

<400> 338  
Met Pro Val Cys Lys Trp His His Ser Gln Asn Ser Glu Leu Thr Leu  
1 5 10 15  
Gln Thr Pro Ser Lys Thr Pro Gly Leu Cys Lys Asn Arg Ser Ser Leu  
20 25 30  
Cys Pro Gln Leu Pro Arg Phe His Val Thr Gln Lys Trp Asn His Ala  
35 40 45  
Ala Glu Ala Gly Ile Thr Gly Glu Ala Ala Val Asn Ile Cys Phe Arg  
50 55 60  
Leu Leu Cys Lys Gln Ala Pro Ser Cys Gln Pro Val Ser Arg Ser Asn  
65 70 75 80  
Val Arg Gly Ser Gly Gly Gly His Thr Ser Asn Phe Ile Arg Asn Asp  
85 90 95  
Arg Phe Pro Asp Gly His Arg Asp Leu Gln Gly Gln Gln Ala  
100 105 110

<210> 339  
<211> 588  
<212> DNA  
<213> Homo sapiens

<400> 339

tctagaatga agcgctgtat cctagcaccg gcagacgtac caagactatc aagggcgta  
 60  
 gatcgtttat cctgcagttg ccattcatca gacaaatcca gtggaacca atggaagaca  
 120  
 ccgacctgca agcgctgatg gccagactcg aattgctaata tgatcgggtc gagcaactta  
 180  
 agagtcaaaa cggactccta ttagctcagg aaaagacctg ggcgcganaa cgcgctcacc  
 240  
 tcattgaaaa aaacgaaatc gcccggcgta aggtcgaatc gatgatttcg cgcctgaagg  
 300  
 ccctggagca agactatgag ttaagcaata gcgttacgtg cagatcctcg acaaagaata  
 360  
 ttgatcatc tgccccagg aagaacgcag cacctgggtga gtgctgcccg ctacctggaa  
 420  
 ggccaaaagg cgtgaaatcc gcagcagcgg caaagtcacg ggtgccgacc gcatcgccgt  
 480  
 gatggccgcg ctgaacatca cccacgatct gctgcataag caggaacggc ctgacgttca  
 540  
 ggccagcggc tcaacgcgcg agcaagtgcg tgacctgctg gaacgcgt  
 588

<210> 340

<211> 123

<212> PRT

<213> Homo sapiens

<400> 340

Met	Glu	Asp	Thr	Asp	Leu	Gln	Ala	Leu	Met	Ala	Arg	Leu	Glu	Leu	Leu
1			5					10					15		
Ile	Asp	Arg	Val	Glu	Gln	Leu	Lys	Ser	Gln	Asn	Gly	Leu	Leu	Leu	Ala
			20					25				30			
Gln	Glu	Lys	Thr	Trp	Ala	Arg	Xaa	Arg	Ala	His	Leu	Ile	Glu	Lys	Asn
		35					40				45				
Glu	Ile	Ala	Arg	Arg	Lys	Val	Glu	Ser	Met	Ile	Ser	Arg	Leu	Lys	Ala
	50					55				60					
Leu	Glu	Gln	Asp	Tyr	Glu	Leu	Ser	Asn	Ser	Val	Thr	Cys	Arg	Ser	Ser
65					70					75				80	
Thr	Lys	Asn	Ile	Arg	Ser	Ser	Ala	Pro	Arg	Lys	Asn	Ala	Ala	Pro	Gly
			85					90					95		
Glu	Cys	Cys	Pro	Leu	Pro	Gly	Arg	Pro	Lys	Gly	Val	Lys	Ser	Ala	Ala
			100					105					110		
Ala	Ala	Lys	Ser	Ser	Val	Pro	Thr	Ala	Ser	Pro					
			115					120							

<210> 341

<211> 401

<212> DNA

<213> Homo sapiens

<400> 341

ngccgcgcgg cctacctgct gtacctggcc tatgccacct ggcgtgaccg ctccggccttt  
 60  
 gcaatgaacg acacgccgac agttgcgacc gcgcgcagcc tgatcctgcg tggcttcttg  
 120

ctgaacattc ttaaccccaa gctgacaatt ttcttctctgg ccttctctgcc tcaattcgta  
 180  
 acgccaggcg gcaccgcgcc ggccttgacag atgctggtac tgagcggcgt gttcatggcg  
 240  
 atgacgcttg cagtgtttgt gctgtatggc ctgttggcga atgtgtttcg tctgcagtg  
 300  
 gtcgagtcgc cacgtgtgca gaactggctg cgacgcagtt ttgccacggc ctttgccggg  
 360  
 ctgggggttg acctggcggt tgcgcagcgc tgaggacgcg t  
 401

<210> 342

<211> 130

<212> PRT

<213> Homo sapiens

<400> 342

Xaa	Arg	Ala	Ala	Tyr	Leu	Leu	Tyr	Leu	Ala	Tyr	Ala	Thr	Trp	Arg	Asp
1				5					10					15	
Arg	Ser	Ala	Phe	Ala	Met	Asn	Asp	Thr	Pro	Thr	Val	Ala	Thr	Ala	Arg
		20						25				30			
Ser	Leu	Ile	Leu	Arg	Gly	Phe	Leu	Leu	Asn	Ile	Leu	Asn	Pro	Lys	Leu
		35					40					45			
Thr	Ile	Phe	Phe	Leu	Ala	Phe	Leu	Pro	Gln	Phe	Val	Thr	Pro	Gly	Gly
	50					55					60				
Thr	Ala	Pro	Ala	Leu	Gln	Met	Leu	Val	Leu	Ser	Gly	Val	Phe	Met	Ala
65					70				75					80	
Met	Thr	Leu	Ala	Val	Phe	Val	Leu	Tyr	Gly	Leu	Leu	Ala	Asn	Val	Phe
			85					90					95		
Arg	Arg	Ala	Val	Val	Glu	Ser	Pro	Arg	Val	Gln	Asn	Trp	Leu	Arg	Arg
		100						105					110		
Ser	Phe	Ala	Thr	Ala	Phe	Ala	Gly	Leu	Gly	Leu	Asn	Leu	Ala	Phe	Ala
		115					120					125			
Gln	Arg														
	130														

<210> 343

<211> 389

<212> DNA

<213> Homo sapiens

<400> 343

gtgttgcgca actacatggc gtccctgccg ttcagcgtgg tcgagtcggc gcgcacgcac  
 60  
 ggggtgctcca acttccagat cttctggaag ctgatcgccc cgatggcgat gccggcgatg  
 120  
 gcggcgttcg cgaccctgca gttcctgtgg gtgtggaacg acctgctcat cgccaagctc  
 180  
 ttcctcacca acgacaaccc cacgggtgatc gtcaagctcc aacagctttc cnnngggcccc  
 240  
 aaggcccagg gtgcggagct gctgacggcg ggcgccttca tctccatcgt gctacccatg  
 300  
 atcgtcttct tctgctcca gaacttctg gtgcgcggta tgacgtcggg tgccgtcaag  
 360

gggtgaccgc tcaactgcag tggccccggg

389

<210> 344

<211> 121

<212> PRT

<213> Homo sapiens

<400> 344

Val	Leu	Arg	Asn	Tyr	Met	Ala	Ser	Leu	Pro	Phe	Ser	Val	Val	Glu	Ser
1			5					10					15		
Ala	Arg	Ile	Asp	Gly	Cys	Ser	Asn	Phe	Gln	Ile	Phe	Trp	Lys	Leu	Ile
		20					25					30			
Ala	Pro	Met	Ala	Met	Pro	Ala	Met	Ala	Ala	Phe	Ala	Thr	Leu	Gln	Phe
	35					40				45					
Leu	Trp	Val	Trp	Asn	Asp	Leu	Leu	Ile	Ala	Lys	Leu	Phe	Leu	Thr	Asn
	50			55						60					
Asp	Asn	Pro	Thr	Val	Ile	Val	Lys	Leu	Gln	Gln	Leu	Ser	Xaa	Gly	Pro
65				70					75					80	
Lys	Ala	Gln	Gly	Ala	Glu	Leu	Leu	Thr	Ala	Gly	Ala	Phe	Ile	Ser	Ile
			85					90					95		
Val	Leu	Pro	Met	Ile	Val	Phe	Phe	Val	Leu	Gln	Asn	Phe	Leu	Val	Arg
		100						105					110		
Gly	Met	Thr	Ser	Gly	Ala	Val	Lys	Gly							
		115					120								

<210> 345

<211> 360

<212> DNA

<213> Homo sapiens

<400> 345

ctagtacttt atgctgatgg tgaacgtcgt tacatccttg cccctaaagg catggttgct  
60  
gggtgatgtga tccaatctgg tgaagatgca tcaattaaag taggtaactg cttaccgatg  
120  
cgtaatatcc cagttggtac aacagtacac gctgtagaaa tgaaacctgc taaagggtgca  
180  
caaattgcac gttctgctgg ttcttacagc caaattatag ctctgatgg tgcttacgtt  
240  
actctacgtt tacgtagtgg tgaaatgcgt aaaatccctg ctgagtgtcg tgcaacaatc  
300  
gggtgaagttg gtaatgcaga acatatgcta cgtcaactag gtaaagctgg tgctacgcgt  
360

<210> 346

<211> 120

<212> PRT

<213> Homo sapiens

<400> 346

Leu	Val	Leu	Tyr	Ala	Asp	Gly	Glu	Arg	Arg	Tyr	Ile	Leu	Ala	Pro	Lys
1			5					10					15		
Gly	Met	Val	Ala	Gly	Asp	Val	Ile	Gln	Ser	Gly	Glu	Asp	Ala	Ser	Ile

	20		25		30										
Lys	Val	Gly	Asn	Cys	Leu	Pro	Met	Arg	Asn	Ile	Pro	Val	Gly	Thr	Thr
	35		40		45										
Val	His	Ala	Val	Glu	Met	Lys	Pro	Ala	Lys	Gly	Ala	Gln	Ile	Ala	Arg
	50		55		60										
Ser	Ala	Gly	Ser	Tyr	Ser	Gln	Ile	Ile	Ala	Arg	Asp	Gly	Ala	Tyr	Val
65			70		75				80						
Thr	Leu	Arg	Leu	Arg	Ser	Gly	Glu	Met	Arg	Lys	Ile	Pro	Ala	Glu	Cys
			85		90				95						
Arg	Ala	Thr	Ile	Gly	Glu	Val	Gly	Asn	Ala	Glu	His	Met	Leu	Arg	Gln
	100		105		110										
Leu	Gly	Lys	Ala	Gly	Ala	Thr	Arg								
	115		120												

&lt;210&gt; 347

&lt;211&gt; 565

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 347

```

accggtgatg ccaaaggtgc tgtgacaagg ggattcatcg gttcgggcaa ggtcgtcacg
60
gcagctgccg tcatcatgat ttcggtgttc gtcttcttca tccccgaggg catgaacgcc
120
atcaaggaaa tcgccctggc cctggccgtc gggatcctca cggatgcctt cttggtgcgg
180
atgaccctcg tccccgccgt gatggccctg ctaggtgaca aggcattggtg gttgcccggg
240
tggctggatc gacgcctacc ccgcctcgac atcgaggag aagggatcac ccacgaggaa
300
aagctggccg cctggcccac agcggatcac accgaggccc tgcacgccga ggggatcggg
360
gtggaggggc tcttcgaagg cctcgatctg cacgtcgaac cgcgtcaggt gcaagccgtc
420
gtcggatcgc agaacagtgt ctcgccgtc ctgctggcga tcgggggacg gctgcccttg
480
gatcacggcc ggatgaggtc gggaggattg ctgctaccgc agcgggcttc cagagtgcgt
540
cgggtgacgt ggttcctcga cgcgt
565

```

&lt;210&gt; 348

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 348

Thr	Gly	Asp	Ala	Lys	Gly	Ala	Val	Thr	Arg	Gly	Phe	Ile	Gly	Ser	Gly
1				5				10					15		
Lys	Val	Val	Thr	Ala	Ala	Ala	Val	Ile	Met	Ile	Ser	Val	Phe	Val	Phe
			20					25					30		
Phe	Ile	Pro	Glu	Gly	Met	Asn	Ala	Ile	Lys	Glu	Ile	Ala	Leu	Ala	Leu
	35						40					45			
Ala	Val	Gly	Ile	Leu	Thr	Asp	Ala	Phe	Leu	Val	Arg	Met	Thr	Leu	Val



```

      50              55              60
Pro Ala Val Met Ala Leu Leu Gly Asp Lys Ala Trp Trp Leu Pro Gly
65              70              75              80
Trp Leu Asp Arg Arg Leu Pro Arg Leu Asp Ile Glu Gly Glu Gly Ile
      85              90              95
Thr His Glu Glu Lys Leu Ala Ala Trp Pro Thr Ala Asp His Thr Glu
      100             105             110
Ala Leu His Ala Glu Gly Ile Gly Val Glu Gly Leu Phe Glu Gly Leu
      115             120             125
Asp Leu His Val Glu Pro Arg Gln Val Gln Ala Val Val Gly Ser Gln
      130             135             140
Asn Ser Val Ser Ala Val Leu Leu Ala Ile Gly Gly Arg Leu Pro Leu
145             150             155             160
Asp His Gly Arg Met Arg Ser Gly Gly Leu Leu Leu Pro Glu Arg Ala
      165             170             175
Ser Arg Val Arg Arg Val Thr Trp Phe Leu Asp Ala
      180             185

```

<210> 349  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

```

<400> 349
ntgctggcca cggataatga ccgtactctg cgtgatgtcg ttgccgctga ccctacccat
60
gagctcgggt cggctaccgc tcatacgttt gcggacaatt tgccgttcct tcttaaactg
120
ctcgcggcag aagagccact atcgttgcag gtcacacca gtttggcgca agcacaggaa
180
gggtacgggc gggagaatcg caaaggggtg ccattagatg cccagaccg gaattaccac
240
gatcccaacc ataaaccgga gcttattgtt gggctgacgc gattccacgc actagccggc
300
ttccgtgaac cacaacgcac acttgagctt tttgacgcg
339

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<210> 350  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

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<400> 350
Xaa Leu Ala Thr Asp Asn Asp Arg Thr Leu Arg Asp Val Val Ala Ala
1              5              10              15
Asp Pro Thr His Glu Leu Gly Ser Ala Thr Ala His Thr Phe Ala Asp
      20              25              30
Asn Leu Pro Phe Leu Leu Lys Leu Leu Ala Ala Glu Glu Pro Leu Ser
      35              40              45
Leu Gln Ala His Pro Ser Leu Ala Gln Ala Gln Glu Gly Tyr Gly Arg
      50              55              60
Glu Asn Arg Lys Gly Val Pro Leu Asp Ala Pro Asp Arg Asn Tyr His
65              70              75              80
Asp Pro Asn His Lys Pro Glu Leu Ile Val Gly Leu Thr Arg Phe His

```

85 90 95  
 Ala Leu Ala Gly Phe Arg Glu Pro Gln Arg Thr Leu Glu Leu Phe Asp  
 100 105 110  
 Ala

<210> 351  
 <211> 354  
 <212> DNA  
 <213> Homo sapiens

<400> 351  
 gcgcgccccca gtgccgagac ccgggggcttc aggagccggc cccgggagag aagagtgcgg  
 60  
 cggcgggacgg agaaaacaac tccaaagttg gcgaaaggca ccgcccctac tccggggctg  
 120  
 ccgcgccttc cccgccccca gccctggcat ccagagtacg ggtcgagccc gngggccatgg  
 180  
 agcccccttg gggaggcggc accagggagc ctggggccccg gggctccgcc gcgaccccat  
 240  
 cgggtagacc acagaagctc cgggaccctt ccggcacctc tggacagccc aggatgctgt  
 300  
 tggccaccen ntectectcc tectcttgg aggcgctctg gcccatccag accg  
 354

<210> 352  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 352  
 Ala Arg Pro Ser Ala Glu Thr Arg Gly Phe Arg Ser Arg Pro Arg Glu  
 1 5 10 15  
 Arg Arg Val Arg Arg Thr Glu Lys Thr Thr Pro Lys Leu Ala Lys  
 20 25 30  
 Gly Thr Ala Pro Thr Pro Gly Leu Pro Pro Pro Pro Arg Pro Gln Pro  
 35 40 45  
 Trp His Pro Glu Tyr Gly Ser Ser Pro Xaa Pro Trp Ser Pro Pro Gly  
 50 55 60  
 Glu Ala Ala Pro Gly Ser Leu Gly Pro Gly Ala Pro Pro Arg Pro His  
 65 70 75 80  
 Arg Val Asp His Arg Ser Ser Gly Thr Leu Pro Ala Pro Leu Asp Ser  
 85 90 95  
 Pro Gly Cys Cys Trp Pro Pro Xaa Pro Pro Pro Pro Trp Arg Arg  
 100 105 110  
 Ser Gly Pro Ser Arg Pro  
 115

<210> 353  
 <211> 1469  
 <212> DNA  
 <213> Homo sapiens

<400> 353

nntcatgaag gcttgaactt gcgtgatctt cagcctgcgg acctggcggg tgacggcggt  
60  
attgagccgg tggacctcgt ggtcggagat gtctctttta tctccttgac gatgatecctt  
120  
gaacccattt cagctgttgt cagcccacac ggccctcatgc tgttgctggg gaagcctcaa  
180  
tttgaggttg gttgcaaggc tttgggagcc catggcggtg tcacggacct ggccctgcgc  
240  
ttgcaggcca tcgcgggtgt catggcagca gcggtagatt tgggttggcg tatgcgtgac  
300  
gagtgcgata gcccggttgc cgggcaggat ggaaacgttg agcacttcgt cttgctggaa  
360  
cgtacgggtc ggtgacagac gtccgggcat atcatgggcc gctactgtgg tcttgtgaac  
420  
gacacgagcc cttcgagata cgttgctcgtc gtcacccatg ccacgcggga cgacgctttt  
480  
gacgcggctg ccgaattcat ctctgaaatg gcggggcgag acattggttg cgcggttcg  
540  
gatgatcagg tgaagccgat gtcaagcaag ctgccaggga tcgatcttga aagcttgga  
600  
gagttcgccc acgaggcgga ggtggtcgtc gtctttggcg gcgacggcac gatcttgca  
660  
gctgctgaat ggtcattacc tcgccacgtt cccatgattg gcgtcaacct tggccatgtc  
720  
ggttttctgg ctgagctgga gcgtccgat atggcggatc tagtgaacaa ggtgtgttcg  
780  
cgcgactaca ccgttgagga tcgcctcgtg cttaaaacca ccgtcaccga gcattccgga  
840  
caacaccgtt ggagttcttt tgccgtcaac gagttgtctc tggaaaaggc agcccgcgcg  
900  
cgcgtgctcg acgttctggc gtctgtcgac gagttgcgg tgcaacgctg gagttgctgac  
960  
gggatcctgg tctcgacccc gaccggatcg acggcctacg cgttctcagc tggcgggccc  
1020  
gtcatgtggc ccgatctcga cgccatgctc atggtgccgt tgagcgctca cgctctcttt  
1080  
gctcgaccgc tggatcatgag ccagctgct cgagtgacc ttgacatcca gccagacggt  
1140  
tcagaatcgg cggttctgtg gtgcgacggg cgccgatcgt gcaccgtacg accgggggaa  
1200  
agaatcacgg tcgtccgcca tcccgaccgt ctgcgcattg ctgctctggc cgcgcagccc  
1260  
ttcacatcgc gtctgggtcaa gaagtttgag ctcccggta gcgggtggcg tcagggtcgt  
1320  
gaccgtcatc acctagagga gacttcgtga tacgtagtgt gcgaattcgt ggactcggcg  
1380  
tcacgatga gacggtcctc gaacctcat ccgcgctgac ggcagtcacc ggcgagaccg  
1440  
gcgccgaaa gaccatggtg gtcaccggt  
1469

&lt;210&gt; 354

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 354

```

Met Gly Arg Tyr Cys Gly Leu Val Asn Asp Thr Ser Pro Ser Arg Tyr
 1           5           10           15
Val Val Val Val Thr His Ala Thr Arg Asp Asp Ala Phe Asp Ala Ala
 20           25           30
Ala Glu Phe Ile Ser Glu Met Ala Gly Arg Asp Ile Gly Cys Ala Val
 35           40           45
Pro Asp Asp Gln Val Lys Pro Met Ser Ser Lys Leu Pro Gly Ile Asp
 50           55           60
Leu Glu Ser Leu Gly Glu Phe Ala His Glu Ala Glu Val Val Val Val
 65           70           75           80
Phe Gly Gly Asp Gly Thr Ile Leu Arg Ala Ala Glu Trp Ser Leu Pro
 85           90           95
Arg His Val Pro Met Ile Gly Val Asn Leu Gly His Val Gly Phe Leu
100           105           110
Ala Glu Leu Glu Arg Ser Asp Met Ala Asp Leu Val Asn Lys Val Cys
115           120           125
Ser Arg Asp Tyr Thr Val Glu Asp Arg Leu Val Leu Lys Thr Thr Val
130           135           140
Thr Glu His Ser Gly Gln His Arg Trp Ser Ser Phe Ala Val Asn Glu
145           150           155           160
Leu Ser Leu Glu Lys Ala Ala Arg Arg Arg Met Leu Asp Val Leu Ala
165           170           175
Ser Val Asp Glu Leu Pro Val Gln Arg Trp Ser Cys Asp Gly Ile Leu
180           185           190
Val Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
195           200           205
Pro Val Met Trp Pro Asp Leu Asp Ala Met Leu Met Val Pro Leu Ser
210           215           220
Ala His Ala Leu Phe Ala Arg Pro Leu Val Met Ser Pro Ala Ala Arg
225           230           235           240
Val Asp Leu Asp Ile Gln Pro Asp Gly Ser Glu Ser Ala Val Leu Trp
245           250           255
Cys Asp Gly Arg Arg Ser Cys Thr Val Arg Pro Gly Glu Arg Ile Thr
260           265           270
Val Val Arg His Pro Asp Arg Leu Arg Ile Ala Arg Leu Ala Ala Gln
275           280           285
Pro Phe Thr Ser Arg Leu Val Lys Lys Phe Glu Leu Pro Val Ser Gly
290           295           300
Trp Arg Gln Gly Arg Asp Arg His His Leu Glu Glu Thr Ser
305           310           315

```

&lt;210&gt; 355

&lt;211&gt; 558

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 355

```

nggatccccac ctcttggaat ggaaaccac ataccagttc tcttcctcga tttgaatgcg
60
gatgacctca gtgccaatga gcagcttggt ggccccatg catccggcgt gaactccatc
120

```

ctgcccagg agcatggcag ccagtttttc tacctgcca tcataaagca cagtgatgat  
 180  
 gaggtttcag ccacagcctc ttgggattcc tcggtgcatg attctgttca cttgaatggg  
 240  
 gtcacaccac agaataaaag gatttaccta attgtgaaaa ccacagttca actcagccac  
 300  
 cctgctgcta tggagttagt attacgaaaa cgaattgcag ccaatattta caacaaacag  
 360  
 agtttcacgc agagtttgaa gaggagaata tccttgaaaa atatatttta ttctgtggt  
 420  
 gtaacctatg aaatagtatc caatatacca aaggcaactg aggagataga ggaccgggaa  
 480  
 acgctggctc tcctggcagc aaggagtga aacgaaggca catcagatgg gaagacgtac  
 540  
 attgagaagt acactcga  
 558

&lt;210&gt; 356

&lt;211&gt; 186

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 356

Xaa	Ile	Pro	Pro	Gly	Met	Glu	Thr	His	Ile	Pro	Val	Leu	Phe	Leu
1			5				10					15		
Asp	Leu	Asn	Ala	Asp	Asp	Leu	Ser	Ala	Asn	Glu	Gln	Leu	Val	Gly
		20					25					30		Pro
His	Ala	Ser	Gly	Val	Asn	Ser	Ile	Leu	Pro	Lys	Glu	His	Gly	Ser
		35				40					45			Gln
Phe	Phe	Tyr	Leu	Pro	Ile	Ile	Lys	His	Ser	Asp	Asp	Glu	Val	Ser
	50					55				60				Ala
Thr	Ala	Ser	Trp	Asp	Ser	Ser	Val	His	Asp	Ser	Val	His	Leu	Asn
65				70					75					80
Val	Thr	Pro	Gln	Asn	Glu	Arg	Ile	Tyr	Leu	Ile	Val	Lys	Thr	Thr
			85						90				95	Val
Gln	Leu	Ser	His	Pro	Ala	Ala	Met	Glu	Leu	Val	Leu	Arg	Lys	Arg
		100						105				110		Ile
Ala	Ala	Asn	Ile	Tyr	Asn	Lys	Gln	Ser	Phe	Thr	Gln	Ser	Leu	Lys
		115				120					125			Arg
Arg	Ile	Ser	Leu	Lys	Asn	Ile	Phe	Tyr	Ser	Cys	Gly	Val	Thr	Tyr
	130					135					140			Glu
Ile	Val	Ser	Asn	Ile	Pro	Lys	Ala	Thr	Glu	Glu	Ile	Glu	Asp	Arg
145				150					155					160
Thr	Leu	Ala	Leu	Leu	Ala	Ala	Arg	Ser	Glu	Asn	Glu	Gly	Thr	Ser
			165						170				175	Asp
Gly	Lys	Thr	Tyr	Ile	Glu	Lys	Tyr	Thr	Arg					
		180						185						

&lt;210&gt; 357

&lt;211&gt; 323

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 357

acgcgtgcgt gtgttgtgtg agtcgggtgt gtgcatgcgt gtgggtgtgc agcaggtggg  
 60  
 gtacgatcag gctgaaggct gatcaggcac aaggctcttg gggagagccc tggttccagc  
 120  
 cctgggggtca gagcagcagg ggccagaaag acggcagggg tgagcactgc acccgctggg  
 180  
 cagggcaggg ccacagaagg cagggcatgg aggccacgtg aagggttga cagagtggat  
 240  
 ggatgtctcc ggaagcacct gcgtggccca gtcagcagga tcagactcgc atgtgtcagg  
 300  
 gtcaccatgg gtcagcgagg atn  
 323

<210> 358

<211> 102

<212> PRT

<213> Homo sapiens

<400> 358

Met	Val	Thr	Leu	Thr	His	Ala	Ser	Leu	Ile	Leu	Leu	Thr	Gly	Pro	Arg
1				5					10					15	
Arg	Cys	Phe	Arg	Arg	His	Pro	Ser	Thr	Leu	Ser	Ser	Pro	Ser	Arg	Gly
			20					25					30		
Leu	His	Ala	Leu	Pro	Ser	Val	Ala	Leu	Pro	Cys	Pro	Ala	Gly	Ala	Val
		35					40					45			
Leu	Thr	Pro	Ala	Val	Phe	Leu	Ala	Pro	Ala	Ala	Leu	Thr	Pro	Gly	Leu
	50					55					60				
Glu	Pro	Gly	Leu	Ser	Pro	Arg	Ala	Leu	Cys	Leu	Ile	Ser	Leu	Gln	Pro
65					70					75				80	
Asp	Arg	Thr	Pro	Pro	Ala	Ala	His	Pro	His	Ala	Cys	Thr	His	Pro	Thr
				85					90					95	
His	Thr	Thr	His	Ala	Arg										
															100

<210> 359

<211> 265

<212> DNA

<213> Homo sapiens

<400> 359

acgcgtaccg acaagcgcgc ggtgatggcc gaccttcgcg aatcgggcgc aatcgagcag  
 60  
 gatgcggaca tgatcgtctt catctaccgc gacgattact acaacaagga aaattcgccg  
 120  
 gacaaggggc tggcagagat catcatcggc aagcatcggg ggggccccac cggctcgtgc  
 180  
 aagctgaagt tcttcggcga gtacacccgt ttcgacaacc tggcccacaa ctcggttggt  
 240  
 tcgttcgaat aacggatgat tccgg  
 265

<210> 360

<211> 83

<212> PRT

<213> Homo sapiens

<400> 360

```

Thr Arg Thr Asp Lys Arg Pro Val Met Ala Asp Leu Arg Glu Ser Gly
 1           5           10           15
Ala Ile Glu Gln Asp Ala Asp Met Ile Val Phe Ile Tyr Arg Asp Asp
      20           25           30
Tyr Tyr Asn Lys Glu Asn Ser Pro Asp Lys Gly Leu Ala Glu Ile Ile
      35           40           45
Ile Gly Lys His Arg Gly Gly Pro Thr Gly Ser Cys Lys Leu Lys Phe
      50           55           60
Phe Gly Glu Tyr Thr Arg Phe Asp Asn Leu Ala His Asn Ser Val Gly
65           70           75           80
Ser Phe Glu

```

<210> 361

<211> 453

<212> DNA

<213> Homo sapiens

<400> 361

```

gctttgacagg aggaaatctc tatctctggc tgcaagatga ggctgagcta cctgagcagc
60
cggacccctg gctacaaatc tgtcctgagg atcagcctca cccacccgac catccccctc
120
aacctcatga aggtgcacct catggtagcg gtggagggcc gcctcttcag gaagtggttc
180
gctgcagccc cagacctgtc ctattatttc atttgggaca agacagacgt ctacaaccag
240
aaggtgtttg ggctttcaga agcctttggt tccgtggggt atgaatatga atcctgcccc
300
gatctaattc tgtgggaaaa aagaacaaca gtgctgcagg gctatgaaat tgacgcgtcc
360
aagcttggag gatggagcct agacaaacat catgcctca acattcaaag tggcatcctg
420
caciaaggga atgngagaa ccagtttgtg tct
453

```

<210> 362

<211> 151

<212> PRT

<213> Homo sapiens

<400> 362

```

Ala Leu Gln Glu Glu Ile Ser Ile Ser Gly Cys Lys Met Arg Leu Ser
 1           5           10           15
Tyr Leu Ser Ser Arg Thr Pro Gly Tyr Lys Ser Val Leu Arg Ile Ser
      20           25           30
Leu Thr His Pro Thr Ile Pro Phe Asn Leu Met Lys Val His Leu Met
      35           40           45
Val Ala Val Glu Gly Arg Leu Phe Arg Lys Trp Phe Ala Ala Ala Pro
      50           55           60
Asp Leu Ser Tyr Tyr Phe Ile Trp Asp Lys Thr Asp Val Tyr Asn Gln

```

```

65          70          75          80
Lys Val Phe Gly Leu Ser Glu Ala Phe Val Ser Val Gly Tyr Glu Tyr
          85          90          95
Glu Ser Cys Pro Asp Leu Ile Leu Trp Glu Lys Arg Thr Thr Val Leu
          100          105          110
Gln Gly Tyr Glu Ile Asp Ala Ser Lys Leu Gly Gly Trp Ser Leu Asp
          115          120          125
Lys His His Ala Leu Asn Ile Gln Ser Gly Ile Leu His Lys Gly Asn
          130          135          140
Gly Glu Asn Gln Phe Val Ser
145          150

```

<210> 363  
 <211> 502  
 <212> DNA  
 <213> Homo sapiens

```

<400> 363
ggtagcaaaa aagtttgcca cagtattcac actccaggtc tccataaacc ttccagatcc
60
gctcacacaa gctgggtgttc atttgcttct tctgtaaact gttcaggacc ttcataaaag
120
cggtgatgcc tgaccgggtgc tcaggggagc ctttgcaaga gtcaggctga tgtgtgatgg
180
tgtccccacc accagctact ggagggagga ggtctgagga ctcagctggg ttgacctga
240
gacacctgct gggatctggg tcaccagctg aaagcacagc catgttctgc cttccccta
300
gggggctctg ggcgccatgg ctttcctgat ctgaccagc actctgggccc ttggacagca
360
gtagtgtgat cacttcacct tgcgtctgga ctgagcttct gtgctgcatg tctgggggct
420
tctcaggagc agcatgagcc tctgcggagg aggtatcatt tttcaacaaa aaatcatctg
480
aaaccacctc ttgagaatgc ag
502

```

<210> 364  
 <211> 136  
 <212> PRT  
 <213> Homo sapiens

```

<400> 364
Met Gln His Arg Ser Ser Val Gln Thr Gln Gly Glu Val Ile Thr Leu
1          5          10          15
Leu Leu Ser Lys Ala Gln Ser Ala Gly Ser Asp Gln Glu Ser His Gly
          20          25          30
Ala Gln Ser Pro Leu Gly Glu Gly Gln Asn Met Ala Val Leu Ser Ala
          35          40          45
Gly Asp Pro Asp Pro Ser Arg Cys Leu Arg Ser Asn Pro Ala Glu Ala
          50          55          60
Ser Asp Leu Leu Pro Pro Val Ala Gly Gly Gly Asp Thr Ile Thr His
65          70          75          80
Gln Pro Asp Ser Cys Lys Ala Ala Pro Glu His Arg Ser Gly Ile Thr

```



[illegible]

```
<210> 365
<211> 333
<212> DNA
<213> Homo sapiens
```

```
<400> 365
atctcaacgg atgcatccat caaggagatg atccccccag gtgctcttgt tatgtctcac
60
ccactgatcg ttgggattct atttgggggt gagaccctct ctggagtcct tgctggtgcc
120
cttgtctctg gtgttcagat tgccatttct gcatccaaca ctggtggtgc ctgggacaac
180
gccaagaagt acattgaggc tggagtttca gagcatgcc a ggacccttg cccaaaaggt
240
tctgaccctc acaaggcggc tgtcattggt gacaccattg gagatcctct caaggacacg
300
tctggccctt cctcaacat cctcatcaag ctt
333
```

```
<210> 366
<211> 111
<212> PRT
<213> Homo sapiens
```

```

<400> 366
Ile Ser Thr Asp Ala Ser Ile Lys Glu Met Ile Pro Pro Gly Ala Leu
 1          5          10          15
Val Met Leu Thr Pro Leu Ile Val Gly Ile Leu Phe Gly Val Glu Thr
          20          25          30
Leu Ser Gly Val Leu Ala Gly Ala Leu Val Ser Gly Val Gln Ile Ala
          35          40          45
Ile Ser Ala Ser Asn Thr Gly Gly Ala Trp Asp Asn Ala Lys Lys Tyr
          50          55          60
Ile Glu Ala Gly Val Ser*Glu His Ala Arg Thr Leu Gly Pro Lys Gly
65          70          75          80
Ser Asp Pro His Lys Ala Ala Val Ile Gly Asp Thr Ile Gly Asp Pro
          85          90          95
Leu Lys Asp Thr Ser Gly Pro Ser Leu Asn Ile Leu Ile Lys Leu
          100          105          110

```

```
<210> 367
<211> 381
<212> DNA
<213> Homo sapiens
```

<400> 367

gcgttcgtcg cactacccgg cggcgccgga acccttgacg agctactcga agcatggaca  
60  
tggcagcagc tcggtgtaca cagcaaaccg gtngccttg tacgactcga cnncttctgg  
120  
gcaccgctga ccgcgctact caaccacatg accatcgaaa gcttcattcg ccctgaggac  
180  
cgcgccctgc tcgtgatcgc cgataccata catcagctga tggccgatct tgagggatgg  
240  
accccaccac caccgaagtg gcgctcgtga catagaacaa atgattctga ctatggctca  
300  
ttgacatctg cgcagcggct actagctcca ttgacttcaa atcgggcctt ggccgaggct  
360  
cngttcaggt ggcccgaat g  
381

&lt;210&gt; 368

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 368

Ala	Phe	Val	Ala	Leu	Pro	Gly	Gly	Gly	Gly	Thr	Leu	Asp	Glu	Leu	Leu
1				5					10					15	
Glu	Ala	Trp	Thr	Trp	Gln	Gln	Leu	Gly	Val	His	Ser	Lys	Pro	Val	Xaa
			20					25					30		
Leu	Val	Arg	Leu	Asp	Xaa	Phe	Trp	Ala	Pro	Leu	Thr	Ala	Leu	Leu	Asn
			35				40					45			
His	Met	Thr	Ile	Glu	Ser	Phe	Ile	Arg	Pro	Glu	Asp	Arg	Ala	Ser	Leu
			50				55				60				
Val	Ile	Ala	Asp	Thr	Ile	His	Gln	Leu	Met	Ala	Asp	Leu	Glu	Gly	Trp
65					70					75				80	
Thr	Pro	Pro	Pro	Pro	Lys	Trp	Arg	Ser							
															85

&lt;210&gt; 369

&lt;211&gt; 313

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 369

gatacatgat cctctcatatc cgcacacaca ccgctcccct ctgccgcaat tcgcagacaa  
60  
acttgccgag gcttcacagc aagccgtcaa ggctgcttcc tgtgggctac cgatagtctc  
120  
gtacgcgagt tctcggacat caacgccaac gtcgggcaag atactgtcaa cgccatctac  
180  
acattctacg agcagcaagc gaccagtctc cttcgccagc tgaacgacct cccacccgaa  
240  
gagcttcccg acgtcatcga ggacttcttc cgctgtcca ctgatgtcct tctttaccat  
300  
ttccagcaag ctt  
313

&lt;210&gt; 370

<211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 370  
 Ser Ser His Thr Ala His Thr Pro Leu Pro Ser Ala Ala Ile Arg Arg  
 1 5 10 15  
 Gln Thr Cys Ala Gly Phe Thr Ala Ser Arg Gln Gly Cys Phe Leu Trp  
 20 25 30  
 Ala Thr Asp Ser Leu Val Arg Glu Phe Ser Asp Ile Asn Ala Asn Val  
 35 40 45  
 Gly Gln Asp Thr Val Asn Ala Ile Tyr Thr Phe Tyr Glu Gln Gln Ala  
 50 55 60  
 Thr Ser Phe Leu Arg Gln Leu Asn Asp Leu Pro Pro Glu Glu Leu Pro  
 65 70 75 80  
 Asp Val Ile Glu Asp Phe Phe Arg Leu Ser Thr Asp Val Leu Leu Tyr  
 85 90 95  
 His Phe Gln Gln Ala  
 100

<210> 371  
 <211> 380  
 <212> DNA  
 <213> Homo sapiens

<400> 371  
 atgacgggtc acgtcatcct ggcgattcca caggtgggtga cgtcatggat cggcctcatc  
 60  
 tgcacgcgca ttggcacggg ctttatcaag ccgaacctct ccacgggtgg aggaggtctt  
 120  
 tacgatgacg gtgacccccg ccgcgatcag ggtttcctgt acttctacat gtcgatcagt  
 180  
 attggatctc tcttcgcgcc gatcgtcacc ggcctcctca aggaccatta cggctaccac  
 240  
 gtaggtttca ttgccgctgc tateggtatg gctctgggtc tgatcgcctt cttccacggt  
 300  
 cgttccaaac tgcgtgagct cgccttcgac atccccaatc cgctggcccc cggcgagggt  
 360  
 cgccggatgg tgctccgcgg  
 380

<210> 372  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 372  
 Met Thr Gly His Val Ile Leu Ala Ile Pro Gln Val Val Thr Ser Trp  
 1 5 10 15  
 Ile Gly Leu Ile Cys Ile Ala Ile Gly Thr Gly Phe Ile Lys Pro Asn  
 20 25 30  
 Leu Ser Thr Val Val Gly Gly Leu Tyr Asp Asp Gly Asp Pro Arg Arg  
 35 40 45  
 Asp Gln Gly Phe Leu Tyr Phe Tyr Met Ser Ile Ser Ile Gly Ser Leu

```

      50              55              60
Phe Ala Pro Ile Val Thr Gly Leu Leu Lys Asp His Tyr Gly Tyr His
65              70              75              80
Val Gly Phe Ile Ala Ala Ala Ile Gly Met Ala Leu Gly Leu Ile Ala
      85              90              95
Phe Phe His Gly Arg Ser Lys Leu Arg Glu Leu Ala Phe Asp Ile Pro
      100              105              110
Asn Pro Leu Ala Pro Gly Glu Gly Arg Arg Met Val Leu Arg
      115              120              125

```

&lt;210&gt; 373

&lt;211&gt; 475

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 373

```

acatgttgga aaaattgcct ccactctgg tgctacaggt atgaatctca gccacagtga
60
tgactgtggc agctacaggc ctgatgaaca cccaccaag aaaaggagca tcatgtgcct
120
gcttctctct ggttcctaaa tcctttggcc aaacattttc cccacaacc tccactccag
180
ttggctggtc actgcctctc agaaagaagt ccaggtccc tgtcagcccc agagcgctg
240
catggactct gccactgtc cctttccaac acggaggccc ccaattctgg ggaccctac
300
accctaccct gtaccaccac atccccatgc ctgctccaga cagcactaac ctcccatgac
360
agtgggacca aagcagttct taaaggcca atccactcag ttcttaaatg aaaaacagtt
420
gcccatgagt ccccccaaa gacgtccgca catatgcca acattcggtg tgcac
475

```

&lt;210&gt; 374

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 374

```

Met Gly Met Trp Trp Tyr Arg Val Gly Cys Arg Gly Pro Gln Asn Trp
1              5              10              15
Gly Pro Pro Cys Trp Lys Gly Thr Val Gly Arg Val His Ala Gly Ala
      20              25              30
Leu Gly Leu Thr Gly Thr Trp Asp Phe Phe Leu Arg Gly Ser Asp Gln
      35              40              45
Pro Thr Gly Val Glu Gly Cys Gly Glu Asn Val Trp Pro Lys Asp Leu
      50              55              60
Gly Thr Arg Glu Lys Gln Ala His Asp Ala Pro Phe Leu Gly Gly Val
65              70              75              80
Phe Ile Arg Pro Val Ala Ala Thr Val Ile Thr Val Ala Glu Ile His
      85              90              95
Thr Cys Ser Thr Arg Val Gly Gly Asn Phe Ser Asn Met
      100              105

```

<210> 375  
 <211> 332  
 <212> DNA  
 <213> Homo sapiens

<400> 375  
 nnacgcgtcg cctccacctc gaaacccgcc ggcggtcggt ttttcaccat ggccgaccgc  
 60  
 aaggcccaag ttgcgacggg cacggacacg ctgtatttca cgccgtcgca atgggatgga  
 120  
 tgcattggcac ggatgcgtgg ggataagata tcagcactga agtggaaatca gatgcagatg  
 180  
 gcggcatgct ccttcatagc ggcagtgggt gcgaagctgg gctgcccga gcgcactatg  
 240  
 ggcaaggcgc agctgctgta ccagcgtttc catctatttc atgcgccgac tgagttttcg  
 300  
 ttacatgagg tggctttgac gtgtctcttc ac  
 332

<210> 376  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 376  
 Xaa Arg Val Ala Ser Thr Ser Lys Pro Ala Gly Gly Arg Phe Phe Thr  
 1 5 10 15  
 Met Ala Asp Arg Lys Ala Gln Val Ala Thr Val Thr Asp Thr Leu Tyr  
 20 25 30  
 Phe Thr Pro Ser Gln Trp Asp Gly Cys Met Ala Arg Met Arg Gly Asp  
 35 40 45  
 Lys Ile Ser Ala Leu Lys Trp Asn Gln Met Gln Met Ala Ala Cys Ser  
 50 55 60  
 Phe Ile Ala Ala Val Gly Ala Lys Leu Gly Cys Pro Gln Arg Thr Met  
 65 70 75 80  
 Gly Thr Ala Gln Leu Tyr Gln Arg Phe His Leu Phe His Ala Pro  
 85 90 95  
 Thr Glu Phe Ser Leu His Glu Val Ala Leu Thr Cys Leu Phe  
 100 105 110

<210> 377  
 <211> 369  
 <212> DNA  
 <213> Homo sapiens

<400> 377  
 cgcggtccag gtatgtcaac tgatctgtcg gatatttccg aggttgagta ccgtcaactg  
 60  
 aggctggaac gagtgggtgct gtgttcggtg tggactcagg gaactgccgc agacgccgag  
 120  
 aacgctatgg cggagctgaa agcccttgct gaaacggcgg gatctcaggt actcgaagct  
 180  
 gtcattgcaac gtcggactac cccggatccg gcgacgtaca ttggttcggg caaggtggct  
 240

gagcttgccg aggtggtgcg ggcgactggt gccgatactg tcatttgtga cgggtgaactt  
 300  
 gacgccgctc agttgcgcaa cctcgaggat cgggtcaagn gcaaagttgt ggaccggtcg  
 360  
 gtctgattc  
 369

<210> 378  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 378  
 Arg Val Pro Gly Met Ser Thr Asp Leu Ser Asp Ile Ser Glu Val Glu  
 1 5 10 15  
 Tyr Arg Gln Leu Arg Leu Glu Arg Val Val Leu Cys Ser Val Trp Thr  
 20 25 30  
 Gln Gly Thr Ala Ala Asp Ala Glu Asn Ala Met Ala Glu Leu Lys Ala  
 35 40 45  
 Leu Ala Glu Thr Ala Gly Ser Gln Val Leu Glu Ala Val Met Gln Arg  
 50 55 60  
 Arg Thr Thr Pro Asp Pro Ala Thr Tyr Ile Gly Ser Gly Lys Val Ala  
 65 70 75 80  
 Glu Leu Ala Glu Val Val Arg Ala Thr Gly Ala Asp Thr Val Ile Cys  
 85 90 95  
 Asp Gly Glu Leu Asp Ala Ala Gln Leu Arg Asn Leu Glu Asp Arg Val  
 100 105 110  
 Lys Xaa Lys Val Val Asp Arg Ser Val  
 115 120

<210> 379  
 <211> 408  
 <212> DNA  
 <213> Homo sapiens

<400> 379  
 acgcgttact taaacttatc tgtaaataat aaattcatta tttctagttg gttaggtact  
 60  
 atgggctgtg gtttaccagg tgctatggca gctaaaattg cttatccaaa ccgtcaagca  
 120  
 gtagctatca caggcgacgg tgcgttccaa atggtaatgc aagactttgc tacagctgtt  
 180  
 caatataact taccaatgac aatctttgta ttaaataaca aacaattgtc attcatta  
 240  
 tatgaacaac aagctgctgg tgaattagag tatgccattg atttctctga tatggatcat  
 300  
 gctaaatttg ctgaagctgc tgggtggtaaa ggctatgttg tgagagatgt aagtcgtctt  
 360  
 gacgacatcg ttgaagaggc aatggctcaa gatgttccaa caatcggt  
 408

<210> 380  
 <211> 136  
 <212> PRT

<213> Homo sapiens

<400> 380

```

Thr Arg Tyr Leu Asn Leu Ser Val Asn Asn Lys Phe Ile Ile Ser Ser
 1           5           10           15
Trp Leu Gly Thr Met Gly Cys Gly Leu Pro Gly Ala Met Ala Ala Lys
      20           25           30
Ile Ala Tyr Pro Asn Arg Gln Ala Val Ala Ile Thr Gly Asp Gly Ala
      35           40           45
Phe Gln Met Val Met Gln Asp Phe Ala Thr Ala Val Gln Tyr Asn Leu
      50           55           60
Pro Met Thr Ile Phe Val Leu Asn Asn Lys Gln Leu Ser Phe Ile Lys
      65           70           75           80
Tyr Glu Gln Gln Ala Ala Gly Glu Leu Glu Tyr Ala Ile Asp Phe Ser
      85           90           95
Asp Met Asp His Ala Lys Phe Ala Glu Ala Ala Gly Gly Lys Gly Tyr
      100          105          110
Val Val Arg Asp Val Ser Arg Leu Asp Asp Ile Val Glu Glu Ala Met
      115          120          125
Ala Gln Asp Val Pro Thr Ile Val
      130          135

```

<210> 381

<211> 613

<212> DNA

<213> Homo sapiens

<400> 381

```

nacgcgtcat aggcggggccc agtgaagac caccgaaca cagttggttg agatccgcgt
60
tgagggcaag gtcctgcgcg tcccgcgaaa tctgtcaag gcctaccact ctgggctgat
120
cgacgtcgag gactgaaccc tgggagcctg ggcggtccag catgactgct caggctcatt
180
accaaaacgc gtcgatcccg tagggttgtc gtcatgagca agcccgaagt gaccctgccc
240
gattccgccc ccgacgacct cgtcgttgag gacatcacca tcggcgacgg ccctgaagcg
300
tccgctggca acctcgtcga agtgcactac gtcggcgtgg ccttaagcaa tggctcgtgag
360
ttcgattctt cctggaaccg cggggagccg ctgaccttcc aactaggggc tggccagggtg
420
atccccgagt gggatgaagg tgtccaaggt atgaaggctg gtggacgacg caaactcgtc
480
atccccacc accttgctta cggtcgcaa ggaatctccg gtgtgatcgc tggcgggtgag
540
acgctggtct tcgtctgcga ccttgtcaac atcatctgac gtgacccccg ctcaagcagt
600
cttcgcgccc ggg
613

```

<210> 382

<211> 137

<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 382

```

Leu Leu Arg Leu Ile Thr Lys Thr Arg Arg Ser Arg Arg Val Val Val
 1           5           10           15
Met Ser Lys Pro Glu Val Thr Leu Pro Asp Ser Ala Pro Asp Asp Leu
      20           25           30
Val Val Glu Asp Ile Thr Ile Gly Asp Gly Pro Glu Ala Ser Ala Gly
      35           40           45
Asn Leu Val Glu Val His Tyr Val Gly Val Ala Leu Ser Asn Gly Arg
      50           55           60
Glu Phe Asp Ser Ser Trp Asn Arg Gly Glu Pro Leu Thr Phe Gln Leu
65           70           75           80
Gly Ala Gly Gln Val Ile Pro Glu Trp Asp Glu Gly Val Gln Gly Met
      85           90           95
Lys Val Gly Gly Arg Arg Lys Leu Val Ile Pro His His Leu Ala Tyr
      100          105          110
Gly Pro Gln Gly Ile Ser Gly Val Ile Ala Gly Gly Glu Thr Leu Val
      115          120          125
Phe Val Cys Asp Leu Val Asn Ile Ile
      130          135

```

&lt;210&gt; 383

&lt;211&gt; 352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 383

```

nggagcaaca cctggctcctt ggggaatgaag tgtaggaggt gcatttgctg aggttggtgt
60
ttgccaaaga gatgccagct tcttcgaact actgctgtgc aactcttcat gttcaaaacc
120
cagttttctg tttttcacac ctgaacatac acccccctgc agttgggtgg ctcccccggt
180
accagctggg ctctatctac agagagagca atggcttccc ttcccttgaa ggaagtctca
240
ccctcacaag gacacttgat ccgctgcaaa gcagaaagtg tgcggaccct ttgggaaggg
300
cgttcttttc ttgttagaa cctaggattc tgttttccc aaacaggatc an
352

```

&lt;210&gt; 384

&lt;211&gt; 93

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 384

```

Met Pro Ala Ser Ser Asn Tyr Cys Cys Ala Thr Leu His Val Gln Asn
 1           5           10           15
Pro Val Phe Cys Phe Ser His Leu Asn Ile His Pro Pro Ala Val Gly
      20           25           30
Trp Leu Pro Arg Tyr Gln Leu Gly Ser Ile Tyr Arg Glu Ser Asn Gly
      35           40           45
Phe Pro Ser Leu Glu Gly Ser Leu Thr Leu Thr Arg Thr Leu Asp Pro

```



50                      55                      60  
 Leu Gln Ser Arg Lys Cys Ala Asp Pro Leu Gly Arg Ala Phe Phe Ser  
 65                      70                      75                      80  
 Cys Leu Glu Pro Arg Ile Leu Phe Phe Pro Asn Arg Ile  
                     85                      90

<210> 385  
 <211> 342  
 <212> DNA  
 <213> Homo sapiens

<400> 385  
 gccggcgcca cgaaatgcaa aatgcgccct tcaccggacg ccaggttgat cgagccgcca  
 60  
 gcacctcggg caatgtcctg ggcctgactg gcacacgcaa tcaaagcgag caacaacaca  
 120  
 caaaaacgca tcatgaggca gacgccaggg aagtacaga agccgcagca ggcgcgcggc  
 180  
 gattggaaat atcggtgagg ctaatggtca ccagcgcttg caggttgat tgggtggcca  
 240  
 attcgcgga cgcagcacc gccagttcca gctcgccgag cagcaccagg cgacgcaagc  
 300  
 tgcggcgcaa ctccgggtgc accaacaaca ccgactgtt ca  
 342

<210> 386  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 386  
 Met Gln Asn Ala Pro Phe Thr Gly Arg Gln Val Asp Arg Ala Ala Ser  
 1                      5                      10                      15  
 Thr Ser Gly Asn Val Leu Gly Leu Thr Gly Thr Arg Asn Gln Ser Glu  
                     20                      25                      30  
 Gln Gln His Thr Lys Thr His His Glu Ala Asp Ala Arg Glu Val Thr  
                     35                      40                      45  
 Glu Ala Ala Ala Gly Ala Arg Arg Leu Glu Ile Ser Val Arg Leu Met  
 50                      55                      60  
 Val Thr Ser Ala Cys Arg Leu Tyr Ser Val Ala Asn Ser Arg Asn Asp  
 65                      70                      75                      80  
 Ser Thr Ala Ser Ser Ser Ser Pro Arg Ser Thr Arg Arg Arg Lys Leu  
                     85                      90                      95  
 Arg Arg Asn Ser Gly Cys Thr Asn Asn Thr Ala Leu Phe  
                     100                      105

<210> 387  
 <211> 379  
 <212> DNA  
 <213> Homo sapiens

<400> 387  
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 60

ggacgtgctg gcacgtctga catggtgcgt ggacccgcct tctcttcgcc tgcgcatgcc  
 120  
 atgcaagagg agcttgacaa tgtgctgat ctcgcccattg cgcggcagca agcgctcgat  
 180  
 gctgttcgtt ccgagctgct cgaagcgcag caagcatgtg cctcgtgccg gctgcagctg  
 240  
 cagcatgtgc cagatgatcg tgtgcgagcg catcccatat accaggcgct ccatgcggac  
 300  
 gttgcttaca tgcagcaaga acttgatcac gtacgagacg cattggcttc ggcagaatct  
 360  
 gagaatgcga gcctgcgcg  
 379

<210> 388

<211> 114

<212> PRT

<213> Homo sapiens

<400> 388

Met	Arg	Leu	Val	Arg	Asp	Gln	Val	Leu	Ala	Ala	Cys	Lys	Gln	Arg	Pro
1				5					10					15	
His	Gly	Ala	Pro	Gly	Ile	Trp	Asp	Ala	Leu	Ala	His	Asp	His	Leu	Ala
			20					25					30		
His	Ala	Ala	Ala	Ala	Ala	Gly	Thr	Arg	His	Met	Leu	Ala	Ala	Leu	Arg
		35					40				45				
Ala	Ala	Arg	Asn	Glu	Gln	His	Arg	Ala	Leu	Ala	Ala	Ala	His	Gly	Arg
	50					55				60					
Asp	His	Ala	His	Cys	Gln	Ala	Pro	Leu	Ala	Trp	His	Ala	Gln	Ala	Lys
65					70					75				80	
Arg	Arg	Arg	Val	His	Ala	Pro	Cys	Gln	Thr	Cys	Gln	His	Val	Pro	Gln
				85					90					95	
Pro	Arg	Ala	Arg	Ser	Ser	Leu	Gln	Ser	Thr	Leu	Pro	Met	Pro	Ala	Arg
			100					105						110	
His	Ala														

<210> 389

<211> 382

<212> DNA

<213> Homo sapiens

<400> 389

ngatggccga ctgtcccact gtcagtacgc gaagctcgcc gtcgagtcgg tccacgtccg  
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 ggctctccac gtgctccgca accctccgaa gcgatgacct ggcccggggg cggcaacgag  
 120  
 gtattgcgtt tggagacgct tggggtaaat tacggccagg tgcgcgccgt cgatgccctg  
 180  
 acgaccaccg tagagcgcgg caccatcacc tgcctcatgg gtcgaaatgg atcaggcaag  
 240  
 tcgtctctga tgtggggcat ccaaggggca acaaagtcct caggaggagg actggtaaac  
 300  
 cagcagggtt cttgggctga cccccgaaa gccgacgccg cgaccgctcg acgaatgggt  
 360

agcttagtcc cgcagtcagc cn  
382

<210> 390  
<211> 127  
<212> PRT  
<213> Homo sapiens

<400> 390  
Xaa Trp Pro Thr Val Pro Leu Ser Val Arg Glu Ala Arg Arg Arg Val  
1 5 10 15  
Gly Pro Arg Pro Gly Leu Pro Arg Ala Pro Gln Pro Ser Glu Ala Met  
20 25 30  
Thr Trp Pro Gly Gly Gly Asn Glu Val Leu Arg Leu Glu Thr Leu Gly  
35 40 45  
Val Asn Tyr Gly Gln Val Arg Ala Val Asp Ala Leu Thr Thr Thr Val  
50 55 60  
Glu Arg Gly Thr Ile Thr Cys Leu Met Gly Arg Asn Gly Ser Gly Lys  
65 70 75 80  
Ser Ser Leu Met Trp Ala Ile Gln Gly Ala Thr Lys Ser Ser Gly Arg  
85 90 95  
Val Leu Val Asn His Glu Gly Ser Trp Ala Asp Pro Arg Lys Ala Asp  
100 105 110  
Ala Ala Thr Ala Arg Arg Met Val Ser Leu Val Pro Gln Ser Ala  
115 120 125

<210> 391  
<211> 456  
<212> DNA  
<213> Homo sapiens

<400> 391  
nnacgcgttg ccgctctgtg aggcgcctat cacggtgaca ctctcggtgc tatgagcgtg  
60  
tgcgacccta tcggtggcat gcacgccttg ttcagcgact ctattcccca gcagatcttc  
120  
ctgcccgcgc cctccttctt tcgccgccga cgaggccgac gtggagacgt ggtgcagcga  
180  
ggccgatgaa tcctggacac ccaccgcgac gacctggccg ggatcattgt cgagcccatc  
240  
ttgcaaggag ccggaggcat gtggccgtgg tctccgtcct gtctgaagca cctgcgccgt  
300  
cgtgctgatg aacttgacct agttcttata gccgacgagg tcgctactgg atttgggcgg  
360  
actggcaaac ttttcgcatg cgagtgggcc gatatcgttc ctgacatcat ggtggttggg  
420  
aaatccatga ctggcggata cctgacccag tcggcc  
456

<210> 392  
<211> 55  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 392

Gly Ala Tyr His Gly Asp Thr Leu Gly Ala Met Ser Val Cys Asp Pro  
 1 5 10 15  
 Ile Gly Gly Met His Ala Xaa Phe Ser Asp Ser Ile Pro Gln Gln Ile  
 20 25 30  
 Phe Leu Pro Ala Pro Ser Phe Phe Arg Arg Arg Arg Gly Arg Arg Gly  
 35 40 45  
 Asp Val Val Gln Arg Gly Arg  
 50 55

&lt;210&gt; 393

&lt;211&gt; 371

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 393

nacgcgttgc tcgtcattgg tggctactcg gcctacgaag gtatctacac catgatgact  
 60  
 gagcgggacc ggtacccggc tttccgtatt ccgacgggtgt gcatcccggc ttctatcgac  
 120  
 aacaacctcc ccggttcgga actgtccatc ggcaccgaca ccgctctcaa cgtcatcgtc  
 180  
 gaggcgatgg acaagattaa ggagtcgggt atcgcgcca gacgctgctt cgtcgctcag  
 240  
 acgatggggtc gtgactgcgg atacctcgcg ttgatgtcgg gtatcgagc tggcgctgag  
 300  
 cggatctata ccaacgagga cggatatctc ctggacgatc tagccaacga cgtccattgg  
 360  
 ttgcgggagt c  
 371

&lt;210&gt; 394

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 394

Xaa Ala Leu Leu Val Ile Gly Gly Tyr Ser Ala Tyr Glu Gly Ile Tyr  
 1 5 10 15  
 Thr Met Met Thr Glu Arg Asp Arg Tyr Pro Ala Phe Arg Ile Pro Thr  
 20 25 30  
 Val Cys Ile Pro Ala Ser Ile Asp Asn Asn Leu Pro Gly Ser Glu Leu  
 35 40 45  
 Ser Ile Gly Thr Asp Thr Ala Leu Asn Val Ile Val Glu Ala Met Asp  
 50 55 60  
 Lys Ile Lys Glu Ser Gly Ile Ala Ser Arg Arg Cys Phe Val Val Glu  
 65 70 75 80  
 Thr Met Gly Arg Asp Cys Gly Tyr Leu Ala Leu Met Ser Gly Ile Ala  
 85 90 95  
 Ala Gly Ala Glu Arg Ile Tyr Thr Asn Glu Asp Gly Ile Ser Leu Asp  
 100 105 110  
 Asp Leu Ala Asn Asp Val His Trp Leu Arg Glu  
 115 120

<210> 395  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 395  
 gaattctagt tgggagattc attgaccaga cttttggaat aaacactagt catcatgcta  
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 ggcacaggtg gtcttgtgca tggtagaaag gcagtccaag cctatgtctc tgaaacctgc  
 120  
 tctcatttct gttttctact ttacgattta tggtatctca tactcccat gttgcctgtt  
 180  
 ctccagtttt tttacttgtg ttatttccat tcttctattc ctgctcaatt tctgcctcag  
 240  
 ggcagaattg tgtccaacag ctcttaaagt cagcgcagaa actgtgatgt taaaaacatc  
 300  
 ttgttatccg gccccaaaac atgttgtcct tggtaactct tactggtttg t  
 351

<210> 396  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 396  
 Met Val Glu Arg Gln Ser Lys Pro Met Ser Leu Lys Pro Ala Leu Ile  
 1 5 10 15  
 Ser Val Phe Tyr Phe Thr Ile Tyr Val Ile Ser Tyr Ser Pro Cys Cys  
 20 25 30  
 Leu Phe Ser Ser Phe Phe Thr Cys Val Ile Ser Ile Leu Leu Phe Leu  
 35 40 45  
 Leu Asn Phe Cys Leu Arg Ala Glu Leu Cys Pro Thr Ala Leu Lys Cys  
 50 55 60  
 Ser Ala Glu Thr Val Met Leu Lys Thr Ser Cys Tyr Pro Ala Pro Lys  
 65 70 75 80  
 His Val Val Leu Gly Asn Ser Tyr Trp Phe  
 85 90

<210> 397  
 <211> 483  
 <212> DNA  
 <213> Homo sapiens

<400> 397  
 gccgtcatta aagagatcac cctctcctc caacctggtg atgtcctcgt cgacgggtggt  
 60  
 aatgcttatt ttggtgatac ccgcccgtg gaggaggaaa tacgtccac cggcattcac  
 120  
 tatgttggtg ctggcatctc cgggtggggga gtcggggccc tgagggtccc atcaattatg  
 180  
 cctggcgggg ttaaggaatc ttacgaaatc atcggaccgg tcttagaaaa aatctccgcc  
 240  
 cacgtcgacg gtgaaccctg ctgcgcatgg atgggtactg acggcgccgg acatttcgtc  
 300

aagatgggtcc ataatggcat cgagtacgcc gatatgcagt tcattggcga ggcgcccttc  
 360  
 ctttttgcgn tgcccgccgg tttagaccaat gctgaggccg ccgatgcctt cgagtctgtg  
 420  
 aaccatggcg acctcaattc ctacctcgtc gaaatcactt ctcgggtact gcgtgccaaag  
 480  
 gat  
 483

<210> 398

<211> 161

<212> PRT

<213> Homo sapiens

<400> 398

Ala	Val	Ile	Lys	Glu	Ile	Thr	Pro	Leu	Leu	Gln	Pro	Gly	Asp	Val	Leu
1				5					10					15	
Val	Asp	Gly	Gly	Asn	Ala	Tyr	Phe	Gly	Asp	Thr	Arg	Arg	Arg	Glu	Glu
		20						25				30			
Glu	Ile	Arg	Pro	Thr	Gly	Ile	His	Tyr	Val	Gly	Thr	Gly	Ile	Ser	Gly
		35				40					45				
Gly	Gly	Val	Gly	Ala	Leu	Arg	Val	Pro	Ser	Ile	Met	Pro	Gly	Gly	Val
	50				55						60				
Lys	Glu	Ser	Tyr	Glu	Ile	Ile	Gly	Pro	Val	Leu	Glu	Lys	Ile	Ser	Ala
65				70					75					80	
His	Val	Asp	Gly	Glu	Pro	Cys	Cys	Ala	Trp	Met	Gly	Thr	Asp	Gly	Ala
			85					90					95		
Gly	His	Phe	Val	Lys	Met	Val	His	Asn	Gly	Ile	Glu	Tyr	Ala	Asp	Met
			100					105					110		
Gln	Phe	Ile	Gly	Glu	Ala	Pro	Phe	Leu	Phe	Ala	Xaa	Pro	Ala	Gly	Leu
	115					120						125			
Thr	Asn	Ala	Glu	Ala	Ala	Asp	Ala	Phe	Glu	Ser	Trp	Asn	His	Gly	Asp
	130				135							140			
Leu	Asn	Ser	Tyr	Leu	Val	Glu	Ile	Thr	Ser	Arg	Val	Leu	Arg	Ala	Lys
145				150						155				160	
Asp															

<210> 399

<211> 314

<212> DNA

<213> Homo sapiens

<400> 399

nngggaatga agaccaccca gcccttcctt tcttcaaate ttctccaggc ttctgtgcat  
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 ggctcatcca cccatccact cattcaccca tctatccatc cactcatcca cccatccagt  
 120  
 cattcactca ttgtccatc cactcatgta cccatccact cattcgccca tttatccatc  
 180  
 cactcaacca tccactcatc caccatcca nctcatcatc cgtccagtca cccatctatc  
 240  
 caccatgta tccatccact catccaccca tccactcatc tgtccatcca cttatccacc  
 300

catctactca ccca  
314

<210> 400  
<211> 104  
<212> PRT  
<213> Homo sapiens

<400> 400  
Xaa Gly Met Lys Thr Thr Gln Pro Phe Leu Ser Ser Asn Leu Leu Gln  
1 5 10 15  
Ala Ser Val His Gly Ser Ser Thr His Pro Leu Ile His Pro Ser Ile  
20 25 30  
His Pro Leu Ile His Pro Ser Ser His Ser Leu Ile Cys Pro Ser Thr  
35 40 45  
His Val Pro Ile His Ser Phe Ala His Leu Ser Ile His Ser Thr Ile  
50 55 60  
His Ser Ser Thr His Pro Xaa His His Pro Ser Ser His Pro Ser Ile  
65 70 75 80  
His Pro Cys Ile His Pro Leu Ile His Pro Ser Thr His Leu Ser Ile  
85 90 95  
His Leu Ser Thr His Leu Leu Thr  
100

<210> 401  
<211> 2165  
<212> DNA  
<213> Homo sapiens

<400> 401  
gagaaaatgg aactacctgt atataaatta ggtgagcaaa cagtgatata ggtagtttta  
60  
agaagcaaat atatacagtc aatttaacag tgtttacttc tctggattgt ttaatggtgt  
120  
caaaatgaaa gatctattga agtttcacta tacattgcat tgattgaacc ttggagagtt  
180  
ttatgaaaaa gaggggcatc ccttgccatc tgtttgccag tcttccttgc cccttccttt  
240  
gaaatgcctg cctctttttt gccagattg tttcctgacc atccgaactc agatgggggc  
300  
ctctaagttc ttcttgata ttcacaaatc ccttcacaag gccacgtgc gaagtgaatg  
360  
atctggaggt gcctgggcat ctgtgttga agggagtcaa gactcaccag ccagtcagtt  
420  
tgtgggtac agttgtcca caaaaatcag gcatgttcac ctcccctctg ggcccctaca  
480  
gctgggactg atcatagcct cagattagaa gaaatactga cttctaactc tataagccag  
540  
cactcctggg taaggagtga agctctgttg gccatgccgc tttggactgc tgggcagagc  
600  
tgagcctaca gttttgtact ggggtgcacg gatgacagct gggaagatgg aaaggcagct  
660  
tgaggattta tagcagctaa agggtaaatg ctgttatgca aaagggtccc atatgaactt  
720

cctacaggtg tagccgcagc caagtgtctg tacagctgct gagaatttgt cggatgatga  
780  
aaaattcctc tttgcatcac aagcgagtgg aaagccaggg gctgcatgag tggagaaaagc  
840  
acagtctggt ttttcaagta ctgcagagaa tgagaatacc cagccgggag cctggagttg  
900  
aggcccagat tacacaggct cccggaatac agacctggga agatagggga ggagagggga  
960  
agcttgtggc cttttgatcc gccccggaa tgcccaccgt gcgctgcttt gctgccttca  
1020  
tctcctgctc agaggccttc tccttcccag agacctcctt ggatgggtct aaggagaca  
1080  
ctgcccgggc ctttttccct gcaatcaciaa ggtccaaatc ctccaggctg cgcttgatcg  
1140  
gccgcgccgc cccaatgttc tacgggctca ttttccgggtg caggattggg tggaccatgc  
1200  
cttccatctt cctgaaatc tccagtctca catggtgagg ttttctgat cttgaaagcg  
1260  
attcagggtg ttttttaggg cctgacatgg tcatgggtga taccgcacag gctttggggt  
1320  
gacagtctcg actctggctg cctaagacct ggaactggga gatgcctttg ctctcctggg  
1380  
gccctgtggt ggaatgagcc agggccagga ccttgccgggt aggtttgtgc gggttcttgg  
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1500  
cttgagggtg cagggacgtg agataattta catggagctt ttcttggtgt ctgtgggaag  
1560  
gaaaagaact gttttccgat tccctgtaca tgtccctgga agggatattt gatgtctgtt  
1620  
cattatgaag atggtgctcg gtgtgtctgt agaggctatg gagatgaggg gacgagtaga  
1680  
agtcagccag gaagctaggc atgtgggaat gggggagggc ctttttctct aagagtttat  
1740  
ccttgccctc ctgaatttct tgcttcagga cgtaggagtc agcaaggggg ttaaggtagt  
1800  
gcttgagaaa gctgcagcgg tggggatctg atcgactcag tttctcatgc ttaaagatgt  
1860  
cattgatggt ctttctctct tccgagggtc tgcttctgaa actctggacg tgctgaatca  
1920  
ctgatggccg gctgaccgcc atatggtcag tgctttggcc atggtgggtc tgggacaaac  
1980  
tggaacacaa gtcaccccta gcaatcagtt tctttttgct gatcaaaggg ggtggggagc  
2040  
cataagggtg gctgctggag aggtggccc cactcacttg ggacaaaagc ttttcttgg  
2100  
ccagtgggga catcatgcct ggggtgcccc tagagtagag caggggcgtg taattaagtc  
2160  
catgg  
2165

&lt;210&gt; 402

&lt;211&gt; 87

&lt;212&gt; PRT



<213> Homo sapiens

<400> 402

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Glu Tyr Pro Ala Gly Ser Leu Glu Leu Arg Pro Glu Leu His Arg Leu
 1             5             10             15
Pro Glu Tyr Arg Pro Gly Lys Ile Gly Glu Glu Arg Gly Ser Leu Trp
      20             25             30
Pro Phe Asp Pro Pro Pro Glu Cys Pro Pro Cys Ala Ala Leu Leu Pro
      35             40             45
Ser Ser Pro Ala Gln Arg Pro Ser Pro Ser Gln Arg Pro Pro Trp Met
      50             55             60
Gly Leu Arg Glu Thr Leu Pro Gly Pro Phe Ser Leu Gln Ser Gln Gly
65             70             75             80
Pro Asn Pro Pro Gly Cys Ala
      85

```

<210> 403

<211> 369

<212> DNA

<213> Homo sapiens

<400> 403

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cccatggggtg tgtcccagga cggcgatcatg aagcgatcagg taaatgacaa ggaaacgggc
60
gcgcacttgtg tcgaatacac gacgcaagtg tctgtcgact cgacgccgca actcgtccag
120
ccttcgcccc cgtcgcacga caacctcgtg cctgtccaga tgatcttttg cttcaagcag
180
cgcaacgcga aaaagatcaa tagccaccgc tgggtatttc atgcactggg ccgcatgcta
240
cagcccgaca tggctgtctt ggtggacgtc ggcacgaagc ccggccacct cgccctatac
300
catctatggc aggcattcta tcaccgacct accttgggcg gtgcttgcg cgaaattcat
360
gctatgatc
369

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<210> 404

<211> 123

<212> PRT

<213> Homo sapiens

<400> 404

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Pro Met Gly Val Ser Gln Asp Gly Val Met Lys Arg Gln Val Asn Asp
 1             5             10             15
Lys Glu Thr Val Ala His Leu Phe Glu Tyr Thr Thr Gln Val Ser Val
      20             25             30
Asp Ser Thr Pro Gln Leu Val Gln Pro Ser Pro Thr Ser His Asp Asn
      35             40             45
Leu Val Pro Val Gln Met Ile Phe Cys Phe Lys Gln Arg Asn Ala Lys
      50             55             60
Lys Ile Asn Ser His Arg Trp Val Phe His Ala Leu Gly Arg Met Leu
65             70             75             80
Gln Pro Asp Met Val Val Leu Val Asp Val Gly Thr Lys Pro Gly His

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<210> 405
<211> 840
<212> DNA
<213> Homo sapiens
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<210> 406
<211> 91
<212> PRT
<213> Homo sapiens
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634

50                      55                      60  
 Ser Glu Asn Lys Leu Arg Gln Leu Asn Leu Asn Glu Trp Thr Leu  
 65                      70                      75                      80  
 Asp Lys Leu Arg Tyr Gly Glu Lys Thr Thr Arg  
                     85                      90

<210> 407  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<400> 407  
 gcctattgta ccagctctcc agggctgggg acttgetaga gcagggttcc cagtgtcccc  
 60  
 aggtcttact ttgctctgcc tggcttcagg gtgtagggga tggagagctg gacttccagc  
 120  
 ctgcttcttg gctgtctagg ggccaggggc tcgggacaca gagctcctgg aggccgagca  
 180  
 caagccttgg gcagaggtga ggcagagctc tgactgtttc attcgactac gttgccaaagg  
 240  
 agatgctcgc tcggagtggt tgctctggct ctgggattcc aaaccaagct gccttctctg  
 300  
 atgtggcctt agtgcctctg gcggatgtac cttggctctg cctggaccct ctctctcttc  
 360  
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 420  
 ccccgagctt cccattccgt gtctctctgg agggcccatc atcatcctgg tggaggtggt  
 480  
 gcactgagga ccacagcagc cctcgcatc ccacgggcaa aggggtatgt gtagg  
 535

<210> 408  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 408  
 Met Leu Ala Arg Ser Gly Cys Ser Gly Ser Gly Ile Pro Asn Gln Ala  
 1                      5                      10                      15  
 Ala Phe Ser Asp Val Ala Leu Val Leu Trp Ala Asp Val Pro Trp Leu  
                     20                      25                      30  
 Cys Leu Asp Pro Leu Ser Leu Pro Gly Leu Cys Pro Thr Arg Met Met  
                     35                      40                      45  
 Pro Ile Gln Ser Ser Leu Ser Ser Pro Thr Ser Ser Pro Ser Phe Pro  
                     50                      55                      60  
 Phe Arg Val Ser Leu Glu Gly Pro Ser Ser Ser Trp Trp Arg Cys Cys  
 65                      70                      75                      80  
 Thr Glu Asp His Ser Ser Pro Arg Ile Pro Thr Gly Lys Gly Val Cys  
                     85                      90                      95  
 Val

<210> 409  
 <211> 375

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 409

ngtgtcatgg gtgtctatac cagcgatgag gccaaactg ccaagacttt tggatttggg  
 60  
 ggacttccga ttacgactaa tatttctctt gccacaact tcaatatgga tgaaatttct  
 120  
 gatattgtct tccgtgtcaa tgataccagt ttgacaccaa ctgtgggacc agaattagct  
 180  
 agaaaattga ccgaaattgc tggctctcag caaggggagt atcaggtgtc agatgcgact  
 240  
 gcagccttcc aagaagtgc acaattgttc ggctttataa ctacgattat tagtgccatt  
 300  
 gcaggaattt ccctttttgt tggagggact ggtgttatga acatcatgct ggtttcgggtg  
 360  
 acggagcgta cgcgt  
 375

&lt;210&gt; 410

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 410

Xaa	Val	Met	Gly	Val	Tyr	Thr	Ser	Asp	Glu	Ala	Lys	Thr	Ala	Lys	Thr
1				5					10					15	
Phe	Gly	Ile	Gly	Gly	Leu	Pro	Ile	Thr	Thr	Asn	Ile	Ser	Leu	Ala	Asn
			20					25					30		
Asn	Phe	Asn	Met	Asp	Glu	Ile	Ser	Asp	Ile	Val	Phe	Arg	Val	Asn	Asp
		35					40					45			
Thr	Ser	Leu	Thr	Pro	Thr	Val	Gly	Pro	Glu	Leu	Ala	Arg	Lys	Leu	Thr
	50					55					60				
Glu	Ile	Ala	Gly	Leu	Gln	Gly	Glu	Tyr	Gln	Val	Ser	Asp	Ala	Thr	
65					70				75					80	
Ala	Ala	Phe	Gln	Glu	Val	Gln	Gln	Leu	Phe	Gly	Phe	Ile	Thr	Thr	Ile
			85					90					95		
Ile	Ser	Ala	Ile	Ala	Gly	Ile	Ser	Leu	Phe	Val	Gly	Gly	Thr	Gly	Val
		100						105					110		
Met	Asn	Ile	Met	Leu	Val	Ser	Val	Thr	Glu	Arg	Thr	Arg			
		115					120					125			

&lt;210&gt; 411

&lt;211&gt; 409

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 411

ccacatactt caccctcctc acccctcca cctactccac cacctggcag tcgccatcga  
 60  
 ggatgggacg caactccacg tccacatgct ccggaccacg cggcgtgtgg tggatgtgca  
 120  
 gcacgcggtc ggggcccctt gagctcgaag gcgcggcgca tcgggcagtg ctgcgcggcc  
 180

tggtegacagg gcacgtcgta ctggtgagac acgcggaagc acttgtggcc gatgtaggcg  
 240  
 cgatcggtcg tcccgaactg ggcgtgatag gccgtgtaca caacacaaac tgttgtactc  
 300  
 ccggtccacc acgatcatgg gctgggactc gtgttccagg tggggggcca gggcttgggc  
 360  
 ctgcggtgag cgcgtggggg ggatggggca tagcgtcggg gaggagggtg  
 409

<210> 412  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 412  
 Met Pro His Pro Pro His Ala Leu Thr Ala Gly Pro Ser Pro Gly Pro  
 1 5 10 15  
 Pro Pro Gly Thr Arg Val Pro Ala His Asp Arg Gly Gly Pro Gly Val  
 20 25 30  
 Gln Gln Phe Val Leu Cys Thr Arg Pro Ile Ser Ala Ser Ser Gly Gln  
 35 40 45  
 Pro Ile Ala Pro Thr Ser Ala Thr Ser Ala Ser Ala Ser Arg Thr Ser  
 50 55 60  
 Thr Thr Cys Pro Ala Thr Arg Pro Ala Ser Thr Ala Arg Cys Ala Ala  
 65 70 75 80  
 Pro Ser Ser Ser Arg Gly Pro Asp Arg Val Leu His Ile His His Thr  
 85 90 95  
 Pro Arg Gly Pro Glu His Val Asp Val Glu Leu Arg Pro Ile Leu Asp  
 100 105 110  
 Gly Asp Cys Gln Val Val Glu  
 115

<210> 413  
 <211> 357  
 <212> DNA  
 <213> Homo sapiens

<400> 413  
 ccgggcatcc caccaccggg tgtcatgaac caagtagtgg cccctatggg agggactcca  
 60  
 gcaccgggtg gaagtccata tggacaacag gtgggagttt tggggcctcc agggcagcag  
 120  
 gcaccacctc catatcccg gcccacatcca gctggacccc ctgtcataca gcagccaaca  
 180  
 acacccatgt ttgtagctcc cccccaaag acccagcggc ttcttcactc agaggcctac  
 240  
 ctgaaatata ttgaaggact cagtgcggag tccaacagca ttagcaagtg ggatcagaca  
 300  
 ctggcagctc ggagacgga cgtccatttg tcgaaagaac aggagagccg cctaccc  
 357

<210> 414  
 <211> 119  
 <212> PRT

<213> Homo sapiens

<400> 414

```

Pro Gly Ile Pro Pro Pro Gly Val Met Asn Gln Val Val Ala Pro Met
 1           5           10           15
Val Gly Thr Pro Ala Pro Gly Gly Ser Pro Tyr Gly Gln Gln Val Gly
          20           25           30
Val Leu Gly Pro Pro Gly Gln Gln Ala Pro Pro Pro Tyr Pro Gly Pro
          35           40           45
His Pro Ala Gly Pro Pro Val Ile Gln Gln Pro Thr Thr Pro Met Phe
          50           55           60
Val Ala Pro Pro Pro Lys Thr Gln Arg Leu Leu His Ser Glu Ala Tyr
65           70           75           80
Leu Lys Tyr Ile Glu Gly Leu Ser Ala Glu Ser Asn Ser Ile Ser Lys
          85           90           95
Trp Asp Gln Thr Leu Ala Ala Arg Arg Arg Asp Val His Leu Ser Lys
          100          105          110
Glu Gln Glu Ser Arg Leu Pro
          115

```

<210> 415

<211> 332

<212> DNA

<213> Homo sapiens

<400> 415

```

tctagagcca acttggttat cgtaatgaat agagagacta catctatatac aattattacg
60
ctctatagta atcatgaagc ttgggttata tgtatgacaa aaattgcaga aaaatcgaaa
120
caagaatatg ggcacttact aaaagaaaaa gaccatttac aagatatgga acagcttgag
180
atgactatcg tctcgatcca tacgccgtat ccgtccattg tcagaattca aggaaaaatc
240
aacacattac agccagagct ttggcaagct cccaatttag caattcggtt aattgtgagc
300
aatccgccag agggacaacc catctcacgc gt
332

```

<210> 416

<211> 102

<212> PRT

<213> Homo sapiens

<400> 416

```

Met Asn Arg Glu Thr Thr Ser Ile Ser Ile Ile Thr Leu Tyr Ser Asn
 1           5           10           15
His Glu Ala Trp Val Ile Cys Met Thr Lys Ile Ala Glu Lys Ser Lys
          20           25           30
Gln Glu Tyr Gly Asp Leu Leu Lys Glu Lys Asp His Leu Gln Asp Met
          35           40           45
Glu Gln Leu Glu Met Thr Ile Val Ser Ile His Thr Pro Tyr Pro Ser
          50           55           60
Ile Val Arg Ile Gln Gly Lys Ile Asn Thr Leu Gln Pro Glu Leu Trp

```



130	135	140
Gly Pro Arg Ala Leu Asn Ala Asn Gly Ile Lys Val Leu Ala Asp Pro		
145	150	155
Arg		160

<210> 419  
 <211> 797  
 <212> DNA  
 <213> Homo sapiens

<400> 419  
 atttcacccc aggaaaacca gtaaggacca atgattaagc ccaaggttgg gtaccgagtt  
 60  
 cggatccata agtaccggcc gccaggggtg ctggaatttg ggctcccccc ggtgaaaata  
 120  
 tccatgcagc cgcgttgtct taggtagaaa agggagactg ggggtgggtg ggctgagctc  
 180  
 aagccccctgc ctacatactt tagtagtaac gactcccgat ctgcatccaa cacatttacc  
 240  
 gaacttctag taagcgcccc cgcgtgcaag cgaaagcact cccctgcaa gaaacagatc  
 300  
 ttttcactt aaaattccca aactcagacc ttccactttt tactgaacaa aaagcgtgta  
 360  
 catgatctga agggttgaca tgacattttc taaattgggc gaatcaggaa gaggttgatg  
 420  
 aaaatccttg acgttttctg gggataggac atttgtgtgt gataacgttc ttaagtcgaa  
 480  
 tttcagtgtg gcagtgcacg cagattcttc attggtgtta gtgtatttcc atacggtatg  
 540  
 tattagtaca agaaatagtg ttccctttga cactcgaacc caaggagtgg tccgaggctt  
 600  
 tttgaggcaa cgtaggatca atgtctctga agcagatttg gtgaaggatg caggtctcat  
 660  
 aatttacaga gcaatcacag ccttctttga aacggagaaa ttagattcta tgaaattttg  
 720  
 tcagtgcaga tagatatgat gtggagaaac ggggaaaatt gagtacaaaa agatgaggct  
 780  
 tgaatgatgg ctggcca  
 797

<210> 420  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 420  
 Met Arg Pro Ala Ser Phe Thr Lys Ser Ala Ser Glu Thr Leu Ile Leu  
 1 5 10 15  
 Arg Cys Leu Lys Lys Pro Arg Thr Thr Pro Trp Val Arg Val Ser Lys  
 20 25 30  
 Gly Thr Leu Phe Leu Val Leu Ile His Thr Val Trp Lys Tyr Thr Asn  
 35 40 45  
 Thr Asn Glu Glu Ser Ala Cys Thr Ala Thr Leu Lys Phe Asp Leu Arg



```

      50              55              60
Thr Leu Ser His Thr Asn Val Leu Ser Pro Glu Asn Val Lys Asp Phe
65              70              75              80
His Gln Pro Leu Pro Asp Ser Pro Asn Leu Glu Asn Val Met Ser Thr
      85              90              95
Leu Gln Ile Met Tyr Thr Leu Phe Val Gln
      100              105

```

<210> 421  
 <211> 406  
 <212> DNA  
 <213> Homo sapiens

```

<400> 421
ggatccacca tgatggagcc caccaccca tcctcagtc acctgctgca gcttctccat
60
aaccaaacac aggtcaatct tgtctcccta aacacaccat gtgctctcat gctgccatgg
120
tttgctgggg gccctctcta cctcctctgc tttctggaga acccttgac tcctcccaag
180
ccttcaagtt ggaaagtga cagtcagcat atgtctctag ctcagccctt actgcgtgga
240
ttcatgaaga ttggttcact gtcagcccet gaccagaacg tgtgttttag gaaagcagga
300
accaagtctt accaatgtct gtagtcccag cctccaccct ggcatacagt aggtgctcat
360
tgaatgtggg agggaaagag gagacacatg gaagggaatg tcattc
406

```

<210> 422  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

```

<400> 422
Met Met Glu Pro Thr His Pro Ser Ser Val His Leu Leu Gln Leu Leu
1              5              10              15
His Asn Pro Thr Gln Val Asn Leu Val Ser Leu Asn Thr Pro Cys Ala
      20              25              30
Leu Met Leu Pro Trp Phe Ala Trp Gly Pro Leu Tyr Leu Leu Cys Phe
      35              40              45
Leu Glu Asn Pro Cys Thr Pro Pro Lys Pro Ser Ser Trp Lys Val Asn
      50              55              60
Ser Gln His Met Ser Leu Ala Gln Pro Leu Leu Arg Gly Phe Met Lys
65              70              75              80
Ile Gly Ser Leu Ser Ala Pro Asp Gln Asn Val Cys Phe Arg Lys Ala
      85              90              95
Gly Thr Lys Ser Tyr Gln Cys Leu
      100

```

<210> 423  
 <211> 628  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 423

ngccacccta cgcctcgcct gcaatggcaa cttcagatcc ccggtggcac cgtagtctta  
 60  
 gagccaccgg ttctgagcgg ggaggacgac ggggttgggg cggaggaagg agagggagaa  
 120  
 ggagatgggg atttgctgac gcagacccaa gcccacacgc cgactccagc acccgcttgg  
 180  
 ccggcgcccc cagccacacc gcgcttcttg gccctcgcaa atggctccct gttggtgccc  
 240  
 ctcttgagtg ccaaggaggc gggcgtctac acttgccgtg cacacaatga gctgggcgccc  
 300  
 aactctacgt caatacgcgt ggcggtggca gcaaccgggc ccccaaaaca cgcgcctggc  
 360  
 gccgggggag aaccgcagcg acaggccccg acctctgagc gcaagtccac agccaagggc  
 420  
 cggggcaaca gcgtcctgcc ttccaaaccc gagggcaaaa tcaaaggcca aggcctggcc  
 480  
 aaggtcagca ttctcgggga gaccgagacg gagccggagg aggacacaag tgagggagag  
 540  
 gaggccgaag accagatcct cgcggaccgc gcggaggagc agcgtgtgtg caacggggac  
 600  
 ccctctcggt acgtttctaa ccacgcgt  
 628

&lt;210&gt; 424

&lt;211&gt; 209

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 424

Xaa His Pro Thr Pro Arg Leu Gln Trp Gln Leu Gln Ile Pro Gly Gly  
 1 5 10 15  
 Thr Val Val Leu Glu Pro Pro Val Leu Ser Gly Glu Asp Asp Gly Val  
 20 25 30  
 Gly Ala Glu Glu Gly Glu Gly Glu Gly Asp Gly Asp Leu Leu Thr Gln  
 35 40 45  
 Thr Gln Ala Gln Thr Pro Thr Pro Ala Pro Ala Trp Pro Ala Pro Pro  
 50 55 60  
 Ala Thr Pro Arg Phe Leu Ala Leu Ala Asn Gly Ser Leu Leu Val Pro  
 65 70 75 80  
 Leu Leu Ser Ala Lys Glu Ala Gly Val Tyr Thr Cys Arg Ala His Asn  
 85 90 95  
 Glu Leu Gly Ala Asn Ser Thr Ser Ile Arg Val Ala Val Ala Ala Thr  
 100 105 110  
 Gly Pro Pro Lys His Ala Pro Gly Ala Gly Gly Glu Pro Asp Gly Gln  
 115 120 125  
 Ala Pro Thr Ser Glu Arg Lys Ser Thr Ala Lys Gly Arg Gly Asn Ser  
 130 135 140  
 Val Leu Pro Ser Lys Pro Glu Gly Lys Ile Lys Gly Gln Gly Leu Ala  
 145 150 155 160  
 Lys Val Ser Ile Leu Gly Glu Thr Glu Thr Glu Pro Glu Glu Asp Thr  
 165 170 175  
 Ser Glu Gly Glu Glu Ala Glu Asp Gln Ile Leu Ala Asp Pro Ala Glu

180                      185                      190  
 Glu Gln Arg Cys Gly Asn Gly Asp Pro Ser Arg Tyr Val Ser Asn His  
          195                      200                      205  
 Ala

<210> 425  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

<400> 425  
 ccggccgctcg aagactttga ggacgatgta gctcgcagcg cagcggttacg agccctggag  
 60  
 tacgtggatt tgaccccgagg cactnaagtg cgcgtcatcg ccattgacac cgtgttccta  
 120  
 ggatcgtgca cgaatggccg tgaggactta cggctggctg ctgaggttcc caaaggacga  
 180  
 catatcgag cgggcaccg gatgctcgtc gcccctggat ctgctcgtgt ccgtctgcag  
 240  
 gctatggagg aaggcctcga cgagatcggg tcccggtttg ctgacatctt tcgcaataac  
 300  
 tctgcgaaca atggcttggt actggctcag gttgacccg aggtcgtcga agagttgtgg  
 360  
 gactttgccg agcagcatcc tgggtgagcag ctcaccgtct ccctcgagaa tcggacgatc  
 420  
 aacettccgg gtcgcacgac ctaccggttc catattgatg acgtcacgcg t  
 471

<210> 426  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 426  
 Pro Ala Val Glu Asp Phe Glu Asp Asp Val Ala Arg Ser Ala Ala Leu  
 1                      5                      10                      15  
 Arg Ala Leu Glu Tyr Val Asp Leu Thr Pro Gly Thr Xaa Val Arg Val  
          20                      25                      30  
 Ile Ala Ile Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Gly Arg Glu  
          35                      40                      45  
 Asp Leu Arg Leu Ala Ala Glu Val Pro Lys Gly Arg His Ile Ala Ala  
          50                      55                      60  
 Gly Thr Arg Met Leu Val Ala Pro Gly Ser Ala Arg Val Arg Leu Gln  
 65                      70                      75                      80  
 Ala Met Glu Glu Gly Leu Asp Glu Ile Gly Ser Arg Phe Ala Asp Ile  
          85                      90                      95  
 Phe Arg Asn Asn Ser Ala Asn Asn Gly Leu Leu Leu Ala Gln Val Asp  
          100                      105                      110  
 Pro Glu Val Val Glu Glu Leu Trp Asp Phe Ala Glu Gln His Pro Gly  
          115                      120                      125  
 Glu Gln Leu Thr Val Ser Leu Glu Asn Arg Thr Ile Asn Leu Pro Gly  
          130                      135                      140  
 Arg Thr Thr Tyr Pro Phe His Ile Asp Asp Val Thr Arg

145

150

155

&lt;210&gt; 427

&lt;211&gt; 546

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 427

ctagcggtag tagaaggat gacgtttgat cgcggctact tgtctccgta tttcatcaac  
60

aatcaagaaa caatgaatgc agagctagaa aaccatttta ttcttcttgt tgataagaaa  
120

atttctaata tccgtgactt gctaccaatt ttggaagggt ttgctaaagc atcgcgccca  
180

ttgttgatca ttgcggaaga cgttgaaggc gaagcgttgg caaccttggg tgtaaacact  
240

atcgcgcgca tcgtaaaagt agcggcagcg aaagcgccag gttttgggtga tcgccgtaaa  
300

gcaatgcttc aagacattgc tgtgctaacg ggttcaactg ttatttcaga agaaattggc  
360

attaagcttg aagaagcgac aattgaacag ttgggtacag cgaagcgctg tacattgaca  
420

aaagaaaagta caacgattgt tgatgggtgcg ggtgttgagc ctaatattac tggctcgtgt  
480

gagcaaattc gtgcagaaat tgctaactct tcttctgggt acgataaaga gaaattgcaa  
540

gaacgc

546

&lt;210&gt; 428

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 428

Leu Ala Val Val Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro  
1 5 10 15

Tyr Phe Ile Asn Asn Gln Glu Thr Met Asn Ala Glu Leu Glu Asn Pro  
20 25 30

Phe Ile Leu Leu Val Asp Lys Lys Ile Ser Asn Ile Arg Asp Leu Leu  
35 40 45

Pro Ile Leu Glu Gly Val Ala Lys Ala Ser Arg Pro Leu Leu Ile Ile  
50 55 60

Ala Glu Asp Val Glu Gly Glu Ala Leu Ala Thr Leu Val Val Asn Thr  
65 70 75 80

Met Arg Gly Ile Val Lys Val Ala Ala Ala Lys Ala Pro Gly Phe Gly  
85 90 95

Asp Arg Arg Lys Ala Met Leu Gln Asp Ile Ala Val Leu Thr Gly Ser  
100 105 110

Thr Val Ile Ser Glu Glu Ile Gly Ile Lys Leu Glu Glu Ala Thr Ile  
115 120 125

Glu Gln Leu Gly Thr Ala Lys Arg Val Thr Leu Thr Lys Glu Ser Thr  
130 135 140

Thr Ile Val Asp Gly Ala Gly Val Ala Ala Asn Ile Thr Gly Arg Val

145                      150                      155                      160  
 Glu Gln Ile Arg Ala Glu Ile Ala Asn Ser Ser Ser Gly Tyr Asp Lys  
                                  165                      170                      175  
 Glu Lys Leu Gln Glu Arg  
                                  180

<210> 429  
 <211> 425  
 <212> DNA  
 <213> Homo sapiens

<400> 429  
 gctagcagcc cttacaggag acgggctaata aataatgcag cagtggctcc gacaacttgc  
 60  
 ccgttgacgc cggtcacgga tccatttgct tttagtagac aggcgctcca aagtacacca  
 120  
 ctgggcagtt cgtccaaaag cagtccacct gtcttgcaag gccagcccc cgcagggttt  
 180  
 tctcaacacc ccggtttgct tgtgccttac acacaatgca aaaaatagct ctcagggacc  
 240  
 ctgtgagccc ctgcctggac ctctgacaca gccagagca catgccagtc cgttttctgg  
 300  
 tgcattgaca ccttcagcac ctctggggcc tgagatgaac aggagtgcag aggtcggctcc  
 360  
 cagttcagag cctgaagttc agactctgcc atatcttctt cactacattc caggagtgga  
 420  
 tcctg  
 425

<210> 430  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 430  
 Met Gln Gln Trp Leu Arg Gln Leu Ala Arg Cys Ser Arg Ser Arg Ile  
 1                      5                      10                      15  
 His Leu Leu Leu Val Asp Arg Arg Ser Lys Val His His Trp Ala Val  
                                  20                      25                      30  
 Arg Pro Lys Ala Val His Leu Ser Cys Lys Ala Gln Pro Pro Gln Gly  
                                  35                      40                      45  
 Phe Leu Asn Thr Pro Val Cys Leu Cys Leu Thr His Asn Ala Lys Asn  
                                  50                      55                      60  
 Ser Ser Gln Gly Pro Cys Glu Pro Leu Pro Gly Pro Leu Thr Gln Pro  
 65                      70                      75                      80  
 Arg Ala His Ala Ser Pro Phe Ser Gly Ala Leu Thr Pro Ser Ala Pro  
                                  85                      90                      95  
 Pro Gly Pro Glu Met Asn Arg Ser Ala Glu Val Gly Pro Ser Ser Glu  
                                  100                      105                      110  
 Pro Glu Val Gln Thr Leu Pro Tyr Leu Pro His Tyr Ile Pro Gly Val  
                                  115                      120                      125  
 Asp Pro  
 130

<210> 431  
 <211> 192  
 <212> DNA  
 <213> Homo sapiens

<400> 431  
 ctagccatcc accagcgtag acacacggga gagaggccct aactggcct cgggtgcaac  
 60  
 cgccgcttcc gccagcgcac ggccctcgtc atccaccagc gcatccacac gggcgagaag  
 120  
 cctnaccgt gcccgactg cgagcggcgc ttctctcct cctctcgct ggtcagtcac  
 180  
 cggcgtgtgc ac  
 192

<210> 432  
 <211> 64  
 <212> PRT  
 <213> Homo sapiens

<400> 432  
 Leu Ala Ile His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Thr Gly  
 1 5 10 15  
 Leu Gly Cys Asn Arg Arg Phe Arg Gln Arg Thr Ala Leu Val Ile His  
 20 25 30  
 Gln Arg Ile His Thr Gly Glu Lys Pro Xaa Pro Cys Pro Asp Cys Glu  
 35 40 45  
 Arg Arg Phe Ser Ser Ser Ser Arg Leu Val Ser His Arg Arg Val His  
 50 55 60

<210> 433  
 <211> 635  
 <212> DNA  
 <213> Homo sapiens

<400> 433  
 nngccggcgg ctgcgttggg atacgacgtc gctgcgattg ggcgtgagta tctttggtac  
 60  
 ctcatggagg agcgtggcgc gtatgaggag gccgcgcgc tcatgccgct gctgctccgg  
 120  
 accgaccgag gcgcgtggga cacgtttgtg tgctgctacc tcgagcggca ccaaaggat  
 180  
 gcgatactcc cgcacattcc gacgcaggac cccagctga gtgagatggt gtacgatctc  
 240  
 gtgctggtgc atctgctgca gcacgatccc acgcagctgt tggcgacgct ccgcgcatgg  
 300  
 ccgagtcaca tctactcgaa gcaggcgggtg gctgcggcga tcggcgatca cgcacgaacc  
 360  
 agccgcacgc tgctcgagt cctgcacag ctgtacatgg ccgcacatca gcccggaag  
 420  
 gctctgacat actacatgcg cctgcgtgat ccatgcgtgt ttgatctcat tcgcgagtac  
 480  
 gatctgctga tcgatgtgca gcaccacatc ggcacgctcg tcgagctcga tcaggaatgc  
 540

gccggctcca ctgagccgcg ctccagcgcg cttatgccgc tgctcgtgcc atataccac  
 600  
 tcgattccca tccagcgcgc catggcgcag ctcga  
 635

<210> 434  
 <211> 211  
 <212> PRT  
 <213> Homo sapiens

<400> 434  
 Xaa Pro Ala Ala Leu Gly Tyr Asp Val Ala Ala Ile Gly Arg Glu  
 1 5 10 15  
 Tyr Leu Trp Tyr Leu Met Glu Glu Arg Gly Ala Tyr Ala Glu Ala Ala  
 20 25 30  
 Ala Leu Met Pro Leu Leu Leu Arg Thr Asp Arg Gly Ala Trp Asp Thr  
 35 40 45  
 Phe Val Cys Cys Tyr Leu Glu Arg His Gln Arg Asp Ala Ile Leu Pro  
 50 55 60  
 His Ile Pro Thr Gln Asp Pro Gln Leu Ser Glu Met Val Tyr Asp Leu  
 65 70 75 80  
 Val Leu Val His Leu Leu Gln His Asp Pro Thr Gln Leu Leu Ala Thr  
 85 90 95  
 Leu Arg Ala Trp Pro Ser His Ile Tyr Ser Lys Gln Ala Val Ala Ala  
 100 105 110  
 Ala Ile Gly Asp His Ala Arg Thr Ser Arg Thr Leu Leu Glu Cys Leu  
 115 120 125  
 Ala Gln Leu Tyr Met Ala Ala His Gln Pro Gly Lys Ala Leu Thr Tyr  
 130 135 140  
 Tyr Met Arg Leu Arg Asp Pro Cys Val Phe Asp Leu Ile Arg Glu Tyr  
 145 150 155 160  
 Asp Leu Leu Ile Asp Val Gln His His Ile Gly Thr Leu Val Glu Leu  
 165 170 175  
 Asp Gln Glu Cys Ala Gly Ser Thr Glu Pro Arg Ser Ser Ala Leu Met  
 180 185 190  
 Pro Leu Leu Val Pro Tyr Thr His Ser Ile Pro Ile Gln Arg Ala Met  
 195 200 205  
 Ala Gln Leu  
 210

<210> 435  
 <211> 493  
 <212> DNA  
 <213> Homo sapiens

<400> 435  
 nncgtacgtt cgcgtatattt ccgcgcccgg gaagctatcg ataataaagt tcaaccgctg  
 60  
 atccagcgtt agcaatggcg ggcacaggaa gggtagcttag gcatgcagaa agaaaagctt  
 120  
 tccgctctga tggatgggtga atcggttcgac agcgagctgt tgagttctct gtcgcaagat  
 180  
 cgaacgcttc aacaaagctg gcagggctat cacctgatac gtgacacact gcgaggtgat  
 240

gtcgggcaag tgatgcatct cgacatcgcc gatcgcgtag ccgctgcact tgagaaagaa  
 300  
 cccgcccggc tgggtgccttc cgccgttcag gaatctcagc cgcagcctca cacctggcag  
 360  
 aaaatgccgt tctgggacaa agtgcgcccc tgggcgagcc agattacgca aatcggtag  
 420  
 gcggcctgcg tgtcgctggc ggtgatcgtc ggcgtgcagc agtacaacca gccttctgcg  
 480  
 ccatcgaacg cgt  
 493

<210> 436

<211> 130

<212> PRT

<213> Homo sapiens

<400> 436

Met Gln Lys Glu Lys Leu Ser Ala Leu Met Asp Gly Glu Ser Phe Asp  
 1 5 10 15  
 Ser Glu Leu Leu Ser Ser Leu Ser Gln Asp Arg Thr Leu Gln Gln Ser  
 20 25 30  
 Trp Gln Gly Tyr His Leu Ile Arg Asp Thr Leu Arg Gly Asp Val Gly  
 35 40 45  
 Gln Val Met His Leu Asp Ile Ala Asp Arg Val Ala Ala Ala Leu Glu  
 50 55 60  
 Lys Glu Pro Ala Arg Leu Val Pro Ser Ala Val Gln Glu Ser Gln Pro  
 65 70 75 80  
 Gln Pro His Thr Trp Gln Lys Met Pro Phe Trp Asp Lys Val Arg Pro  
 85 90 95  
 Trp Ala Ser Gln Ile Thr Gln Ile Gly Met Ala Ala Cys Val Ser Leu  
 100 105 110  
 Ala Val Ile Val Gly Val Gln Gln Tyr Asn Gln Pro Ser Ala Pro Ser  
 115 120 125  
 Asn Ala  
 130

<210> 437

<211> 447

<212> DNA

<213> Homo sapiens

<400> 437

ntggtaaccg gtgtccctga tatggaccct gctgtgtag agcgtaaatt atttatttta  
 60  
 cgtaattatg taacacgcat ctgtttggag tctgttaatg gaattaagga caacttttac  
 120  
 attaatacat tctcatacaa aacaatcggt tataaagggtc agttaaccac tgaacaagt  
 180  
 ccacaatatt tcttagattt acaaaatcca agtatggtaa cggcattagc gcttggtcat  
 240  
 tcacgtttct caacaaatac atttcctcgt tggcggttag cacaaccatt ccgttacatc  
 300  
 gctcataatg gcgaaatcaa tacggttcgc ggtaatatca attggatgaa agcacgtgaa  
 360



gcgttacttg aagctgaatt ttctactcgc tcagaattag atatgttaat gccaatctgt  
 420  
 acggatggta tgtctgactc ggcaagg  
 447

<210> 438  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

<400> 438  
 Xaa Val Thr Gly Val Pro Asp Met Asp Pro Ala Val Leu Glu Arg Lys  
 1 5 10 15  
 Leu Phe Ile Leu Arg Asn Tyr Val Thr Arg Ile Cys Leu Glu Ser Val  
 20 25 30  
 Asn Gly Ile Lys Asp Asn Phe Tyr Ile Asn Thr Phe Ser Tyr Lys Thr  
 35 40 45  
 Ile Val Tyr Lys Gly Gln Leu Thr Thr Glu Gln Val Pro Gln Tyr Phe  
 50 55 60  
 Leu Asp Leu Gln Asn Pro Ser Met Val Thr Ala Leu Ala Leu Val His  
 65 70 75 80  
 Ser Arg Phe Ser Thr Asn Thr Phe Pro Arg Trp Arg Leu Ala Gln Pro  
 85 90 95  
 Phe Arg Tyr Ile Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn  
 100 105 110  
 Ile Asn Trp Met Lys Ala Arg Glu Ala Leu Leu Glu Ala Glu Phe Phe  
 115 120 125  
 Thr Arg Ser Glu Leu Asp Met Leu Met Pro Ile Cys Thr Asp Gly Met  
 130 135 140  
 Ser Asp Ser Ala Arg  
 145

<210> 439  
 <211> 395  
 <212> DNA  
 <213> Homo sapiens

<400> 439  
 nacgcgtgaa gggagagtgg ggccgagccc caggaggctg tcctgcagca gctgcaccag  
 60  
 cttcccaggg gccggctgga cctggccacg caaagcctga cggtggagac ctgcagggcc  
 120  
 ctgggcaagc tgctgccgag ggagacgctg tgcacggagc tggtcctgag tgactgcatg  
 180  
 ctcagcgagg aaggggccac actgctgctc cgaggcctgt gtgccaacac cgtgctgcgc  
 240  
 tttctggact taaagggcaa caaccttcgg gctgcagggg ccgaggctct gggaaaactc  
 300  
 ctccaacaga acaagtccat tcagagcctc acgctggagt ggaacagcct gggcacgtgg  
 360  
 gacgatgcct tcgccacctt ctgcgggggc ctggc  
 395

<210> 440

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 440

```

Arg Glu Ser Gly Ala Glu Pro Gln Glu Ala Val Leu Gln Gln Leu His
 1           5           10           15
Gln Leu Pro Arg Gly Arg Leu Asp Leu Ala Thr Gln Ser Leu Thr Val
          20           25           30
Glu Thr Cys Arg Ala Leu Gly Lys Leu Leu Pro Arg Glu Thr Leu Cys
          35           40           45
Thr Glu Leu Val Leu Ser Asp Cys Met Leu Ser Glu Glu Gly Ala Thr
          50           55           60
Leu Leu Leu Arg Gly Leu Cys Ala Asn Thr Val Leu Arg Phe Leu Asp
65           70           75           80
Leu Lys Gly Asn Asn Leu Arg Ala Ala Gly Ala Glu Ala Leu Gly Lys
          85           90           95
Leu Leu Gln Gln Asn Lys Ser Ile Gln Ser Leu Thr Leu Glu Trp Asn
          100          105          110
Ser Leu Gly Thr Trp Asp Asp Ala Phe Ala Thr Phe Cys Gly Gly Leu
          115          120          125

```

&lt;210&gt; 441

&lt;211&gt; 364

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 441

```

gccagtgact acgtgaacat gttcgatgcc gagcagggct tcttcgacag gcgcagccccg
60
ggcggcgagt tccaagccgg cttggatccg gaatcctggg gcggtctgtt cactgagacc
120
gacgggttga acttcgcctt ccacgctcca caggacggcc gggggctggc cgcgctctac
180
ggcgggtccga aaggcttga gaacaagctc gatgcctttt tcgcgacgcc ggaaaacgcy
240
gacaagccgg cgtacggcgg aatccacgaa atggtcgagg ccagagcggt ccggatgggc
300
caattgggca tgtccaacga gccctcgac catattccct acatctacaa ctatgccggc
360
gcgc
364

```

&lt;210&gt; 442

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 442

```

Ala Gln Tyr Tyr Val Asn Met Phe Asp Ala Glu Gln Gly Phe Phe Asp
 1           5           10           15
Arg Arg Ser Pro Gly Gly Glu Phe Gln Ala Gly Leu Asp Pro Glu Ser
          20           25           30
Trp Gly Gly Leu Phe Thr Glu Thr Asp Gly Trp Asn Phe Ala Phe His

```

```

      35              40              45
Ala Pro Gln Asp Gly Arg Gly Leu Ala Ala Leu Tyr Gly Gly Pro Lys
      50              55              60
Gly Leu Glu Asn Lys Leu Asp Ala Phe Phe Ala Thr Pro Glu Asn Ala
65              70              75              80
Asp Lys Pro Ala Tyr Gly Gly Ile His Glu Met Val Glu Ala Arg Ala
      85              90              95
Val Arg Met Gly Gln Leu Gly Met Ser Asn Glu Pro Ser His His Ile
      100              105              110
Pro Tyr Ile Tyr Asn Tyr Ala Gly Ala
      115              120

```

&lt;210&gt; 443

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 443

```

accggttacg gctcagtgc acaagagatg ttcgccaaca acctcgtgcg gatgccgctg
60
ctcatggtgc tggcaatccc cttcgccaag atcctctcga cgaccctgtc catcggatcg
120
ggcgggtccgg cggcgctcttc cggccctggc atgggtcatcg gcggagccac tggcgcgggca
180
ctgtggcgcc tcctcgaggg gctgccaggt atcccatcct caccgatgag ttctgtcatt
240
gtcggcatga tcgectgctt cgggtgcggtt gcccatgccc cactcggcgt gctgctcatg
300
gttggcgaga tgaccggaaa cctgtcgctg ctcgctcctg gcatgatcgc cgtcgccgtc
360
gctggccgag ttgtcgggga cacttcgatc tacacctctc agctcaagga tcgectggag
420
ggcgacgcgt
430

```

&lt;210&gt; 444

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 444

```

Thr Gly Tyr Gly Ser Val Gln Gln Glu Met Phe Ala Asn Asn Leu Val
1      5      10      15
Arg Met Pro Leu Leu Met Val Leu Ala Ile Pro Phe Ala Lys Ile Leu
      20      25      30
Ser Thr Thr Leu Ser Ile Gly Ser Gly Gly Pro Ala Ala Ser Ser Gly
      35      40      45
Pro Gly Met Val Ile Gly Gly Ala Thr Gly Ala Ala Leu Trp Arg Leu
      50      55      60
Leu Glu Gly Leu Pro Gly Ile Pro Ser Ser Pro Met Ser Phe Val Ile
65      70      75      80
Val Gly Met Ile Ala Cys Phe Gly Ala Val Ala His Ala Pro Leu Gly
      85      90      95
Val Leu Leu Met Val Gly Glu Met Thr Gly Asn Leu Ser Leu Leu Ala

```

	100		105		110										
Pro	Gly	Met	Ile	Ala	Val	Ala	Val	Ala	Gly	Arg	Val	Val	Gly	Asp	Thr
	115		120		125										
Ser	Ile	Tyr	Thr	Ser	Gln	Leu	Lys	Asp	Arg	Leu	Glu	Gly	Asp	Ala	
	130		135		140										

<210> 445  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 445  
 ccatggggct gcctagcctc tggggaggcc cctcagctgg tgacaccagc agggcagatt  
 60  
 tcttgcttta ttgctcacc tgtccagggt tccctctgtt tgtgaggag ctgctgccac  
 120  
 cttgggtcca ggaagcatga agctccgcag gtcagcctcc tgggtgggagg acttttcctt  
 180  
 agttttcttt gctcttctgc tctgagtcca gccctggctg gacctttgat cccttctctc  
 240  
 tttatcagga aattttctga ctttcttctt ttgccttttc aagatctgtg atgccatctc  
 300  
 caagtgggaa caagccatga aggagctgca ccccgaaaag tctgagggtg ggacacgcgt  
 360

<210> 446  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

Met	Ala	Cys	Ser	His	Leu	Glu	Met	Ala	Ser	Gln	Ile	Leu	Lys	Arg	Gln
1				5					10					15	
Lys	Lys	Lys	Val	Arg	Lys	Phe	Pro	Asp	Lys	Glu	Arg	Arg	Asp	Gln	Arg
			20					25					30		
Ser	Ser	Gln	Gly	Trp	Thr	Gln	Ser	Arg	Arg	Ala	Lys	Lys	Thr	Lys	Glu
		35				40					45				
Lys	Ser	Ser	His	Gln	Glu	Ala	Asp	Leu	Arg	Ser	Phe	Met	Leu	Pro	Gly
	50				55					60					
Pro	Lys	Val	Ala	Ala	Ala	Pro	Ser	Gln	Thr	Glu	Gly	Thr	Leu	Asp	Arg
65				70				75					80		
Val	Ser	Asn	Lys	Ala	Arg	Asn	Leu	Pro	Cys	Trp	Cys	His	Gln	Leu	Arg
		85					90						95		
Gly	Leu	Pro	Arg	Gly											
		100													

<210> 447  
 <211> 487  
 <212> DNA  
 <213> Homo sapiens

<400> 447  
 acgcgtgaag ggggaaattg ctcgtgccac ctgaggatta atcattaccc tggaaccctt  
 60

cccaaggcca tcaaggaaca cgcacccctt accagacctt ccagctgctg ggggctctcc  
 120  
 gaggtaggct gaggtcatgg agaagggaat ggggggcccc catggccagc tggacctgat  
 180  
 cactgcctcc ccactcagcc acagccctca gggccctgtg ccagtccaga agccatttca  
 240  
 gggacacctt tggccaatgt tctgtttcat ctgcgaggca accttccccca gtgccccaac  
 300  
 catagcgttt tccccaaac accctcagga aggagggacc actacctgtg cagggggggc  
 360  
 caggagcctc ctgagagcct catatgggga ggaagtggta ccatctcacc cccattgcct  
 420  
 ttctctceta cttccacctg gccagcttcc ctcagtgcc ctcctgcctc agtgcccctt  
 480  
 cacgcgt  
 487

&lt;210&gt; 448

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 448

Met	Glu	Lys	Gly	Met	Gly	Gly	Pro	His	Gly	Gln	Leu	Asp	Leu	Ile	Thr
1			5				10				15				
Ala	Ser	Pro	Leu	Ser	His	Ser	Pro	Gln	Gly	Pro	Val	Pro	Val	Gln	Lys
			20				25				30				
Pro	Ile	Gln	Gly	His	Leu	Trp	Pro	Met	Phe	Cys	Phe	Ile	Cys	Glu	Ala
			35				40				45				
Thr	Phe	Pro	Ser	Ala	Pro	Thr	Ile	Ala	Phe	Ser	Pro	Lys	His	Pro	Gln
			50				55				60				
Glu	Gly	Gly	Thr	Thr	Thr	Cys	Ala	Gly	Gly	Ala	Arg	Ser	Leu	Leu	Arg
65						70				75				80	
Ala	Ser	Tyr	Gly	Glu	Val	Val	Pro	Ser	His	Pro	His	Cys	Leu	Ser	
				85			90					95			
Leu	Leu	Leu	Pro	Pro	Gly	Gln	Leu	Pro	Ser	Val	Pro	Leu	Leu	Pro	Gln
			100				105					110			
Cys	Pro	Phe	Thr	Arg											
			115												

&lt;210&gt; 449

&lt;211&gt; 353

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 449

gagctcagcc agttggagtt tgagaagcgg cagctgcaca gggacttgga gcaggccaag  
 60  
 gagaaggggg agcgggcaga gaagctggag agggagctac agcgactcca ggaggagaac  
 120  
 gggaggctgg ccaggaaggt gacctccctg gagacagcca ccgagaaagt cgaggccctg  
 180  
 gagcatgaga gccagggcct gcagctggag aaccggactc tgaggaagtc tctggacacc  
 240

ttgcagaacg tgtccctgca gcttgagggc ctggagcgtg acaacaagca gctggacgca  
 300  
 gagaacctgg agctgcgcag gctggtggag accatgcgga gacgacaacg cgt  
 353

<210> 450  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 450  
 Glu Leu Ser Gln Leu Glu Phe Glu Lys Arg Gln Leu His Arg Asp Leu  
 1 5 10 15  
 Glu Gln Ala Lys Glu Lys Gly Glu Arg Ala Glu Lys Leu Glu Arg Glu  
 20 25 30  
 Leu Gln Arg Leu Gln Glu Glu Asn Gly Arg Leu Ala Arg Lys Val Thr  
 35 40 45  
 Ser Leu Glu Thr Ala Thr Glu Lys Val Glu Ala Leu Glu His Glu Ser  
 50 55 60  
 Gln Gly Leu Gln Leu Glu Asn Arg Thr Leu Arg Lys Ser Leu Asp Thr  
 65 70 75 80  
 Leu Gln Asn Val Ser Leu Gln Leu Glu Gly Leu Glu Arg Asp Asn Lys  
 85 90 95  
 Gln Leu Asp Ala Glu Asn Leu Glu Leu Arg Arg Leu Val Glu Thr Met  
 100 105 110  
 Arg Arg Arg Gln Arg  
 115

<210> 451  
 <211> 444  
 <212> DNA  
 <213> Homo sapiens

<400> 451  
 gtgatgcggc tgactaagcc tactttattc accaatatcc cagtaacatg tgaagagaaa  
 60  
 gacttacctg gagatctctt taaccagctg atgagagatg atccttcaac cggttaatggt  
 120  
 gcagaagtgt taatgttggg agaaatgctg actttaccac agaattttgg gaatatattt  
 180  
 ttgggagaga ccttttccag ttatatcagc gttcataatg atagcaatca agttgtaaaa  
 240  
 gacatattag taaaagctga tcttcagaca agttctcagc gtttaaattct ttcagcctcc  
 300  
 aatgctgcag tggctgaact taaaccggat tgttgatttg atgatgtcat acatcatgaa  
 360  
 gtcaaagaaa ttggaacaca catcttggtg tgtgctgtga gttatacaac tcaggctgga  
 420  
 gaaaaaatgt atttcagaaa attt  
 444

<210> 452  
 <211> 148  
 <212> PRT

<213> Homo sapiens

<400> 452

```

Val Met Arg Leu Thr Lys Pro Thr Leu Phe Thr Asn Ile Pro Val Thr
 1           5           10           15
Cys Glu Glu Lys Asp Leu Pro Gly Asp Leu Phe Asn Gln Leu Met Arg
      20           25           30
Asp Asp Pro Ser Thr Val Asn Gly Ala Glu Val Leu Met Leu Gly Glu
      35           40           45
Met Leu Thr Leu Pro Gln Asn Phe Gly Asn Ile Phe Leu Gly Glu Thr
      50           55           60
Phe Ser Ser Tyr Ile Ser Val His Asn Asp Ser Asn Gln Val Val Lys
65           70           75           80
Asp Ile Leu Val Lys Ala Asp Leu Gln Thr Ser Ser Gln Arg Leu Asn
      85           90           95
Leu Ser Ala Ser Asn Ala Ala Val Ala Glu Leu Lys Pro Asp Cys Cys
      100          105          110
Ile Asp Asp Val Ile His His Glu Val Lys Glu Ile Gly Thr His Ile
      115          120          125
Leu Val Cys Ala Val Ser Tyr Thr Thr Gln Ala Gly Glu Lys Met Tyr
      130          135          140
Phe Arg Lys Phe
145

```

<210> 453

<211> 373

<212> DNA

<213> Homo sapiens

<400> 453

```

gctagctctg accccacctt tgccaagtgg cactaggggtg gccaatgggg actaggggtg
60
tataattgga aaatacagtc tcccctgttg toccaagaaag gccccagatg acctgggggt
120
tgaaaggcac tcccgctggg tgcttctctg gagcaggtgg ggggcagcgg ggcggcgggg
180
cctgtctgtg ctgagcatcc ccagctccag ggcaggtgct gggctctgag cccactgggt
240
gcgttttggg atgggctggc ctgcgcggct gtcgtttcag agcacacaga agagaccctg
300
ccacaggagg agtgggagga gaagctgttg atgttctctg gagacaccct ggccatcatt
360
tctgacaacg cgt
373

```

<210> 454

<211> 108

<212> PRT

<213> Homo sapiens

<400> 454

```

Met Met Ala Arg Val Ser Arg Arg Asn Ile Asn Ser Phe Ser Ser His
 1           5           10           15
Ser Ser Cys Gly Arg Val Ser Ser Val Cys Ser Glu Thr Thr Ala Ala

```

```

          20          25          30
Gln Ala Ser Pro Ser Gln Asn Ala Pro Val Gly Leu Arg Ala Gln His
          35          40          45
Leu Pro Trp Ser Trp Gly Cys Ser Ala Gln Thr Gly Pro Ala Ala Pro
          50          55          60
Leu Pro Pro Thr Cys Ser Gln Glu Ala Pro Ser Gly Ser Ala Phe Gln
65          70          75          80
Ala Pro Gly His Leu Gly Pro Phe Leu Asp Asn Arg Gly Asp Cys Ile
          85          90          95
Phe Gln Leu Tyr Asn Pro Ser Pro His Trp Pro Pro
          100          105

```

<210> 455  
 <211> 602  
 <212> DNA  
 <213> Homo sapiens

```

<400> 455
cctaggcaaaa gcatgcccac cctacctccc cttaccctta cccttcattt tcccctaagc
60
acccatcacc accgatgtta ctgtatgtgt ttgcttaacgc tgacagccca ccaccacac
120
tggaatgtcc gcacgacaaa ggcaggactc ttggctgcct tagccacagc tggatcccca
180
gagcttttcta ggggtgttggg cacagagtgg agtgggtact taataagtat ctgtggaatg
240
aacatgtaca gagtgaagcc ctgtgcccag aacaggctca aaataagctc aattcctttc
300
cttgccactt actaagtcct ttttctctcg cccctctca ctgacctggt tttgatgcca
360
gacagcacag atgggctagg gaggcagggtg gggaagcaga gatctgcgtc tcttggaagt
420
ggagctggtg ggtggggctc cttcctggtg ctgcggaggc tcattgggga ggtggcagcg
480
acccctcag gagcctctgt cgcctgcact cagatctgtg cctttccaca gcgcccggag
540
gaagacttgc tcaggagata aattcaaaga caacaggaag ctggacgtgg tggctcacgc
600
gt
602

```

<210> 456  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

```

<400> 456
Met Pro Thr Leu Pro Pro Leu Thr Leu Thr Leu His Phe Pro Leu Ser
1          5          10          15
Thr His His His Arg Cys Tyr Cys Met Cys Leu Leu Thr Leu Thr Ala
          20          25          30
His His Pro His Trp Asn Val Arg Thr Thr Lys Ala Gly Leu Leu Ala
          35          40          45
Ala Leu Ala Thr Ala Gly Ser Pro Glu Leu Cys Arg Val Leu Gly Thr

```



50                      55                      60  
 Glu Trp Ser Gly Tyr Leu Ile Ser Ile Cys Gly Met Asn Met Tyr Arg  
 65                      70                      75                      80  
 Val Lys Pro Cys Ala Gln Asn Arg Leu Lys Ile Ser Ser Ile Pro Phe  
                     85                      90                      95  
 Leu Ala Thr Tyr  
                     100

<210> 457  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

<400> 457  
 acgcgtcatg tggatattcc tgggagggtc ccaggaacgt ttctggacgg gccccgacc  
 60  
 agaggtcagg gaacttttct tattattctg cacgtgccca gggatagtca aaccaggctct  
 120  
 tcccccttctg ctggccgcaa cacgccagcc gccgccacga ccgcacgctg aattcatgac  
 180  
 ccgacacgcg acgtggcagc gagcacaccc accgctagga gaaagagcgc tcatcgaaga  
 240  
 tcgttttctg tccactggcc agcgccacta tgatcagggtg gggatatccgc ccggcggcgg  
 300  
 gagcaccggg acgccggggc gccg  
 324

<210> 458  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 458  
 Met Trp Ile Phe Leu Gly Gly Ser Gln Glu Arg Phe Trp Thr Gly Pro  
 1                      5                      10                      15  
 Arg Pro Glu Val Arg Glu Leu Phe Leu Leu Phe Cys Thr Cys Pro Gly  
                     20                      25                      30  
 Ile Val Lys Pro Gly Leu Pro Leu Leu Ala Ala Thr Arg Gln Pro  
                     35                      40                      45  
 Pro Pro Arg Pro His Ala Glu Phe Met Thr Arg His Ala Thr Trp Gln  
                     50                      55                      60  
 Arg Ala His Pro Pro Leu Gly Glu Arg Ala Leu Ile Glu Asp Arg Phe  
 65                      70                      75                      80  
 Leu Ser Thr Gly Gln Arg His Tyr Asp Gln Val Gly Tyr Pro Pro Gly  
                     85                      90                      95  
 Gly Gly Ser Thr Gly Thr Pro Gly Arg  
                     100                      105

<210> 459  
 <211> 415  
 <212> DNA  
 <213> Homo sapiens

<400> 459

acgcgttcat tccgcatctg cttccatgga tttcctgcgg ggaggcgcg cccagagtg  
 60  
 ggggtgctgaa caccgacctt cagtgatcgt ttcaaccacc ggccgagatg ggtcctgacg  
 120  
 ctgggcttca agccgcttgc gctcgcgctc ctgatctcgg gcagcgcgat tccgggtggtt  
 180  
 tatgtgcccg gcagacgact gcgcacgccc ctcacgaggt atctgcacat gcttaaaggg  
 240  
 agaggcctca cccgacagct gggcatcgga tttacgaagc ccacgacgaa tcttctcgc  
 300  
 ctcctcaaag ccgatcatcg gcatgccagg tttgtggttg aatgcttcga tcaacacact  
 360  
 aggatcggtg ggggtccacca catacccgga gcggcaatcg agcggatacg acctc  
 415

&lt;210&gt; 460

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 460

Met	Pro	Met	Ile	Gly	Phe	Glu	Glu	Ala	Arg	Lys	Ile	Arg	Arg	Gly	Leu
1				5					10					15	
Arg	Lys	Ser	Asp	Ala	Gln	Leu	Ser	Gly	Glu	Ala	Ser	Pro	Phe	Lys	His
			20					25					30		
Val	Gln	Ile	Pro	Arg	Glu	Gly	Arg	Ala	Gln	Ser	Ser	Ala	Gly	Ser	Ile
			35				40					45			
Asn	His	Arg	Asn	Arg	Ala	Ala	Arg	Asp	Gln	Glu	Arg	Glu	Arg	Lys	Arg
			50			55					60				
Leu	Glu	Ala	Gln	Arg	Gln	Asp	Pro	Ser	Arg	Pro	Val	Val	Glu	Thr	Ile
65					70				75					80	
Thr	Glu	Val	Ser	Cys	Ser	Thr	Pro	Ala	Leu	Ser	Ala	Ala	Pro	Pro	Arg
				85					90					95	
Arg	Lys	Ser	Met	Glu	Ala	Asp	Ala	Glu							
			100					105							

&lt;210&gt; 461

&lt;211&gt; 357

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 461

acgcgttcga ggtcggctaa atttatcatg cgcacgacaa agagagtagt ggctcacaac  
 60  
 cgggtcacat gcatgatgac aaaaactggc agaataagagt tgatgtcatc ccgtctacca  
 120  
 gctcctagaa ccagctcaga gagtcccggg gtcggtagcg tcgagactca gtacacaact  
 180  
 gtcgcgatac cggacgaccc tcttcatctg gttgcagatg ggcgtctcaa tcacgtcact  
 240  
 gtcgcttacg aaacctacgg gaagctcaat acgtccagcg acaatgcggg ctatacctgt  
 300  
 catgcgctta ctggtgatgc ccatgcagcc ggatttcacc ccggtgtagt ccgtccg  
 357

<210> 462  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 462  
 Thr Arg Ser Arg Ser Ala Lys Phe Ile Met Arg Thr Thr Lys Arg Val  
 1 5 10 15  
 Val Ala His Asn Arg Val Thr Cys Met Met Thr Lys Thr Gly Arg Ile  
 20 25 30  
 Glu Leu Met Ser Ser Arg Leu Pro Ala Pro Arg Thr Ser Ser Glu Ser  
 35 40 45  
 Pro Gly Val Gly Thr Val Glu Thr Gln Tyr Thr Thr Val Ala Ile Pro  
 50 55 60  
 Asp Asp Pro Leu His Leu Val Ala Asp Gly Arg Leu Asn His Val Thr  
 65 70 75 80  
 Val Ala Tyr Glu Thr Tyr Gly Lys Leu Asn Thr Ser Ser Asp Asn Ala  
 85 90 95  
 Val Tyr Thr Cys His Ala Leu Thr Gly Asp Ala His Ala Ala Gly Phe  
 100 105 110  
 His Pro Gly Val Val Arg Pro  
 115

<210> 463  
 <211> 434  
 <212> DNA  
 <213> Homo sapiens

<400> 463  
 gtgcacgggg tatgcgaggg atgcggcatt gccaccaatg ccgctgacct gcgcagatac  
 60  
 gaggcagctg gtgacgatga agtggtgcga tgcgaggaat gcgatcgat cctggtgcgt  
 120  
 accggagagt ccatctgagc ccttcttggtg gcggtgatgc cgggatatcc gtagaattag  
 180  
 cggtcggacg agccatccgg gtgatcgcg cagcgggtgag ttgtcgagga aagtcggggc  
 240  
 tccatagagc aggggtggtg gtaacgccca cccggggtga cccgcgggaa agtgccacag  
 300  
 agaacagact gccggtttcg agccgggtgag ggtgaaacgg tggagtaagt gcccaccgcg  
 360  
 tcatcgggtga cggtgacggc atggcaaacc ccacctggag caaggccaag aagaccgtga  
 420  
 ggtcgaggac gcgt  
 434

<210> 464  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

<400> 464  
 Met Pro Ser Pro Ser Pro Met Thr Arg Trp Ala Leu Thr Pro Pro Phe

```

      1             5             10             15
His Pro His Arg Leu Glu Thr Gly Ser Leu Phe Ser Val Ala Leu Ser
      20             25             30
Arg Gly Ser Pro Arg Val Gly Val Thr His His Pro Ala Leu Trp Ser
      35             40             45
Pro Asp Phe Pro Arg Gln Leu Thr Ala Ala Ala Ile Thr Arg Met Ala
      50             55             60
Arg Pro Thr Ala Asn Ser Thr Asp Ile Pro Ala Ser Pro Pro Gln Glu
      65             70             75             80
Gly Leu Arg Trp Thr Leu Arg Tyr Ala Pro Gly Tyr Asp Arg Ile Pro
      85             90             95
Arg Ile Ala Pro Leu His Arg His Gln Leu Pro Arg Ile Cys Ala Gly
      100            105            110
Gln Arg His Trp Trp Gln Cys Arg Ile Pro Arg Ile Pro Arg Ala
      115            120            125

```

&lt;210&gt; 465

&lt;211&gt; 438

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 465

```

gatcatttag aatttatgga agaagctgat gtgaaagcta tgggtcaaadc tggcactgtg
60
gctgtattgc taccaggagc attttacacc ttgaaagaaa ctcaacttcc accgatgaat
120
ttgttacgtc agtacggagt agacattgct atttcgacgg atgctaatacc agggacgtcg
180
ccagcggttat cattacgggtt aatgatgaat atggcatgta ccttgtttgg tatgacacct
240
gaaaccgccc ttgcaggggt aacaattcat gcggcaaaaag cggtggggat tagcgattct
300
catggcactt tagaagttgg caaggtagct gattttgtct gctgggatgt ggaaagcccc
360
ggtgaacttt gttattgggt aggagagcag ttagtaaagc aacgtattca gcacggagta
420
tcccatgaat aatctaga
438

```

&lt;210&gt; 466

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 466

```

Asp His Leu Glu Phe Met Glu Glu Ala Asp Val Lys Ala Met Val Lys
1             5             10             15
Ser Gly Thr Val Ala Val Leu Leu Pro Gly Ala Phe Tyr Thr Leu Lys
      20             25             30
Glu Thr Gln Leu Pro Pro Met Asn Leu Leu Arg Gln Tyr Gly Val Asp
      35             40             45
Ile Ala Ile Ser Thr Asp Ala Asn Pro Gly Thr Ser Pro Ala Leu Ser
      50             55             60
Leu Arg Leu Met Met Asn Met Ala Cys Thr Leu Phe Gly Met Thr Pro

```

```

65          70          75          80
Glu Thr Ala Leu Ala Gly Val Thr Ile His Ala Ala Lys Ala Leu Gly
          85          90          95
Ile Ser Asp Ser His Gly Thr Leu Glu Val Gly Lys Val Ala Asp Phe
          100          105          110
Val Cys Trp Asp Val Glu Ser Pro Gly Glu Leu Cys Tyr Trp Leu Gly
          115          120          125
Glu Gln Leu Val Lys Gln Arg Ile Gln His Gly Val Ser His Glu
          130          135          140

```

<210> 467  
 <211> 460  
 <212> DNA  
 <213> Homo sapiens

```

<400> 467
ntttccctgg ctattggcca tgtgggacac aacgttccgc ctaccccaga gcggttaagc
60
tgcattccctg caccttcttc tcccaccgct tcaaagccac agtgaggaac ttcggagctt
120
ctcgcagtga agatggcggt ggaggaatgg atgccctggc tagaagaggg ggaatatctg
180
ttgatttgtt ggaccgacca caaaaacctg gagtatctcc acacaaccaa gtgcctcaac
240
tccaggcaag caagaagggc ccagctgttt acctgggtcc acttttccct ctccctaccg
300
ccgggggtcca agaacatcag gctggatgcc ctttcttgcc actttatggg catgggcccc
360
ttctccagg cttgcctgtc acccgggctc ccgtcaaacc ctggccttcg tgcgacaaca
420
ctcttggtgc cttctatggt tctgtatggt gccgcaattg
460

```

<210> 468  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

```

<400> 468
Gly Thr Ser Glu Leu Leu Ala Val Lys Met Ala Leu Glu Glu Trp Met
1      5      10      15
Pro Trp Leu Glu Glu Ala Glu Tyr Leu Leu Ile Val Trp Thr Asp His
20     25     30
Lys Asn Leu Glu Tyr Leu His Thr Thr Lys Cys Leu Asn Ser Arg Gln
35     40     45
Ala Arg Arg Ala Gln Leu Phe Thr Trp Phe His Phe Ser Leu Ser Tyr
50     55     60
Arg Pro Gly Ser Lys Asn Ile Arg Leu Asp Ala Leu Ser Cys His Phe
65     70     75     80
Met Gly Met Gly Pro Phe Leu Gln Ala Cys Leu Ser Pro Gly Leu Pro
85     90     95
Ser Asn Pro Gly Leu Arg Ala Thr Thr Leu Leu Val Pro Ser Met Val
100    105    110
Leu Tyr Val Ala Ala Ile

```

115

<210> 469  
 <211> 381  
 <212> DNA  
 <213> Homo sapiens

<400> 469  
 cttgtgcaca cggtattttt ccaatacaaa tagtttaaaa agtaaaactcc aaatacctat  
 60  
 aagccccctc aaagcacctt ccaaatatga accttggtta tgcccaaggt ccagaggggt  
 120  
 cccccagaaa ggcccaggag cctggggcat gggaaagctg tcgggggtccc catgctgact  
 180  
 ccctggactc caagcgatat tccataaagc cagggcctcc tggctgcggg agggaggcct  
 240  
 tgacccaaaa tccattcggc cctggatact ggagaggcag aggcctctgc tgatgagaag  
 300  
 ccctgagttc ctggctagct gtggttaacc acaaaaaatg cgggggggtga tgattttcga  
 360  
 agtccatcgg caaagaaaga c  
 381

<210> 470  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 470  
 Met Asp Phe Glu Asn His His Pro Pro His Phe Leu Trp Leu Thr Thr  
 1 5 10 15  
 Ala Ser Gln Glu Leu Arg Ala Ser His Gln Gln Arg Pro Leu Pro Leu  
 20 25 30  
 Gln Tyr Pro Gly Pro Asn Gly Phe Trp Val Lys Ala Ser Leu Pro Gln  
 35 40 45  
 Pro Gly Gly Pro Gly Phe Met Glu Tyr Arg Leu Glu Ser Arg Glu Ser  
 50 55 60  
 Ala Trp Gly Pro Arg Gln Leu Ser His Ala Pro Gly Ser Trp Ala Phe  
 65 70 75 80  
 Leu Gly Asp Pro Ser Gly Pro Trp Ala Leu Thr Arg Phe Ile Phe Gly  
 85 90 95  
 Arg Cys Phe Glu Gly Ala Tyr Arg Tyr Leu Glu Phe Thr Phe  
 100 105 110

<210> 471  
 <211> 378  
 <212> DNA  
 <213> Homo sapiens

<400> 471  
 accggtgact acctgcagca ctggattgac atgggtaaaa agggcggcga ccgcatgcc  
 60  
 gaggtcttcc tgggttaactg gttccgccgc ggcgacgatg gccgcttcct gtggccngg  
 120

cttggcgaaa acttccccgt cctanagtgg atcatcgacc gcattgaagg caacgtagag  
 180  
 gccgaggaca cggtgggtcgg acgcaccgcc cgcgccgagg acatcgactt gcaaggcctt  
 240  
 gacttcgatg tcgacgacgt tcgcgccgca ctgcgcgttg acccgaagga atgggaaggc  
 300  
 gatatgcaag acaacgccga gtacctgaac ttcttgggct cccgcgtgcc cgaggaagtg  
 360  
 tggaaccagt tccgcgcc  
 378

<210> 472  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 472  
 Thr Gly Asp Tyr Leu Gln His Trp Ile Asp Met Gly Lys Lys Gly Gly  
 1 5 10 15  
 Asp Arg Met Pro Glu Val Phe Leu Val Asn Trp Phe Arg Arg Gly Asp  
 20 25 30  
 Asp Gly Arg Phe Leu Trp Pro Xaa Leu Gly Glu Asn Phe Pro Val Leu  
 35 40 45  
 Xaa Trp Ile Ile Asp Arg Ile Glu Gly Asn Val Glu Ala Glu Asp Thr  
 50 55 60  
 Val Val Gly Arg Thr Ala Arg Ala Glu Asp Ile Asp Leu Gln Gly Leu  
 65 70 75 80  
 Asp Phe Asp Val Asp Asp Val Arg Ala Ala Leu Ala Val Asp Pro Lys  
 85 90 95  
 Glu Trp Glu Gly Asp Met Gln Asp Asn Ala Glu Tyr Leu Asn Phe Leu  
 100 105 110  
 Gly Ser Arg Val Pro Glu Glu Val Trp Asn Gln Phe Arg Ala  
 115 120 125

<210> 473  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

<400> 473  
 accggttggt gggggaaggg acccatccca tgccacctgt cctagaaaat gtttcccctt  
 60  
 gttgagcagc tgctggatct agggctgctg ggtctaagtc caaaaaggga aaaaggaaaa  
 120  
 aggcaccaag taaaagaagg gggaagctgc caaaaccccc cctgccaaaa ctctcccacc  
 180  
 ctgcttccat ttccctctcc aggggaacagg tgtacctccc ctctccctg tctctctcag  
 240  
 atgccccagg ggctctctac ttcatctctg ccgaccctgc caggagtggc ctcaggggta  
 300  
 gaggtctcta gttggagaat ttgcttgacg gaaggtgaa  
 339

<210> 474

<211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 474  
 Met Phe Pro Leu Val Glu Gln Leu Leu Asp Leu Gly Leu Leu Gly Leu  
 1 5 10 15  
 Ser Pro Lys Arg Glu Lys Gly Lys Arg His Gln Val Lys Glu Gly Gly  
 20 25 30  
 Ser Cys Gln Asn Pro Pro Cys Gln Asn Ser Pro Thr Leu Leu Pro Phe  
 35 40 45  
 Pro Ser Pro Gly Asn Arg Cys Thr Ser Pro Pro Pro Cys Pro Pro Gln  
 50 55 60  
 Met Pro Gln Gly Leu Ser Thr Ser Phe Leu Pro Thr Leu Pro Gly Val  
 65 70 75 80  
 Ala Ser Gly Val Glu Ala Pro Ser Trp Arg Ile Cys Leu Gln Glu Gly  
 85 90 95  
 Glu

<210> 475  
 <211> 345  
 <212> DNA  
 <213> Homo sapiens

<400> 475  
 acgcgtgaag ggtccctcc aaactctgag cctccttcca agccttgctg ggagctcccc  
 60  
 agcgcctgcc ggagaggcct ctccctccagg cgggcttccc gcgccgatgt gaaggagagg  
 120  
 ctgccccaga ggggtctgga tcgtaatcca gaaagggaca gtccacacagc cataatcccc  
 180  
 aatgctggga ctcttcagta aaggaagaga tggctttttc gttcatctgc ctttctgaaa  
 240  
 ggtaaaatat ctccagatcc gggctctctg ggcgactgcg tatgtggggg tccctgaagc  
 300  
 ctttgatgga tcttgtaga agtgggttgt tcatcttggg gtttt  
 345

<210> 476  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 476  
 Met Asn Asn Pro Leu Leu Thr Arg Ser Ile Lys Gly Phe Arg Asp Pro  
 1 5 10 15  
 His Ile Arg Ser Arg Pro Glu Ser Pro Asp Leu Glu Ile Phe Tyr Leu  
 20 25 30  
 Ser Glu Arg Gln Met Asn Glu Lys Ala Ile Ser Ser Phe Thr Glu Glu  
 35 40 45  
 Ser Gln His Ser Gly Leu Trp Leu Trp Asp Cys Pro Phe Leu Asp Tyr  
 50 55 60  
 Asp Pro Asp Pro Ser Gly Ala Ala Ser Pro Ser His Arg Arg Gly Lys



```

65              70              75              80
Pro Ala Trp Arg Arg Gly Leu Ser Gly Arg Arg Trp Gly Ala Pro Ser
              85              90              95
Lys Ala Trp Lys Glu Ala Gln Ser Leu Glu Gly Thr Leu His Ala
              100              105              110

```

<210> 477  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

```

<400> 477
acgcgtggcc gagccagcgt gctcaaggaa atggtcaacg gcactcttat taacggctgg
60
gactctcccg aggtggaacg ggcactggac ctgtgcatgg cgtgcaaagg gtgcgcccga
120
gattgccccca ccggaatcga catggccagc taccgcagca cggttcttga cgaaaaatac
180
cgtcaccgtc tccgcctcgc ctccacctg acgatggggc tgctgcccatt gtgggaacgt
240
ttgctcaatc ggaccccagg agcgccgtcg ctggctaacg cagtgccttc gatgccggtc
300
ttgcacgtc ttgctagatg gacagccggg gtggatcagc gtcgtccct ccccgatc
360
cagccctcgg ccagattggc cagtccgcag gccgccccgg ttaaggagat tgtggcggat
420
cc
422

```

<210> 478  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

```

<400> 478
Thr Arg Gly Arg Ala Ser Val Leu Lys Glu Met Val Asn Gly Thr Leu
1      5      10      15
Ile Asn Gly Trp Asp Ser Pro Glu Val Glu Arg Ala Leu Asp Leu Cys
20     25     30
Met Ala Cys Lys Gly Cys Ala Arg Asp Cys Pro Thr Gly Ile Asp Met
35     40     45
Ala Ser Tyr Arg Ser Thr Val Leu Asp Glu Lys Tyr Arg His Arg Leu
50     55     60
Arg Pro Arg Ser His Leu Thr Met Gly Leu Leu Pro Met Trp Glu Arg
65     70     75     80
Leu Leu Asn Arg Thr Pro Gly Ala Pro Ser Leu Ala Asn Ala Val Leu
85     90     95
Ser Met Pro Val Phe Ala Arg Leu Ala Arg Trp Thr Ala Gly Val Asp
100    105    110
Gln Arg Arg Pro Leu Pro Arg Phe Gln Pro Ser Ala Arg Leu Ala Ser
115    120    125
Pro Gln Ala Ala Pro Val Lys Glu Ile Val Ala Asp
130    135    140

```

<210> 479  
 <211> 348  
 <212> DNA  
 <213> Homo sapiens

<400> 479  
 cgcggtggcca ttggccgggc gctgggtgcgg caccgcgcac tggtgattgc cgatgagccg  
 60  
 atctcggcgt tggacatgac catccagaag cagattcttg agctgttcga ggcctgcag  
 120  
 gcgcagtacg gctttgcctg cctgttcac tccacgcacc tggcagcggg ggaacgcac  
 180  
 gcccacccggg tggcgggtgat gagcgagggc aggggtgggg aaatgggtgc ccgcgacgag  
 240  
 atcttcgacc gccgcagca cccctacacc cgcaagctgc tggccgcgcg cagccccctg  
 300  
 gagaaacttg aaaacggtgg ctaccgcac cgccagggcc ccgtaccg  
 348

<210> 480  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 480  
 Arg Val Ala Ile Gly Arg Ala Leu Val Arg His Pro Arg Leu Val Ile  
 1 5 10 15  
 Ala Asp Glu Pro Ile Ser Ala Leu Asp Met Thr Ile Gln Lys Gln Ile  
 20 25 30  
 Leu Glu Leu Phe Glu Arg Leu Gln Ala Gln Tyr Gly Phe Ala Cys Leu  
 35 40 45  
 Phe Ile Ser His Asp Leu Ala Ala Val Glu Arg Ile Ala His Arg Val  
 50 55 60  
 Ala Val Met Ser Glu Gly Arg Val Val Glu Met Gly Ala Arg Asp Glu  
 65 70 75 80  
 Ile Phe Asp Arg Pro Gln His Pro Tyr Thr Arg Lys Leu Leu Ala Ala  
 85 90 95  
 Ala Ser Pro Leu Glu Lys Leu Glu Asn Gly Gly Tyr Arg Ile Arg Gln  
 100 105 110  
 Gly Pro Val Pro  
 115

<210> 481  
 <211> 441  
 <212> DNA  
 <213> Homo sapiens

<400> 481  
 aagcttctga ctgtggcatt ctccctgctt aatatgtcct caatatcccc tacttactgg  
 60  
 gcaaaatcct gcttatgctt tgggactagc tcaaagacca ctcccttgga tgggtgccttc  
 120  
 cctgccctgc cggcttgccg tggcttcctc agtggttagga ttaccatcac attgcatcat  
 180

gagagcagaa gaccatctcc atgtgactgc tgcccctgct cccagcaggg cccacaanca  
 240  
 cccagtccag gacctggctc acgctgggtg gcggatgccc aggaatgggg ctctggatct  
 300  
 gcctcttctc ctgcaggacc aggaaaccgc tgccctgtcc ctgccccagg aaaccctcag  
 360  
 taaatcccca gtcatttgag tttccctca gcgccagaga ccaataacac atctccacca  
 420  
 acctgaaaaa ccttcacgcg t  
 441

<210> 482

<211> 120

<212> PRT

<213> Homo sapiens

<400> 482

Lys	Leu	Leu	Thr	Val	Ala	Phe	Ser	Leu	Leu	Asn	Met	Ser	Ser	Ile	Ser
1				5					10					15	
Pro	Thr	Tyr	Trp	Ala	Lys	Ser	Cys	Leu	Cys	Phe	Gly	Thr	Ser	Ser	Lys
			20					25					30		
Thr	Thr	Pro	Leu	Asp	Gly	Ala	Phe	Pro	Ala	Leu	Pro	Ala	Cys	Ala	Gly
		35				40					45				
Phe	Leu	Ser	Val	Arg	Ile	Thr	Ile	Thr	Leu	His	His	Glu	Ser	Arg	Arg
	50				55					60					
Pro	Ser	Pro	Cys	Asp	Cys	Pro	Cys	Ser	Gln	Gln	Gly	Pro	Gln	Xaa	
65				70					75					80	
Pro	Ser	Pro	Gly	Pro	Gly	Ser	Arg	Trp	Val	Ala	Asp	Ala	Gln	Glu	Trp
			85					90					95		
Gly	Ser	Gly	Ser	Ala	Ser	Ser	Pro	Ala	Gly	Pro	Gly	Asn	Arg	Cys	Pro
			100					105					110		
Val	Pro	Ala	Pro	Gly	Asn	Pro	Gln								
		115					120								

<210> 483

<211> 330

<212> DNA

<213> Homo sapiens

<400> 483

acgcgttcat tccctgatgg ccacgcacga gctaacggag ggatggggcg aaggggaaggc  
 60  
 caagggttgc tcgaagacca aggagtgtgc agggcaggac ctcgttttaa aggaatatcc  
 120  
 tctcaccaga gacacgcggc ggccaggcag ggccggagcg gggcctgtgc ccaggctccg  
 180  
 agcgtctgcc cagcccagca tccctgtccc cagccaggaa tatgtcttcg tggcatagag  
 240  
 ggagctcttg gagccacacc tgcgtgtgca catgtgtcac cccactgctg ggagggggctc  
 300  
 tcccgggacc ctgcagcgtg ggctggggccc  
 330

<210> 484

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 484

```

Met Gly Arg Arg Glu Gly Gln Gly Cys Leu Glu Asp Gln Gly Val Cys
 1           5           10          15
Arg Ala Gly Pro Arg Phe Lys Gly Ile Ser Ser His Gln Arg His Ala
      20          25          30
Ala Ala Arg Gln Gly Arg Ser Gly Ala Cys Ala Gln Ala Pro Ser Val
      35          40          45
Cys Pro Ala Gln His Pro Cys Pro Gln Pro Gly Ile Cys Leu Arg Gly
      50          55          60
Ile Glu Gly Ala Leu Gly Ala Thr Pro Ala Cys Ala His Val Ser Pro
65          70          75          80
His Cys Trp Glu Gly Leu Ser Arg Asp Pro Ala Ala Trp Ala Gly Pro
      85          90          95

```

&lt;210&gt; 485

&lt;211&gt; 377

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 485

```

acgcgtgctc ggcgcggacga agtcggcgct gatcgcccag tcatgcgccc tgcccgtagcc
60
gcccagttcg gcgatcgccg cattcgggccg gccggaatcg agaaggaatg cgtggacgta
120
cgggggatac caaaggaatc ttgtcgaggg cttcgcgggc ctcgacgtgg atcacctgta
180
cccgcgggac gtggggaagc cgccccgcaa gctcacggga ctccgcgaca tcgatgtgcg
240
atacgatttg caccgtcgtc ggctgcggtg ggcacacatg ctccgcgatc gcctcagcgg
300
tggtttccga cgtcagcagg aacgtggcga cgggtggcat ggcggtcgcc gttatgtcgg
360
cattccatt cctcggg
377

```

&lt;210&gt; 486

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 486

```

Met Arg Pro Ala Arg Ala Ala Gln Phe Gly Asp Arg Arg Ile Arg Pro
 1           5           10          15
Ala Gly Ile Glu Lys Glu Cys Val Asp Val Arg Gly Ile Pro Lys Glu
      20          25          30
Ser Cys Arg Gly Leu Arg Gly Pro Arg Arg Gly Ser Pro Val Pro Asp
      35          40          45
Gly Arg Gly Glu Ala Val Pro Gln Ala His Gly Thr Pro Arg His Arg
      50          55          60
Cys Ala Ile Arg Phe Ala Pro Ser Ser Ala Ala Cys Ala Thr His Ala

```

65											70											75											80
Pro	Arg	Ser	Pro	Gln	Arg	Trp	Phe	Pro	Thr	Ser	Ala	Gly	Thr	Trp	Arg																		
					85											90											95						
Arg	Val	Ala	Trp	Arg	Ser	Pro	Leu	Cys	Arg	His	Ser	His	Ser	Ser																			
					100											105											110						

```
<210> 487
<211> 459
<212> DNA
<213> Homo sapiens
```

```
<400> 487
nnacgcgtaa gatcgattgt ggatcagcac cgatgctggg ccccccgacg ttgttggtgg
60
cgggtgttgt tgtaaggagt gtgtgtgatg cgtgttgggtg ttcctactga ggtaagaat
120
agtgagtttc gtgtggctgt gacgccggcg ggtgttcattg cgttggttgg tcgtggtcatt
180
gagggtgttg ttcaggctgg tgctggtgtg ggttcgggta ttccggattc ggattttgtg
240
gggtgctgggtg cgcggttgtt ggggtgatgtg gagtcgggtgt ggggtgatgc tgatttgggtg
300
ttgaagggtga aggagcctgt tgcggaggag tatgggcgggt tgcattgaggg tttggttctt
360
tttacgtatc ttcatttggc tgctgatgag gcgttgactc gtgagctttt ggggcgtggg
420
gtgacgtcga ttgcgtatga gacggtggag ttggccgat
459
```

```
<210> 488
<211> 124
<212> PRT
<213> Homo sapiens
```

```

<400> 488
Met Arg Val Gly Val Pro Thr Glu Val Lys Asn Ser Glu Phe Arg Val
  1              5              10              15
Ala Val Thr Pro Ala Gly Val His Ala Leu Val Gly Arg Gly His Glu
      20              25              30
Val Leu Val Gln Ala Gly Ala Gly Val Gly Ser Gly Ile Pro Asp Ser
      35              40              45
Asp Phe Val Gly Ala Gly Ala Arg Val Val Gly Asp Val Glu Ser Val
      50              55              60
Trp Gly Asp Ala Asp Leu Val Leu Lys Val Lys Glu Pro Val Ala Glu
65      70              75              80
Glu Tyr Gly Arg Leu His Glu Gly Leu Val Leu Phe Thr Tyr Leu His
      85              90              95
Leu Ala Ala Asp Glu Ala Leu Thr Arg Glu Leu Leu Gly Arg Gly Val
      100              105              110
Thr Ser Ile Ala Tyr Glu Thr Val Glu Leu Ala Asp
      115              120

```

<210> 489  
<211> 542

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 489

nacgcgtttg gcgtactgag tgcgggtggtg gatggcgacg acagtggcaa gccgctgctc  
 60  
 aaccagcacg gttgctacaa agtgcgcttt ccatttaccg gcgatcaaaa gccagcact  
 120  
 cggggttcgg catggctgcg cagggtgtcg ttgtctgccg gttccagcca tggcatgcac  
 180  
 tttccgctgc tcaaaggcag tgaagtgtg gtgtcatttc tggggggcga ccccgaccgg  
 240  
 ccgattatcg ttggctgcgt accaaactcg gaaaccccgga gcatggctcg tgagcgtaac  
 300  
 gccaccacaga ggggcttctc cacggccgga gggcacttcc tggcgatgga agaccacccc  
 360  
 ggggctgccc atctgaagct ggggtgcgct ggcggcaaca gcgtcttcac actgggcaat  
 420  
 ggcaaagtcg ccggcgcgca actgcgcacc aacgccccac atgcaattga catcgtcttc  
 480  
 gctcaaacac gaagtgcccg gcgtgtactc attgtcgatg ggcaccgggg acccgggcgg  
 540  
 cg  
 542

&lt;210&gt; 490

&lt;211&gt; 180

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 490

Xaa	Ala	Phe	Gly	Val	Leu	Ser	Ala	Val	Val	Asp	Gly	Asp	Asp	Ser	Gly
1				5					10					15	
Lys	Pro	Leu	Leu	Asn	Gln	His	Gly	Cys	Tyr	Lys	Val	Arg	Phe	Pro	Phe
			20					25					30		
Thr	Arg	Asp	Gln	Lys	Pro	Ser	Thr	Arg	Gly	Ser	Ala	Trp	Leu	Arg	Arg
			35				40					45			
Val	Ser	Leu	Ser	Ala	Gly	Ser	Ser	His	Gly	Met	His	Phe	Pro	Leu	Leu
			50			55					60				
Lys	Gly	Ser	Glu	Val	Leu	Val	Ser	Phe	Leu	Gly	Gly	Asp	Pro	Asp	Arg
65					70					75				80	
Pro	Ile	Ile	Val	Gly	Cys	Val	Pro	Asn	Ser	Glu	Thr	Pro	Ser	Met	Val
				85					90					95	
Val	Glu	Arg	Asn	Ala	Thr	Gln	Ser	Gly	Phe	Ser	Thr	Ala	Gly	Gly	His
			100					105					110		
Phe	Leu	Ala	Met	Glu	Asp	His	Pro	Gly	Ala	Ala	His	Leu	Lys	Leu	Gly
			115				120					125			
Ala	Pro	Gly	Gly	Asn	Ser	Val	Phe	Thr	Leu	Gly	Asn	Gly	Lys	Val	Ala
			130				135					140			
Gly	Ala	Gln	Leu	Arg	Thr	Asn	Ala	Pro	His	Ala	Ile	Asp	Ile	Val	Phe
145					150					155				160	
Ala	Gln	Thr	Arg	Ser	Ala	Arg	Arg	Val	Leu	Ile	Val	Asp	Gly	His	Arg
				165					170					175	
Gly	Pro	Gly	Gly												

180

<210> 491  
 <211> 825  
 <212> DNA  
 <213> Homo sapiens

<400> 491  
 nacgcgtcga ggcgacggtc ggcgccgtca tggcgactgt tctcgagggc acatgggaac  
 60  
 gcatcgggtgc cggattccgg actgccttaa ccacagcctt ggaacgcacc gatgaatggg  
 120  
 tggggggccc tgacagcaag cccctcaacg aagtcgagac actgcgccgg tgcgccgatg  
 180  
 aactcatcgg cggggccgtc ggcgcgggtg ccgcgatgca cggaggggtca atcgaattgg  
 240  
 tcgacgtgtc ggtcgggtgac gaagagcgca gagtcgacgt caccatgaag ggagcatgcc  
 300  
 gaggttgccc ggcagccatc agaccctaca tcagcgcctg gaacatcaac tgagtctgcg  
 360  
 nattgcgcga gccgggtcacc gtgcgggaaa tctgacacct actccgacag ctccacctcg  
 420  
 acgagcacct ccacgacgag gccaaagccac tcgtagacgc attcctctct ggcatccaat  
 480  
 tcttcccggg ccgcccgagc gacttcgtcg gcagtaacct ggtcgatgat ccctagcctg  
 540  
 gcggccatca tgccacgcag cgcattgaca gtacgaagcc aacgttgctg catcacaggg  
 600  
 ttcatggaga tacagccggt tcggtgcaac gtctccacat cagcacttaa ggactgagcg  
 660  
 tcttcccagc gcgccgcgac atcctcggcg tcattggtcga catggaattg cgcgtcagct  
 720  
 gagtcgtcgt cacgataggc gctgggcagg atcaatcgac gcacctcgtc gtcctcctgg  
 780  
 agtccagaaa actggctctc ccaaaaagcg aacgggtccc cctcc  
 825

<210> 492  
 <211> 58  
 <212> PRT  
 <213> Homo sapiens

<400> 492  
 Met Asn Gly Trp Ala Ala Leu Thr Ala Ser Pro Ser Thr Lys Ser Arg  
 1 5 10 15  
 His Cys Ala Gly Ala Pro Met Asn Ser Ser Ala Gly Pro Ser Ala Arg  
 20 25 30  
 Leu Pro Arg Cys Thr Glu Gly Gln Ser Asn Trp Ser Thr Cys Arg Ser  
 35 40 45  
 Val Thr Lys Ser Ala Glu Ser Thr Ser Pro  
 50 55

<210> 493  
 <211> 863

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 493

nacgcgttcc aacctcgtca aaacggctat cgcaggaaat gaccccaact ggggtcgcac  
 60  
 cctcgcggcg atcggtatgtg ttcctgagaa tatagctccc ttcgatcccg accaggtgga  
 120  
 tgtgtccatc aatgacattc agatctgtaa ggccgggggt atcggggagg accgcaacct  
 180  
 cgtcgatatg aggccacgag aggttcacat cgatattgag ctgcatgcgg gtgatgccga  
 240  
 agctgcggta tggactaatg atctgaccca ccaatacgtc gaagagaata gcgcgtatac  
 300  
 atcatgaccc ttgctcttga catccccctc aacgactccc agttctcggc tcagcggaaa  
 360  
 tctgagggcc tggtagaagc gctgccttgg atcaggcggt ttcagggccg cactgtcgtc  
 420  
 gtgaaatatg gcggcaacgc gatggttgat cccggtctgc agcaggcctt cgccgacgac  
 480  
 attgtgttta tggcctctgt ggggattcgc cctattgtcg tccacggtgg tggccctcag  
 540  
 atcaatgcca tgcttctga atccgctacc ccggtggagt tccgtaatgg tttgcgggtg  
 600  
 acatctccgg aggtcatgga ggttgtccgg atggtgctcg tcgggcaggc gggccgtcag  
 660  
 ctcgttaacc gaatcaacgc ctatgcgccg ctagcagctg gcatgtcagg cgaggacttt  
 720  
 ggcctttttt cgcccccggaa gtcgcgggta attgttgatg gcgagcaa at agacatgggt  
 780  
 ttagtgggag acatcgttga cgtcaacatc gatctcgta tctctatgct tgatcgcggt  
 840  
 cagattccgg tcattgcacc ggt  
 863

&lt;210&gt; 494

&lt;211&gt; 186

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 494

Met Thr Leu Ala Leu Asp Ile Pro Leu Asn Asp Ser Gln Phe Ser Ala  
 1 5 10 15  
 Gln Arg Lys Ser Glu Val Leu Val Glu Ala Leu Pro Trp Ile Arg Arg  
 20 25 30  
 Phe Gln Gly Arg Thr Val Val Val Lys Tyr Gly Gly Asn Ala Met Val  
 35 40 45  
 Asp Pro Gly Leu Gln Gln Ala Phe Ala Asp Asp Ile Val Phe Met Ala  
 50 55 60  
 Ser Val Gly Ile Arg Pro Ile Val Val His Gly Gly Gly Pro Gln Ile  
 65 70 75 80  
 Asn Ala Met Leu Ala Glu Ser Ala Thr Pro Val Glu Phe Arg Asn Gly  
 85 90 95  
 Leu Arg Val Thr Ser Pro Glu Val Met Glu Val Val Arg Met Val Leu



```

      100      105      110
Val Gly Gln Val Gly Arg Gln Leu Val Asn Arg Ile Asn Ala Tyr Ala
      115      120      125
Pro Leu Ala Ala Gly Met Ser Gly Glu Asp Phe Gly Leu Phe Ser Ala
      130      135      140
Arg Lys Ser Arg Val Ile Val Asp Gly Glu Gln Ile Asp Met Gly Leu
      145      150      155      160
Val Gly Asp Ile Val Asp Val Asn Ile Asp Leu Val Ile Ser Met Leu
      165      170      175
Asp Arg Gly Gln Ile Pro Val Ile Ala Pro
      180      185

```

<210> 495  
 <211> 514  
 <212> DNA  
 <213> Homo sapiens

```

<400> 495
gcgcgcgaca ccggtgcccc gattagcgtg ccagtgggtg acgtcactaa gggtcacgtc
60
tggaatgtga caggtgacgt tcttaacgcc ngatccctcc acaatcgagg tgacnntgag
120
cgttggccga tccaccggga tccccgggcc ttcgatgacc ttgagccga gaccgagatg
180
ctggagaccg gtattaaggt ccttgacttg ctgactcctt acgtcaaggg cggcaagatt
240
ggcctctttg gcggcgctgg tgtgggtaag acggtgctca ttcaggagat gatttaccgt
300
atcgcccaca acttcggcgg tacttcgggtt ttcgccggtg tcggtgagcg taccgcgag
360
ggtaacgacc tcatcaacga gatggacgag gccggtgtgc tcaaagacac cgccctggta
420
ttcggccaga tggacgagcc cccgggcacg cggtacgagc tgtcgcgctg gcagccctgc
480
ggcccatgcc tggtaactg ctgtgggacc ttgg
514

```

<210> 496  
 <211> 171  
 <212> PRT  
 <213> Homo sapiens

```

<400> 496
Ala Arg Asp Thr Gly Ala Pro Ile Ser Val Pro Val Gly Asp Val Thr
1      5      10      15
Lys Gly His Val Trp Asn Val Thr Gly Asp Val Leu Asn Ala Xaa Ser
      20      25      30
Leu His Asn Arg Gly Asp Xaa Glu Arg Trp Pro Ile His Arg Asp Pro
      35      40      45
Pro Ala Phe Asp Asp Leu Glu Pro Glu Thr Glu Met Leu Glu Thr Gly
      50      55      60
Ile Lys Val Leu Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
65      70      75      80
Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu

```

85								90					95			
Met	Ile	Tyr	Arg	Ile	Ala	His	Asn	Phe	Gly	Gly	Thr	Ser	Val	Phe	Ala	
100								105					110			
Gly	Val	Gly	Glu	Arg	Thr	Arg	Glu	Gly	Asn	Asp	Leu	Ile	Asn	Glu	Met	
115								120					125			
Asp	Glu	Ala	Gly	Val	Leu	Lys	Asp	Thr	Ala	Leu	Val	Phe	Gly	Gln	Met	
130								135					140			
Asp	Glu	Pro	Pro	Gly	Thr	Arg	Tyr	Glu	Leu	Ser	Arg	Trp	Gln	Pro	Cys	
145								150					155			
160								165					170			
Gly	Pro	Cys	Leu	Val	Asn	Cys	Cys	Gly	Thr	Leu						

```
<210> 497
<211> 662
<212> DNA
<213> Homo sapiens
```

```

<400> 497
acgcgcctctg ggatctcaac ccagcagtc tggcttggtt ctcatccca caatttcctg
60
ggttccacca agcagcgaaa actgccagga tgaatgagga aaaaaccag cccacaaaac
120
gagacacacg ctggcgggga gagacgcagc agagctcctt cctgtctgtg gactcggagc
180
aaagacgtgg ggccccatct tttgtgtttt cctcaagcgg ggaaagaatg gactgtttgc
240
atgcttcgtg ccacacgccc gcggtgatcc cagccagggc cccgagcgca gaggcggagc
300
tgtgctcagc acaggcctgg gacctcccc ggtaggcacc tgtgggggggt gcagcccccg
360
ggaaggagggc aactgcctca cttaacatcc tccgctgcaa ggtgggtggc cgagagggc
420
tgtctgtgaa gacaggtacc aggatggcag gaccgcacg cctcttccca cacctgtcag
480
cttcggaagc atctctcgag gactctggtc ccaggatgtc tcccaggaca agccagtctg
540
cctcttcttc ctacttctgc tgtagcctgg gaccagacct ggccaaggtc agccagcggg
600
gagggccgag gtctgagctc tcgtctgcc gtggcccccg cgatggcttg gggtgcaagc
660
tt
662

```

```
<210> 498
<211> 191
<212> PRT
<213> Homo sapiens
```

<400> 498																
Met	Asn	Glu	Glu	Lys	Thr	Gln	Pro	His	Lys	Arg	Asp	Thr	Arg	Trp	Arg	
1				5					10					15		
Gly	Glu	Thr	Gln	Ser	Ser	Phe	Leu	Ser	Val	Asp	Ser	Glu	Gln	Arg		
			20				25					30				
Arg	Gly	Ala	Pro	Ser	Phe	Val	Phe	Ser	Ser	Ser	Gly	Glu	Arg	Met	Asp	

```

      35      40      45
Cys Leu His Ala Ser Cys His Thr Pro Ala Val Ile Pro Ala Arg Ala
  50      55      60
Pro Ser Ala Glu Ala Glu Leu Cys Ser Ala Gln Ala Trp Asp Leu Pro
  65      70      75      80
Arg Gln Ala Pro Val Gly Gly Ala Ala Pro Gly Lys Glu Ala Thr Ala
      85      90      95
Ser Leu Asn Ile Leu Arg Cys Lys Val Val Ala Pro Arg Gly Val Ser
      100      105      110
Val Lys Thr Gly Thr Arg Met Ala Gly Pro Ala Arg Leu Phe Pro His
      115      120      125
Leu Ser Ala Ser Glu Ala Ser Leu Glu Asp Ser Gly Pro Arg Met Ser
      130      135      140
Pro Arg Thr Ser Gln Ser Ala Ser Ser Ser Tyr Phe Cys Cys Ser Leu
      145      150      155      160
Gly Pro Asp Leu Ala Lys Val Ser Gln Arg Gly Gly Pro Arg Ser Glu
      165      170      175
Leu Ser Ser Cys Arg Gly Pro Arg Asp Gly Leu Gly Cys Lys Leu
      180      185      190

```

&lt;210&gt; 499

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 499

```

acgcgtgaag ggtgggcagt gttgagctga gtgagccctc ctccctgcaa tgctggagcc
60
ctgccttctg cctgaccctc tggcttctca agcagtctat acgtgagaag ccctttcttc
120
aagtgaagc ttctgagctc actacgagag cactggagct ggaacctctc tgggttcaaa
180
tcctcaactg gggggttgga ggaggttact tcacttctca aaacctcaat ttccttatct
240
gcaaaatggg gtaataggag cccctcttca tcaatgcttg gagggaatgc ctggcacagt
300
agggcagtta ccgtcatgga gaacagaaag gccccgagct atcctggatg tggtgagaat
360
gggtcctgga tcctgctgc tcggcctttt cattctcttc ttcacctaca ggctoccaca
420
aagggcctct gaaaacacag ggtg
444

```

&lt;210&gt; 500

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 500

```

Met Thr Val Thr Ala Leu Leu Cys Gln Ala Phe Pro Pro Ser Ile Asp
  1      5      10      15
Glu Glu Gly Leu Leu Leu Pro His Phe Ala Asp Lys Glu Ile Glu Val
      20      25      30
Leu Arg Ser Glu Val Thr Ser Ser Asn Pro Pro Val Glu Asp Leu Asn

```

```

          35          40          45
Pro Glu Arg Phe Gln Leu Gln Cys Ser Arg Ser Glu Leu Arg Ser Phe
          50          55          60
His Leu Lys Lys Gly Leu Leu Thr Tyr Arg Leu Leu Arg Lys Pro Glu
65          70          75          80
Gly Gln Ala Glu Gly Arg Ala Pro Ala Leu Gln Gly Gly Gly Leu Thr
          85          90          95
Gln Leu Asn Thr Ala His Pro Ser Arg
          100          105

```

&lt;210&gt; 501

&lt;211&gt; 800

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 501

```

agatctgata cgagaagtgg ctgctcaggg aaatgactac tccatggctt tcttaactca
60
ggtactcctt attcaatgag aggcctgagg tgagaccgc catgcggcgc gtggatcgca
120
tggtgttagt gcacactagc aaggggctta ggtctccagc tgaggtcaga tgcacacttg
180
gaccttgtag tggggagtaa cacacatctc tgtgttcagc gaaccatcca ggagctgttt
240
gaagtttatt ctcccatgga tgatgctggc ttcccggtca aagctgagga gtttgtggtg
300
ctttctcagg aaccttctgt cacggaaacc attgcacca aaattgcaag acctttcata
360
gaggccctca agagtattga gtatctggag gaggatgcc agaagtccgc acaggagggg
420
tgctgtggac cacacactga tgctctgtca tcagactctg agaacatgcc gtgtgatgaa
480
gaaccatccc aattagagga gctagctgac ttcattggagc agcttacacc aattgaaaaa
540
tatgctttaa attacctgga atcttgaggc agggcctgag agagcacgct gcgccgtact
600
tccagcagct gcggcagacc acggctccac gcctgctgca gttccctgag ctgaggctgg
660
tgaggttcga ctgaggtatg cggcagttgg gggcgtggcc cgtgcgggag ctgcactggc
720
cctggatgat gaggcgctct tgatgtgatt cgtttcccag ggaagttgga agcttttagct
780
atcttgcttc agaaactgaa
800

```

&lt;210&gt; 502

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 502

```

Met Asp Asp Ala Gly Phe Pro Val Lys Ala Glu Glu Phe Val Val Leu
1          5          10          15
Ser Gln Glu Pro Ser Val Thr Glu Thr Ile Ala Pro Lys Ile Ala Arg

```

```

      20      25      30
Pro Phe Ile Glu Ala Leu Lys Ser Ile Glu Tyr Leu Glu Glu Asp Ala
      35      40      45
Gln Lys Ser Ala Gln Glu Gly Val Leu Gly Pro His Thr Asp Ala Leu
      50      55      60
Ser Ser Asp Ser Glu Asn Met Pro Cys Asp Glu Glu Pro Ser Gln Leu
      65      70      75      80
Glu Glu Leu Ala Asp Phe Met Glu Gln Leu Thr Pro Ile Glu Lys Tyr
      85      90      95
Ala Leu Asn Tyr Leu Glu Ser
      100

```

&lt;210&gt; 503

&lt;211&gt; 538

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 503

```

nnacgcgttg tcgtctctcc gatcattgat tttgttgat tctgcaatga tgtaaaggaa
60
gatgatgaca cggagaagtt taaagaagcc attgtgaaat ttcataaggct gtttgggatg
120
ccagaggaag agaaactcgt caactattac tcttgacagct attggaaggg gaaggtcccc
180
cgtcagggtt ggatgtacct cagcattaac cacctttgct tttattcttt tcttatggga
240
agggaagcga aactgggtcat ccggtgggta gacatcactc agcttgagaa gaatgcccc
300
ctgcttctgc ctgatgtgat caaagtgagc acacgggtcca gtgagcatatt cttctctgta
360
ttcctcaaca tcaacgagac cttcaagtta atggagcagc ttgccaacat agccatgagg
420
caactcttag acaatgaggg atttgaacaa gatcgatccc tgcccaaact caaaaggaaa
480
tctcctaaaa aagtgtctgc tctaaaacgt gatcttgatg cctgggacct tcacgcgt
538

```

&lt;210&gt; 504

&lt;211&gt; 179

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 504

```

Xaa Arg Val Val Ser Pro Ile Ile Asp Phe Val Val Phe Cys Asn
  1      5      10      15
Asp Val Lys Glu Asp Asp Asp Thr Glu Lys Phe Lys Glu Ala Ile Val
      20      25      30
Lys Phe His Arg Leu Phe Gly Met Pro Glu Glu Glu Lys Leu Val Asn
      35      40      45
Tyr Tyr Ser Cys Ser Tyr Trp Lys Gly Lys Val Pro Arg Gln Gly Trp
      50      55      60
Met Tyr Leu Ser Ile Asn His Leu Cys Phe Tyr Ser Phe Leu Met Gly
      65      70      75      80
Arg Glu Ala Lys Leu Val Ile Arg Trp Val Asp Ile Thr Gln Leu Glu

```

[illegible]

```
<210> 505
<211> 381
<212> DNA
<213> Homo sapiens
```

```
<400> 505
gtgcacgaca ccgaacggta cgaacgtatc tcccaggcac gtcgcgagga acagcaggcc
60
atgctcggct acgacngctc aagaacctgt cgcattgacct tgctcaccgg gcagctggac
120
gacccctcca cgactccttg cggacgctgc gacgtctgtg ctggcccgtg gtactcagtc
180
gaggtcgata agtcagccgc tgtgagagcc gtccaatccc tcaaccgggt gggagttccg
240
gtggaaccac gcgcgccttg gcccgcaggg atggacgccc tccaggttgc gctcaagggt
300
cgcattcagtg ccgaggagat cgctgcagag ggccgcgtca tcgccagact ctccgatctg
360
ggttggggag gggcgctgcg c
381
```

```
<210> 506
<211> 127
<212> PRT
<213> Homo sapiens
```

```

<400> 506
Val His Asp Thr Glu Arg Tyr Glu Arg Ile Ser Gln Ala Arg Arg Glu
 1              5              10              15
Glu Gln Gln Ala Met Leu Gly Tyr Asp Xaa Ser Arg Thr Cys Arg Met
              20              25              30
Thr Leu Leu Thr Gly Gln Leu Asp Asp Pro Ser Thr Thr Pro Cys Gly
          35              40              45
Arg Cys Asp Val Cys Ala Gly Pro Trp Tyr Ser Val Glu Val Asp Gln
          50              55              60
Ser Ala Ala Val Arg Ala Val Gln Ser Leu Asn Arg Val Gly Val Pro
65              70              75              80
Val Glu Pro Arg Ala Ala Trp Pro Ala Gly Met Asp Ala Leu Gln Val
          85              90              95
Ala Leu Lys Gly Arg Ile Ser Ala Glu Glu Ile Ala Ala Glu Gly Arg

```

	100		105		110
Val	Ile	Ala	Arg	Leu	Ser
			Asp	Leu	Gly
			Trp	Gly	Gly
			Ala	Leu	Arg
	115		120		125

<210> 507  
 <211> 499  
 <212> DNA  
 <213> Homo sapiens

<400> 507  
 gccggcggtgt tcaacctcat ggtgtggggc ttcattaccg acgtcatcga tgcccaggag  
 60  
 gtcattgtccg gggagcgtga agacggtgtc atctatggcg tgaactcctt cgcccgcaaa  
 120  
 cttgcccagg ccattgcccgg tggaaatcggc ggagccatgc tgacgatgat cggctaccag  
 180  
 tcctcctccc aagggtggtgc cgttcagtcg gagtccgtcg tcaatcacct gtacacgtc  
 240  
 gccaccgcca tcccagcat ctgctgcctc ggcgctgccc tgctcatgct gggctaccgc  
 300  
 ctcacccgcg acaagggtgt cgccaacgcc gacgagttgg ctcgtcgcca cgagtacag  
 360  
 gccgagcaaa actcctgacc cataacggag gcacatcatg gacacgtca tgccgatcac  
 420  
 cgaccacttg acaacctcgc cgggtatcca attgaaaatt gacaagcgat ggggtgcctc  
 480  
 cgtcacattt gtgacgcgt  
 499

<210> 508  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 508  
 Ala Gly Val Phe Asn Leu Met Val Trp Ala Phe Ile Thr Asp Val Ile  
 1 5 10 15  
 Asp Ala Gln Glu Val Met Ser Gly Glu Arg Glu Asp Gly Val Ile Tyr  
 20 25 30  
 Gly Val Asn Ser Phe Ala Arg Lys Leu Ala Gln Ala Ile Ala Gly Gly  
 35 40 45  
 Ile Gly Gly Ala Met Leu Thr Met Ile Gly Tyr Gln Ser Ser Ser Gln  
 50 55 60  
 Gly Gly Ala Val Gln Ser Glu Ser Val Val Asn His Leu Tyr Thr Leu  
 65 70 75 80  
 Ala Thr Ala Ile Pro Thr Ile Cys Cys Leu Gly Ala Ala Leu Leu Met  
 85 90 95  
 Leu Gly Tyr Pro Leu Thr Arg Asp Lys Val Val Ala Asn Ala Asp Glu  
 100 105 110  
 Leu Ala Arg Arg His Ala Val Gln Ala Glu Gln Asn Ser  
 115 120 125

<210> 509  
 <211> 360

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 509

ttggccatgg atttggctcg caagtccagt cccaaagatg tcacgctcta tctaattggac  
 60  
 ttcgggacca atggtgtggc accactaggc caattaccac aggtggccga caccttgctt  
 120  
 ttggatcata cggagaagat tgccaagttt gtacgcata tggagcggga gctcaaccgg  
 180  
 cgtaagaagc tcttgtccga ctacggtgtt ggtacactag agctctaccg tcaggctagc  
 240  
 ggtagcaag agccggccat cgtcatcctg ctggacagtt atgagtccat gaaggaagag  
 300  
 gcctatgaag cggagctctt cacgctcttg gtgcggatct cccgggaagg tctcagcatc  
 360

&lt;210&gt; 510

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 510

Leu	Ala	Met	Asp	Leu	Ala	Arg	Lys	Phe	Ser	Pro	Lys	Asp	Val	Thr	Leu
1				5					10				15		
Tyr	Leu	Met	Asp	Phe	Gly	Thr	Asn	Gly	Val	Ala	Pro	Leu	Gly	Gln	Leu
			20					25				30			
Pro	Gln	Val	Ala	Asp	Thr	Leu	Leu	Leu	Asp	His	Thr	Glu	Lys	Ile	Ala
		35				40					45				
Lys	Phe	Val	Arg	Ile	Met	Glu	Arg	Glu	Leu	Asn	Arg	Arg	Lys	Lys	Leu
	50				55				60						
Leu	Ser	Asp	Tyr	Gly	Val	Gly	Thr	Leu	Glu	Leu	Tyr	Arg	Gln	Ala	Ser
65				70					75				80		
Gly	Gln	Gln	Glu	Pro	Ala	Ile	Val	Ile	Leu	Leu	Asp	Ser	Tyr	Glu	Ser
			85				90					95			
Met	Lys	Glu	Glu	Ala	Tyr	Glu	Ala	Glu	Leu	Phe	Thr	Leu	Leu	Val	Arg
		100					105					110			
Ile	Ser	Arg	Glu	Gly	Leu	Ser	Ile								
		115				120									

&lt;210&gt; 511

&lt;211&gt; 361

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 511

ntcgcgaacc gcggtctatgc ggtgctccag cccaatttcc gcggatcggg cggttatggc  
 60  
 actgcgttcg gcatgcccgg catcggccag atcgggcgca agatgcagga cgatctcgac  
 120  
 gacgggatgg actggctggt caaggagggc atcgtcgaca agggccgggt gtgcatcgtc  
 180  
 ggggcctcct atggcggcta tgccgcgatg tggggcgaga tccgcaatcc cgaacgctat  
 240



cgctgcgcgg cgagcctggc ggggggttgcc gattaaggcc atgctcaaat ataaccggcg  
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 361

<210> 512  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 512  
 Xaa Ala Asn Arg Gly Tyr Ala Val Leu Gln Pro Asn Phe Arg Gly Ser  
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 Gly Gly Tyr Gly Thr Ala Phe Gly Asp Ala Gly Ile Gly Gln Ile Gly  
 20 25 30  
 Arg Lys Met Gln Asp Asp Leu Asp Asp Gly Met Asp Trp Leu Val Lys  
 35 40 45  
 Glu Gly Ile Val Asp Lys Gly Arg Val Cys Ile Val Gly Ala Ser Tyr  
 50 55 60  
 Gly Gly Tyr Ala Ala Met Trp Gly Ala Ile Arg Asn Pro Glu Arg Tyr  
 65 70 75 80  
 Arg Cys Ala Ala Ser Leu Ala Gly Val Ala Asp  
 85 90

<210> 513  
 <211> 369  
 <212> DNA  
 <213> Homo sapiens

<400> 513  
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 120  
 aataactgtg gtgtagatgg ttttggttta ggggttttgc tagaagataa gcaagtacgc  
 180  
 aaaatggtgt cttcttatgt gggtgaaaat gcaactgttg agaagcaatt attacaaggt  
 240  
 gagttggaag tcgagctcac tctcaaggc actcttgccg aaaaactacg cgctggcggc  
 300  
 gcgggaattc ctgccttttt cacagcaacg ggtgtaggta cacctattgg tgagggtaaa  
 360  
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 369

<210> 514  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 514  
 Xaa Cys Arg Leu Glu Asp Gly Met Thr Val Leu Ala Gly Gly Phe Gly

```

      1           5           10           15
Leu Cys Gly Ile Pro Glu Asn Leu Ile Gln Glu Ile Lys Arg Arg Gln
      20           25           30
Thr Cys Asp Leu Thr Ile Val Ser Asn Asn Cys Gly Val Asp Gly Phe
      35           40           45
Gly Leu Gly Val Leu Leu Glu Asp Lys Gln Val Arg Lys Met Val Ser
      50           55           60
Ser Tyr Val Gly Glu Asn Ala Leu Phe Glu Lys Gln Leu Leu Gln Gly
      65           70           75           80
Glu Leu Glu Val Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Lys Leu
      85           90           95
Arg Ala Gly Gly Ala Gly Ile Pro Ala Phe Phe Thr Ala Thr Gly Val
      100           105           110
Gly Thr Pro Ile Gly Glu Gly Lys Asp Thr Arg
      115           120

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<210> 515  
 <211> 387  
 <212> DNA  
 <213> Homo sapiens

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<400> 515
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gcgatcatcg acgtgctcgt gcagcaggcg ctcgaggccg ggaagaccac cccgtactac
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387

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<210> 516  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

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<400> 516
Ala Trp Asp Glu Lys Ala Ala Gly Asn Cys Ala Ile Asp Tyr Gly Phe
1           5           10           15
His Gln Ile Leu Ser Asp Val Gln Asp Ser Ser Leu Thr Ala Met Asp
20           25           30
Glu Leu Ile Thr Glu Gly Val Thr Ser Phe Lys Leu Phe Val Ala Tyr
35           40           45
Lys Gly Val Phe Leu Ser Asp Asp Gly Gln Ile Leu Arg Ala Phe Gln
50           55           60
Lys Gly Ala Asp Asn Gly Ala Met Met Met Met His Ala Glu Asn Gly
65           70           75           80
Ala Ile Ile Asp Val Leu Val Gln Gln Ala Leu Glu Ala Gly Lys Thr

```

```

      85              90              95
Thr Pro Tyr Tyr His Gly Ile Ser Arg Pro Trp Gln Ala Glu Glu Glu
      100              105              110
Ala Thr His Arg Ala Ile Met Ile Ala Asp Leu Thr Gly Ala Pro Leu
      115              120              125
Tyr

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<210> 517  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

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<400> 517
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120
attcgcgagt tccgggggag ctggggactg agctgcgggc ctctggggct ggggctcttc
180
tccgaggttg gaggcagctt tagaaacttg agacccttag ctggagaggg cagaaggggt
240
ccctgagctt ccccaggaga aggggggcca atttgagct tgcttttcac ctgagatgag
300
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360
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377

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<210> 518  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

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<400> 518
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1          5          10          15
Pro His Ser Ser Ser Gln Val Lys Ser Lys Leu Gln Ile Gly Pro Pro
20        25        30
Ser Pro Gly Glu Ala Gln Gly Pro Leu Leu Pro Ser Pro Ala Arg Gly
35        40        45
Leu Lys Phe Leu Lys Leu Pro Pro Thr Ser Glu Lys Ser Pro Ser Pro
50        55        60
Gly Gly Pro Gln Leu Ser Pro Gln Leu Pro Arg Asn Ser Arg Ile Pro
65        70        75        80
Cys Arg Asn Ser Gly Ser Asp Gly Ser Pro Ser Pro Leu Leu Ala Arg
85        90        95
Arg Gly Leu Gly Gly Gly Glu Leu Ser Pro Glu Gly Ala Gln Gly Leu
100       105       110
Pro Thr Ser Pro Ser Arg
115

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<210> 519  
 <211> 311

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 519

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 agaattttaa ttattataaa ggaacctttt ctgcaactct gaaaaatgtt agaatatcca  
 120  
 aagaaattga taattttcta ggaaaacatg acttaccaaa attaactcta gaaaagaatc  
 180  
 gatacacatc agtaacaaca gaagttgaga aagtagttaa catattgcca aacctggaat  
 240  
 tcatgattga attcttttag atctactgtg agtacatact ctgcctctgt tcagctgttc  
 300  
 cagaacttaa g  
 311

&lt;210&gt; 520

&lt;211&gt; 92

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 520

Met	Arg	Gly	Lys	Tyr	Gln	Ile	Leu	Lys	Asn	Leu	Asn	Tyr	Tyr	Lys	Gly
1			5					10					15		
Thr	Phe	Ser	Ala	Thr	Leu	Lys	Asn	Val	Arg	Ile	Ser	Lys	Glu	Ile	Asp
			20				25					30			
Asn	Phe	Leu	Gly	Lys	His	Asp	Leu	Pro	Lys	Leu	Thr	Leu	Glu	Lys	Asn
		35				40				45					
Arg	Tyr	Thr	Ser	Val	Thr	Thr	Glu	Val	Glu	Lys	Val	Val	Asn	Ile	Leu
	50				55				60						
Pro	Asn	Leu	Glu	Phe	Met	Ile	Glu	Phe	Phe	Glu	Ile	Tyr	Cys	Glu	Tyr
65				70				75						80	
Ile	Leu	Cys	Leu	Cys	Ser	Ala	Val	Pro	Glu	Leu	Lys				
			85					90							

&lt;210&gt; 521

&lt;211&gt; 352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 521

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 60  
 attccagaag agatgcgcgc gcagctgcag ctgtccctgg tgcgtccca ccgcccggc  
 120  
 accggccctg aggtggaaga agaagtaatt cgcgcgctca tgctgctgcg cctatccacc  
 180  
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 240  
 aacgccggca tcgtgccggg ggtgcgcgaa tacgggtcgc tgggctgctc cggcgacttg  
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 352

<210> 522  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 522  
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 20 25 30  
 Leu Val Arg Ser His Ala Ala Gly Thr Gly Pro Glu Val Glu Glu  
 35 40 45  
 Val Ile Arg Ala Leu Met Leu Leu Arg Leu Ser Thr Leu Cys Thr Gly  
 50 55 60  
 Arg Thr Gly Val Arg Pro Val Val Val Glu Thr Tyr Ala Lys Ala Leu  
 65 70 75 80  
 Asn Ala Gly Ile Val Pro Gly Val Arg Glu Tyr Gly Ser Leu Gly Cys  
 85 90 95  
 Ser Gly Asp Leu Ala Pro Leu Ala His Cys Ala Leu Ala Leu Leu Gly  
 100 105 110  
 Glu Gly Glu Val Arg  
 115

<210> 523  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 523  
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 tcagagccac caagctgagg caccatctaa ggagaacatg tcccctggag gtccgtgttag  
 120  
 aagctcctgg ttgagaaggc cctgaagctg ggtggcatca atgtccagcc tctgctgagc  
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 240  
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 300  
 gaactccgct gattttctcc gtgtctgtgc aaccacaaca tagttcccag ggctcagatg  
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 gtaagtcacg gtgaagttgc ggcggaattt attatttgag ctttgacag tgtttctgaa  
 420  
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 600  
 agcatcattt ccgggtcttc ctggcgtgtt tcctagaatc attgcttcct aaacattatt  
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<210> 524  
 <211> 193  
 <212> PRT  
 <213> Homo sapiens

<400> 524  
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 20 25 30  
 Val Thr Val Ala Val Thr Pro Ser Asn Leu Lys Ala Glu Asp Ala Lys  
 35 40 45  
 Phe Pro Leu Asp Phe Gln Val Ile Leu Ala Gly Ser Gln Arg Phe Arg  
 50 55 60  
 Glu Lys Phe Pro Pro Val Phe Phe Ser Ser Phe Arg Asn Thr Val Gln  
 65 70 75 80  
 Ser Ser Asn Asn Lys Phe Arg Arg Asn Phe Thr Met Thr Tyr His Leu  
 85 90 95  
 Ser Pro Gly Asn Tyr Val Val Val Ala Gln Thr Arg Arg Lys Ser Ala  
 100 105 110  
 Glu Phe Leu Leu Arg Ile Phe Leu Lys Met Pro Asp Ser Asp Arg His  
 115 120 125  
 Leu Ser Ser His Phe Asn Leu Arg Met Lys Gly Ser Pro Ser Glu His  
 130 135 140  
 Gly Ser Gln Gln Ser Ile Phe Asn Arg Tyr Ala Gln Gln Arg Leu Asp  
 145 150 155 160  
 Ile Asp Ala Thr Gln Leu Gln Gly Leu Leu Asn Gln Glu Leu Leu Thr  
 165 170 175  
 Gly Pro Pro Gly Asp Met Phe Ser Leu Asp Gly Ala Ala Ala Trp Trp  
 180 185 190  
 Leu

<210> 525  
 <211> 1101  
 <212> DNA  
 <213> Homo sapiens

<400> 525  
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 180  
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 240  
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 300  
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 420

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 1080  
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&lt;210&gt; 526

&lt;211&gt; 290

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 526

Met	Ala	Arg	Phe	Pro	Lys	Ala	Asp	Leu	Ala	Ala	Ala	Gly	Val	Met	Leu
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Leu	Cys	His	Phe	Phe	Thr	Asp	Gln	Phe	Gln	Phe	Ala	Asp	Gly	Lys	Pro
			20				25						30		
Gly	Asp	Gln	Ile	Leu	Asp	Trp	Gln	Tyr	Gly	Val	Thr	Gln	Ala	Phe	Pro
		35					40					45			
His	Thr	Glu	Glu	Glu	Val	Glu	Val	Asp	Ser	His	Ala	Tyr	Ser	His	Arg
		50				55					60				
Trp	Lys	Arg	Asn	Leu	Asp	Phe	Leu	Lys	Ala	Val	Asp	Thr	Asn	Arg	Ala
65				70					75					80	
Ser	Val	Gly	Gln	Asp	Ser	Leu	Glu	Pro	Arg	Ser	Phe	Thr	Asp	Leu	Leu
			85					90						95	
Leu	Asp	Asp	Gly	Gln	Asp	Asn	Asn	Thr	Gln	Ile	Glu	Glu	Asp	Thr	Asp
			100					105						110	
His	Asn	Tyr	Tyr	Ile	Ser	Arg	Ile	Tyr	Gly	Pro	Ser	Asp	Ser	Ala	Ser
		115				120						125			
Arg	Asp	Leu	Trp	Val	Asn	Ile	Asp	Gln	Met	Glu	Lys	Asp	Lys	Val	Lys
		130				135						140			
Ile	His	Gly	Ile	Leu	Ser	Asn	Thr	His	Arg	Gln	Ala	Ala	Arg	Val	Asn
145				150						155				160	
Leu	Ser	Phe	Asp	Phe	Pro	Phe	Tyr	Gly	His	Phe	Leu	Arg	Glu	Ile	Thr
				165				170						175	
Val	Ala	Thr	Gly	Gly	Phe	Ile	Tyr	Thr	Gly	Glu	Val	Val	His	Arg	Met

	180		185		190
Leu Thr Ala Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro					
195		200		205	
Ser Val Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala					
210		215		220	
Leu Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu					
225		230		235	240
Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile					
	245		250		255
Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr					
	260		265		270
Asn His Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His					
275		280		285	
Arg Ile					
290					

&lt;210&gt; 527

&lt;211&gt; 5343

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 527

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120
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960

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&lt;210&gt; 528

&lt;211&gt; 886

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 528

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Leu	Glu	Ala	Cys	Asp	Glu	Ser	Pro	Ala	Ser	Arg	Glu	Leu	Asp	Ile
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														Phe

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Cys 225	Ala	Arg	Thr	Asp 230	Cys	Pro	Pro	His	Leu 235	Ala	Val	Gly	Asp	Trp	Ser	
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Pro 465	Phe	Leu	Arg	Ala 470	Leu	Leu	Gly	His	Cys 475	Ser	Asn	Ser	Ala	Gly	Ser	
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&lt;210&gt; 529

&lt;211&gt; 4566

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 529

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&lt;210&gt; 530

&lt;211&gt; 802

&lt;212&gt; PRT



&lt;213&gt; Homo sapiens

&lt;400&gt; 530

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Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser Asp Pro Asp Gly Gly
65           70           75           80
Pro Arg Asp Arg Asn Phe Leu Phe Val Gly Val Met Thr Ala Gln Lys
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Tyr Leu Gln Thr Arg Ala Val Ala Ala Tyr Arg Thr Trp Ser Lys Thr
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Ile Pro Gly Lys Val Gln Phe Phe Ser Ser Glu Gly Ser Asp Thr Ser
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      130          135          140
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Leu Asp Lys Tyr Glu Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile
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Pro Leu Phe Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly
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Lys Leu Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly
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Val Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
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Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala Ile Thr Leu His
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305          310          315          320
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Glu Ile Val Leu Met Ser Lys Tyr Ser Asn Thr Glu Ile His Lys Glu
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Gln Arg Glu Ala Leu Asp Asp Ile Val Met Gln Val Met Glu Met Ile

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Ser	Leu	Leu	Phe	Phe	Cys	Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe														
				625					630					635					640										
Leu	Gln	Arg	Cys	Arg	Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe														
				645					650					655															
Pro	Ile	Ile	Phe	Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys														
				660					665					670															
Val	Pro	Ser	Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp														
				675					680					685															
Arg	Asn	Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val														
				690					695					700															
Arg	Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	G																			

<210> 531

<211> 321

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 531

ngatgatgaa tccccccgca gcctcgtcaa tatggggggc ttcctacccc agcaaaaggg  
 60  
 acggcaatac gtctcgaaca aaggtctttt gtttcgaaat aacaaggggt tagagctaag  
 120  
 aggaagaagc gtgaaacgct gtaggaccag cgtttcgaac gcccccgagg tgaaccctcg  
 180  
 ggggcgtctg aatcaggcca gttgggcctg ggacgacagc ggttgacgag gcagcaatgg  
 240  
 cgcgtgcgga tcagccttga tcgattcacg ccaggcgccg agccactcgg cgtggccttc  
 300  
 gttccacacc tgctgggtgca g  
 321

&lt;210&gt; 532

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 532

Met	Gly	Gly	Phe	Leu	Pro	Gln	Gln	Lys	Ala	Arg	Gln	Tyr	Val	Ser	Asn
1				5				10					15		
Lys	Gly	Leu	Leu	Phe	Arg	Asn	Asn	Lys	Gly	Leu	Glu	Leu	Arg	Gly	Arg
		20				25				30					
Ser	Val	Lys	Arg	Cys	Arg	Thr	Ser	Val	Ser	Asn	Ala	Pro	Glu	Val	Asn
		35				40				45					
Pro	Arg	Gly	Arg	Leu	Asn	Gln	Ala	Ser	Trp	Ala	Trp	Asp	Asp	Ser	Gly
	50				55				60						
Cys	Ser	Gly	Ser	Asn	Gly	Ala	Cys	Gly	Ser	Ala	Leu	Ile	Asp	Ser	Arg
65				70				75					80		
Gln	Ala	Pro	Ser	His	Ser	Ala	Trp	Pro	Ser	Phe	His	Thr	Cys	Trp	Cys
			85					90					95		

&lt;210&gt; 533

&lt;211&gt; 335

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 533

nagtttccgg tgaaccgctc cgcaatgcct cgtgacatcg acttcagcga agccaacagg  
 60  
 agcatcatcg acaacatggc aactgcctca atcccgcctt tccgaaccca caaaaactgg  
 120  
 gagacgtggt cgagtcaggt ccggcatttc attagccttt tacacccaaa agtcaccctc  
 180  
 accaacattg acaacgtcct caacaaagat cacctgcgtt ggctacactt tcttttggag  
 240  
 ggtcgcctgg agccaaacgt gcgcctgatt gtccagggct actgttcgcc tggcaagctg  
 300  
 taccgcaagc ttgaggagct atatgcccct tctg  
 335

<210> 534  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 534  
 Met Pro Arg Asp Ile Asp Phe Ser Glu Ala Asn Arg Ser Ile Ile Asp  
 1 5 10 15  
 Asn Met Ala Thr Ala Ser Ile Pro Leu Phe Arg Thr His Lys Asn Trp  
 20 25 30  
 Glu Thr Trp Ser Ser Gln Val Arg His Phe Ile Ser Leu Leu His Pro  
 35 40 45  
 Lys Val Thr Leu Thr Asn Ile Asp Asn Val Leu Asn Lys Asp His Leu  
 50 55 60  
 Arg Trp Leu His Phe Leu Leu Glu Gly Arg Leu Glu Pro Asn Val Arg  
 65 70 75 80  
 Leu Ile Val Gln Gly Tyr Cys Ser Pro Gly Lys Leu Tyr Arg Lys Leu  
 85 90 95  
 Glu Glu Leu Tyr Ala Pro Ser  
 100

<210> 535  
 <211> 402  
 <212> DNA  
 <213> Homo sapiens

<400> 535  
 acgcgtctct acagccggac taagcacagg ctcagccccg gtcgccatgc gcccaggctc  
 60  
 ggttatcagc cgaggaatcc acggcgaaat gaccagtagc ggccctaata caactatgct  
 120  
 gccgagcagc agacgtcgag gtcgggtcat gaggatgccg acggccaccg cgaccgggta  
 180  
 taccacaat gcaggaacaa ggctgatagc tagggctgac cacagagcca ggccgctgctg  
 240  
 cgaggaaacg cccccacct ggtgactgcc agtatcagca ccgcgcagct caacgacgtc  
 300  
 aacagtctcg ggattgacca accgccacgt atgcagggcc atgtggggga gaatcacccc  
 360  
 caacgccaat gctgtcaccc agcctcgggc taggcgccgc gc  
 402

<210> 536  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 536  
 Met Ala Leu His Thr Trp Arg Leu Val Asn Pro Glu Thr Val Asp Val  
 1 5 10 15  
 Val Glu Leu Arg Gly Ala Asp Thr Gly Ser His Gln Val Gly Gly Val  
 20 25 30  
 Ser Ser Ala Gly Gly Leu Ala Leu Trp Ser Ala Leu Ala Ile Ser Leu

```

      35              40              45
Val Pro Ala Leu Trp Val Tyr Pro Val Ala Val Ala Val Gly Ile Leu
      50              55              60
Met Thr Arg Pro Arg Arg Leu Leu Leu Gly Ser Ile Val Val Leu Gly
65              70              75              80
Pro Leu Leu Val Ile Ser Pro Trp Ile Pro Arg Leu Ile Thr Glu Pro
      85              90              95
Gly Arg Met Ala Thr Gly Ala Glu Pro Val Leu Ser Pro Ala Val Glu
      100              105              110
Thr Arg

```

<210> 537  
 <211> 404  
 <212> DNA  
 <213> Homo sapiens

```

<400> 537
gtgcacatcg gcggcaccga cttcgacaaa caactctcgc tggctggcat gatgccgctg
60
ttcggctacg gcagccgcat gaagagcggc gcctacatgc ccaccagcca ccacatgaac
120
ctggcgacct ggcacacccat caactcgggtg tactcgcaaa aatcccagct ggccctgggc
180
agcatgcgct acgacatcga agacaccggc ggcacgcgacc gcctgttcaa gctgatcgaa
240
cagcgtgctg ggcactggct tgccatggaa gtggaagaaa ccaagatcca gctcacccat
300
caagacagcc gccacgtgcc gctggaccgc atcgaagcgg gcctgagcgt agacctgagc
360
cggggcgctgt tcgaatcgtc catcgacaac ctgctcgaac gcgt
404

```

<210> 538  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

```

<400> 538
Met Met Pro Leu Phe Gly Tyr Gly Ser Arg Met Lys Ser Gly Ala Tyr
1              5              10              15
Met Pro Thr Ser His His Met Asn Leu Ala Thr Trp His Thr Ile Asn
      20              25              30
Ser Val Tyr Ser Gln Lys Ser Gln Leu Ala Leu Gly Ser Met Arg Tyr
      35              40              45
Asp Ile Glu Asp Thr Gly Gly Ile Asp Arg Leu Phe Lys Leu Ile Glu
      50              55              60
Gln Arg Ala Gly His Trp Leu Ala Met Glu Val Glu Glu Thr Lys Ile
65              70              75              80
Gln Leu Thr His Gln Asp Ser Arg His Val Pro Leu Asp Arg Ile Glu
      85              90              95
Ala Gly Leu Ser Val Asp Leu Ser Arg Ala Leu Phe Glu Ser Ser Ile
      100              105              110
Asp Asn Leu Leu Glu Arg

```

115

<210> 539  
 <211> 534  
 <212> DNA  
 <213> Homo sapiens

<400> 539  
 nnacgcgtga aaaagaagaa aatgaaggaa agcgaggctg acagcgaggt gaagcatcaa  
 60  
 ccaattttca taaaagaaag attgaagctt tttgaaatac tgaagaaaga ccatcagctc  
 120  
 ttacttgcca tttatggaaa aaagggggat acaagcaaca tcatcacagt aagagtggct  
 180  
 gatgggcaaa cagtgcgaagg ggaagtcttg aaaacaacgc cttaccaagt ggctgctgaa  
 240  
 attagtcagg aactggctga aagcacggta atagccaaag tcaatgggtga actgtgggac  
 300  
 ctggaccgcc cattggaagg ggactcttct ctagagctgc ttacatttga taatgaggaa  
 360  
 gctcaagctg tgagtatttt aaaaccagac agccaaactt tgggtagtta tgttgtaaac  
 420  
 tacattatat aagaggccac atattgaatt cacgaatgtt gagttttttg ggggtttcta  
 480  
 agatttaaaa tttgattatt gatgtttaat aaatatttgc ctcatgaatg ttaa  
 534

<210> 540  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 540  
 Xaa Arg Val Lys Lys Lys Lys Met Lys Glu Ser Glu Ala Asp Ser Glu  
 1 5 10 15  
 Val Lys His Gln Pro Ile Phe Ile Lys Glu Arg Leu Lys Leu Phe Glu  
 20 25 30  
 Ile Leu Lys Lys Asp His Gln Leu Leu Leu Ala Ile Tyr Gly Lys Lys  
 35 40 45  
 Gly Asp Thr Ser Asn Ile Ile Thr Val Arg Val Ala Asp Gly Gln Thr  
 50 55 60  
 Val Gln Gly Glu Val Trp Lys Thr Thr Pro Tyr Gln Val Ala Ala Glu  
 65 70 75 80  
 Ile Ser Gln Glu Leu Ala Glu Ser Thr Val Ile Ala Lys Val Asn Gly  
 85 90 95  
 Glu Leu Trp Asp Leu Asp Arg Pro Leu Glu Gly Asp Ser Ser Leu Glu  
 100 105 110  
 Leu Leu Thr Phe Asp Asn Glu Glu Ala Gln Ala Val Ser Ile Leu Lys  
 115 120 125  
 Pro Asp Ser Gln Thr Leu Gly Ser Tyr Val Val Asn Tyr Ile Ile  
 130 135 140

<210> 541  
 <211> 551

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 541

ggtaccgagc tgcgcgtgtg gtatgcggcc ttctatgccca agaagatgga caagcccatg  
 60  
 ctgaagcagg ccggctctgg cgtccacgct gcaggcaccc cagaaaacag cgccccctg  
 120  
 gagtcggagc ccagccagtg ggcgtgtaaa gtgtgttctg ccaccttctt ggagctgcag  
 180  
 ctctcaatg gtaaggagga cgtgtgggga gcccagttg taaaactcct gtgtcgattt  
 240  
 ctctctgact tacgctgtca cctgtctgcg gctgtcgggg gtgtcccaga ctttgcctg  
 300  
 tctgccccat tgccccacaa tgtagtcgcc agaaccaagg ctttctcagg gtttaaagct  
 360  
 tctgggcagt cccgcttccc acccccgacc cctgcaggcc tcaactctca ctctcctgg  
 420  
 ttgggaagtt gcatttcagc tgggcgcctt gactctggag cactggcagg ggccaggggc  
 480  
 caggagccag ccgtggcatg tggtgtgcac tcttgccctt gttgtctcta cttgacagcc  
 540  
 ccctcacgcg t  
 551

&lt;210&gt; 542

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 542

Met Asp Lys Pro Met Leu Lys Gln Ala Gly Ser Gly Val His Ala Ala  
 1 5 10 15  
 Gly Thr Pro Glu Asn Ser Ala Pro Val Glu Ser Glu Pro Ser Gln Trp  
 20 25 30  
 Ala Cys Lys Val Cys Ser Ala Thr Phe Leu Glu Leu Gln Leu Leu Asn  
 35 40 45  
 Gly Lys Glu Asp Val Trp Gly Ala Pro Val Val Lys Leu Leu Cys Arg  
 50 55 60  
 Phe Leu Ser Asp Leu Arg Cys His Leu Ser Ala Ala Val Gly Gly Val  
 65 70 75 80  
 Pro Asp Phe Val Leu Ser Ala Pro Leu Pro His Asn Val Val Ala Arg  
 85 90 95  
 Thr Lys Ala Phe Ser Gly Phe Lys Ala Ser Gly Gln Ser Arg Phe Pro  
 100 105 110  
 Pro Pro Thr Pro Ala Gly Leu Thr Pro His Ser Ser Trp Leu Gly Ser  
 115 120 125  
 Cys Ile Ser Ala Gly Arg Leu Asp Ser Gly Ala Leu Ala Gly Ala Arg  
 130 135 140  
 Gly Gln Glu Pro Ala Val Ala Cys Val Val His Ser Cys Leu Cys Cys  
 145 150 155 160  
 Leu Tyr Leu Thr Ala Pro Ser Arg  
 165

<210> 543  
 <211> 349  
 <212> DNA  
 <213> Homo sapiens

<400> 543  
 nnaaagccgg acatgaatac ccgcattgct ggcaaaactg tcctgacat cattctggcc  
 60  
 ggggggcaaag gcagccgcct ggccccgatg accgatcagg tggccaaacc agccgtgccc  
 120  
 tttatgggga cgtaccgcct gattgacttt tcgctgtcca acattgtcca cagcggcttg  
 180  
 caggacgtct ggatcattga gcaaaacctg ccccatagct taaacgagca cctggctggg  
 240  
 gggcgctcct gggatctgga ccgcaccgcg ggtggcctga aggtcatgcc gcccttttcc  
 300  
 ggccctgccc atgaggacgg tggcttttcc gaaggcaacg cacacgcgt  
 349

<210> 544  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 544  
 Xaa Lys Pro Asp Met Asn Thr Arg Ile Ala Gly Lys Thr Val Leu Thr  
 1 5 10 15  
 Ile Ile Leu Ala Gly Gly Lys Gly Ser Arg Leu Ala Pro Met Thr Asp  
 20 25 30  
 Gln Val Ala Lys Pro Ala Val Pro Phe Met Gly Thr Tyr Arg Leu Ile  
 35 40 45  
 Asp Phe Ser Leu Ser Asn Ile Val His Ser Gly Leu Gln Asp Val Trp  
 50 55 60  
 Ile Ile Glu Gln Asn Leu Pro His Ser Leu Asn Glu His Leu Ala Gly  
 65 70 75 80  
 Gly Arg Ser Trp Asp Leu Asp Arg Thr Arg Gly Gly Leu Lys Val Met  
 85 90 95  
 Pro Pro Phe Ser Gly Pro Ala Asp Glu Asp Gly Gly Phe Ser Glu Gly  
 100 105 110  
 Asn Ala His Ala  
 115

<210> 545  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<400> 545  
 catgatgcaa aaacagacat gcttatttca aaatataaaa gtgaaaaaga tcgttttagca  
 60  
 caagaaattg ttggtgtcat cacagggttct gcaatgccgg gtggttcagc aaaccgtatc  
 120  
 ccaaataaag caggctcaaa tccagaaggt tctattgcaa cgcgttttat tgcagaaaca  
 180



atgtataacg aactcaaaac agtggattta actattcaaa atgctggcgg tgtacgcgca  
 240  
 gatattttac cggggaatgt aacctttaac gatgcttata ctttcttacc tttcgggaat  
 300  
 acgttatata cctataaaat ggaaagtcca ttagtgaaac aagtgcttga agatgcaatg  
 360  
 ctatttgctt tgggtcccc ccccccccc

<210> 546  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 546  
 His Asp Ala Lys Thr Asp Met Leu Ile Ser Lys Tyr Lys Ser Glu Lys  
 1 5 10 15  
 Asp Arg Leu Ala Gln Glu Ile Val Gly Val Ile Thr Gly Ser Ala Met  
 20 25 30  
 Pro Gly Gly Ser Ala Asn Arg Ile Pro Asn Lys Ala Gly Ser Asn Pro  
 35 40 45  
 Glu Gly Ser Ile Ala Thr Arg Phe Ile Ala Glu Thr Met Tyr Asn Glu  
 50 55 60  
 Leu Lys Thr Val Asp Leu Thr Ile Gln Asn Ala Gly Gly Val Arg Ala  
 65 70 75 80  
 Asp Ile Leu Pro Gly Asn Val Thr Phe Asn Asp Ala Tyr Thr Phe Leu  
 85 90 95  
 Pro Phe Gly Asn Thr Leu Tyr Thr Tyr Lys Met Glu Ser Ser Leu Val  
 100 105 110  
 Lys Gln Val Leu Glu Asp Ala Met Leu Phe Ala Leu Gly Pro Pro Pro  
 115 120 125  
 Pro Pro  
 130

<210> 547  
 <211> 306  
 <212> DNA  
 <213> Homo sapiens

<400> 547  
 aagcttggtt ttctgatttt tattcaaate tctatcatgg atgaagcatg cagtttcaga  
 60  
 atcagttcag tgttgacaac atatcaagat attctgcagt caatctcaat gtatgttcat  
 120  
 gaagcctcca acatattttg tgggatacca tctttgtcag gcattgtgct aggcactgtc  
 180  
 cctgcagtga ataagaaaga caggatttct gtatttatgg ggcttagtac caagttgttc  
 240  
 tcaaactttc atgttttgtt atacaaatca gctgaggcct tcactaaact cnnnnncenn  
 300  
 nncenn  
 306

<210> 548

<211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 548  
 Met Asp Glu Ala Cys Ser Phe Arg Ile Ser Ser Val Leu Thr Thr Tyr  
 1 5 10 15  
 Gln Asp Ile Leu Gln Ser Ile Ser Met Tyr Val His Glu Ala Ser Asn  
 20 25 30  
 Ile Phe Cys Gly Ile Pro Ser Leu Ser Gly Ile Val Leu Gly Thr Val  
 35 40 45  
 Pro Ala Val Asn Lys Lys Asp Arg Ile Ser Val Phe Met Gly Leu Ser  
 50 55 60  
 Thr Lys Leu Phe Ser Asn Phe His Val Cys Val Tyr Lys Ser Ala Glu  
 65 70 75 80  
 Ala Phe Thr Lys Leu Xaa Xaa Xaa Xaa Xaa  
 85 90

<210> 549  
 <211> 780  
 <212> DNA  
 <213> Homo sapiens

<400> 549  
 nnacgcgtac ttccaacacc tatgctccag tatggaggac gggtaaagtc tcttgtaaat  
 60  
 gttttaatca tacacatatt gtctgtaagt atgaagagaa aggcataatca gaaatatttc  
 120  
 aattcagcga tttgaaatgt ttactttctg tttattgaaa atttttgttc tttttcacca  
 180  
 tgttattttt ttctcctcgt gtagaatcgg acagtagcaa caccgagcca tggagtatgg  
 240  
 gacatgcgag ggaaacaatt ccacacagga gttgaaatca aaatgtgggc tatcgcttgt  
 300  
 tttgccacac agaggcagtg cagagaagaa atattgaagg gtttcacaga ccagctgcgt  
 360  
 aagatttcta aggatgcagg gatgcccatc cagggccagc catgcttctg caaatatgca  
 420  
 cagggggcag acagcgtaga gcccatgttc cggcatctca agaacacata ttctggccta  
 480  
 cagcttatta tcgtcatcct gccggggaag acaccagtgt atgcggaagt gaaacgtgta  
 540  
 ggagacacac ttttgggtat ggctacacaa tgtgttcaag tcaagaatgt aataaaaaca  
 600  
 tctctcaaaa ctctgtcaaa cttgtgccta aagataaatg ttaaactcgg agggatcaat  
 660  
 aatattcttg tacctcatca aagaccttct gtgttccagc aaccagtgat ctttttggga  
 720  
 gccgatgtca ctcatccacc tgctggtgat ggaaagaagc cttctattgc tgctgttgta  
 780

<210> 550  
 <211> 192  
 <212> PRT

<213> Homo sapiens

<400> 550

```

Asn Arg Thr Val Ala Thr Pro Ser His Gly Val Trp Asp Met Arg Gly
 1             5             10             15
Lys Gln Phe His Thr Gly Val Glu Ile Lys Met Trp Ala Ile Ala Cys
          20             25             30
Phe Ala Thr Gln Arg Gln Cys Arg Glu Glu Ile Leu Lys Gly Phe Thr
          35             40             45
Asp Gln Leu Arg Lys Ile Ser Lys Asp Ala Gly Met Pro Ile Gln Gly
          50             55             60
Gln Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro
65             70             75             80
Met Phe Arg His Leu Lys Asn Thr Tyr Ser Gly Leu Gln Leu Ile Ile
          85             90             95
Val Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val
          100            105            110
Gly Asp Thr Leu Leu Gly Met Ala Thr Gln Cys Val Gln Val Lys Asn
          115            120            125
Val Ile Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Ile
          130            135            140
Asn Val Lys Leu Gly Gly Ile Asn Asn Ile Leu Val Pro His Gln Arg
145            150            155            160
Pro Ser Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala Asp Val Thr
          165            170            175
His Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Ala Ala Val Val
          180            185            190

```

<210> 551

<211> 291

<212> DNA

<213> Homo sapiens

<400> 551

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nnggatccgg attatggggc tattgctaac aggtcaacgg ccatcaaggt gtcggttgcc
60
gtggcaccgc cagccccgga gcctactcgc gagccaccga cgaactccgc tccttccgag
120
gaaccgtcct cgtcgtcaat cgcaccgggtc ccgcccggccc cgacgactgc agtaccacg
180
actagttcgt cgtcggggccg ctgaccgatg cgcccatcgg cggggtcatc tggtgggcg
240
tagcggggggc ttcgatgtcc ccataccaca gcgtccgcta aattgccnc c
291

```

<210> 552

<211> 67

<212> PRT

<213> Homo sapiens

<400> 552

```

Xaa Asp Pro Asp Tyr Gly Ala Ile Ala Asn Arg Ser Thr Ala Ile Lys
 1             5             10             15
Val Leu Val Ala Val Ala Pro Pro Ala Pro Glu Pro Thr Arg Glu Pro

```

```

          20          25          30
Pro Thr Asn Ser Ala Pro Ser Glu Glu Pro Ser Ser Ser Ser Ile Ala
          35          40          45
Pro Val Pro Pro Ala Pro Thr Thr Ala Val Pro Thr Thr Ser Ser Ser
          50          55          60
Ser Gly Arg
65

```

<210> 553  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

```

<400> 553
ctagccgatg taggattagt aggttttccg agcgtgggta aatctacctt actctcaata
60
gtatctaaaag ccaaaccgaa aattggtgca tatcatttca ctacaattaa acctaactta
120
ggtgtgtgtt ccacaaaaga tcaacgtagt tttgttatgg cagatttacc aggtttaatt
180
gaaggtgcat ctgatggcgt tggattagga catcaatttt taagacatgt agagagaaca
240
aaagttattg ttcacatgat tgatatgagc ggttctgaag gtagagaacc tattgaagat
300
tataaagtca ttaatcaaga attagctgcg tacgagcaac gtttagaaga tagacctcaa
360
atcgtagtag ctaacaagat ggattttacct gaatcacaag ataatttaaa cttgtttaaa
420
gaagaaattg gcgaagatgt gccagttatt ccagtttcaa caataacgcg t
471

```

<210> 554  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

```

<400> 554
Leu Ala Asp Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr
1      5      10      15
Leu Leu Ser Ile Val Ser Lys Ala Lys Pro Lys Ile Gly Ala Tyr His
20     25     30
Phe Thr Thr Ile Lys Pro Asn Leu Gly Val Val Ser Thr Lys Asp Gln
35     40     45
Arg Ser Phe Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala Ser
50     55     60
Asp Gly Val Gly Leu Gly His Gln Phe Leu Arg His Val Glu Arg Thr
65     70     75     80
Lys Val Ile Val His Met Ile Asp Met Ser Gly Ser Glu Gly Arg Glu
85     90     95
Pro Ile Glu Asp Tyr Lys Val Ile Asn Gln Glu Leu Ala Ala Tyr Glu
100    105    110
Gln Arg Leu Glu Asp Arg Pro Gln Ile Val Val Ala Asn Lys Met Asp
115    120    125
Leu Pro Glu Ser Gln Asp Asn Leu Asn Leu Phe Lys Glu Glu Ile Gly

```

130 135 140  
 Glu Asp Val Pro Val Ile Pro Val Ser Thr Ile Thr Arg  
 145 150 155

<210> 555  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 555  
 tctagagatt gagaacaatt atggatacag aaatggttga ttccgtcaaa tatattcgag  
 60  
 attcggaaatc atgtgaggct cgcgtgctgg agatcttagc cagaaggccg tccatgatgg  
 120  
 tgcagatctt gcggtggcgac ggcttaatta acgaagacca gagattagtc agattatggc  
 180  
 ttaataaagt acctagaatt gttcgctgc ttctcgggt tagtgtgttc gtcgctgcgg  
 240  
 caataggtgc ccgtgcggta tgggcggcgg cttccggtaa tcccgatctt gttcacgcgt  
 300

<210> 556  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 556  
 Met Asp Thr Glu Met Val Asp Ser Val Lys Tyr Ile Arg Asp Ser Glu  
 1 5 10 15  
 Ser Cys Glu Ala Arg Val Leu Glu Ile Leu Ala Arg Arg Pro Ser Met  
 20 25 30  
 Met Val Gln Ile Leu Arg Gly Asp Gly Leu Ile Asn Glu Asp Gln Arg  
 35 40 45  
 Leu Val Arg Leu Trp Leu Asn Lys Val Pro Arg Ile Val Arg Leu Leu  
 50 55 60  
 Leu Arg Leu Ser Val Phe Val Ala Ala Ala Ile Gly Ala Arg Ala Val  
 65 70 75 80  
 Trp Ala Ala Ala Ser Gly Asn Pro Asp Leu Val His Ala  
 85 90

<210> 557  
 <211> 678  
 <212> DNA  
 <213> Homo sapiens

<400> 557  
 atcttcccgg tttatgagga gaatgcgctg cgtgtcgagt ttttcggcga cgaaattgag  
 60  
 gccctcacga cgatgcaccc gctcaccggg gaggtcatca gcgaggacga gcaggtctac  
 120  
 gtgttcccgg ctaccacta tgctgccggc ccggaacgta tggagcgggc catagcgtcc  
 180  
 atccagcagg agctcgagga ggcctggcc gttctagagc gtgatgggaa actgttgagg  
 240

gcccaacggt tacgtatgcg tactacctac gatatcgaga tgatgcagca ggctcgggtgcc  
 300  
 tgtgctggca tcgaaaacta ttcgcggcac atcgacggac gcgctcccgg ctacagccccg  
 360  
 aactgtctgc ttgactactt tccggaagat tttgtgctcg tcattgatga atccccacgtg  
 420  
 accgtcccgc agattggcgg gatgtatgag ggggacatga gccgcaagcg gacattggta  
 480  
 gaacatgggt tccgactgcc cagcgcgatg gacaaccgtc ctctcaaatt cgacgagttc  
 540  
 acccagcggg tcggccagac tgtctacctg tccgccacgc ccggttcgta cgagaccgaa  
 600  
 cgagctcacg gcgtcgtcga acaaatcatt cgtccgacag gtctggtgga tccggagatt  
 660  
 atcgtcaagc ctacgcgt  
 678

<210> 558

<211> 226

<212> PRT

<213> Homo sapiens

<400> 558

Ile	Phe	Pro	Val	Tyr	Glu	Glu	Asn	Ala	Leu	Arg	Val	Glu	Phe	Phe	Gly
1					5				10					15	
Asp	Glu	Ile	Glu	Ala	Leu	Thr	Thr	Met	His	Pro	Leu	Thr	Gly	Glu	Val
			20					25					30		
Ile	Ser	Glu	Asp	Glu	Gln	Val	Tyr	Val	Phe	Pro	Ala	Thr	His	Tyr	Val
		35					40					45			
Ala	Gly	Pro	Glu	Arg	Met	Glu	Arg	Ala	Ile	Ala	Ser	Ile	Gln	Gln	Glu
		50				55					60				
Leu	Glu	Glu	Arg	Leu	Ala	Val	Leu	Glu	Arg	Asp	Gly	Lys	Leu	Leu	Glu
65					70					75				80	
Ala	Gln	Arg	Leu	Arg	Met	Arg	Thr	Thr	Tyr	Asp	Ile	Glu	Met	Met	Gln
				85					90					95	
Gln	Val	Gly	Ala	Cys	Ala	Gly	Ile	Glu	Asn	Tyr	Ser	Arg	His	Ile	Asp
			100					105					110		
Gly	Arg	Ala	Pro	Gly	Ser	Ala	Pro	Asn	Cys	Leu	Leu	Asp	Tyr	Phe	Pro
		115					120					125			
Glu	Asp	Phe	Val	Leu	Val	Ile	Asp	Glu	Ser	His	Val	Thr	Val	Pro	Gln
						135						140			
Ile	Gly	Gly	Met	Tyr	Glu	Gly	Asp	Met	Ser	Arg	Lys	Arg	Thr	Leu	Val
145					150					155					160
Glu	His	Gly	Phe	Arg	Leu	Pro	Ser	Ala	Met	Asp	Asn	Arg	Pro	Leu	Lys
				165					170					175	
Phe	Asp	Glu	Phe	Thr	Gln	Arg	Ile	Gly	Gln	Thr	Val	Tyr	Leu	Ser	Ala
				180				185					190		
Thr	Pro	Gly	Ser	Tyr	Glu	Thr	Glu	Arg	Ala	His	Gly	Val	Val	Glu	Gln
		195					200					205			
Ile	Ile	Arg	Pro	Thr	Gly	Leu	Val	Asp	Pro	Glu	Ile	Ile	Val	Lys	Pro
		210				215						220			
Thr	Arg														
225															

<210> 559  
 <211> 335  
 <212> DNA  
 <213> Homo sapiens

<400> 559  
 ggatcctatg gagctcaagt tcaagaaaag aaactgtaaa catggagggt ttgtgataaa  
 60  
 tggaatgcag tcagagggaa ggaactgccn gcttaaagtg tcctatgctg cgctttccag  
 120  
 agcaatacag tacacagtgg agggcgctac catggagtct ctgggtgaaa gttaggatgg  
 180  
 tatggtggca ccagccaaac ttctcagggt tcataggcag acagcagctc tggagtggaa  
 240  
 ctaaagtgtg tccaggagct gaagccctta atcagctagg gtcacacag agtcaaggta  
 300  
 gggtcaaaaa cattcagtct gggaccatat ctaga  
 335

<210> 560  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 560  
 Met Glu Cys Ser Gln Arg Glu Gly Thr Ala Xaa Leu Lys Cys Pro Met  
 1 5 10 15  
 Leu Arg Phe Pro Glu Gln Tyr Ser Thr Gln Trp Arg Ala Leu Pro Trp  
 20 25 30  
 Ser Leu Trp Val Lys Val Arg Met Val Trp Trp His Gln Pro Asn Phe  
 35 40 45  
 Ser Gly Phe Ile Gly Arg Gln Gln Leu Trp Ser Gly Thr Lys Val Tyr  
 50 55 60  
 Pro Gly Ala Glu Ala Leu Asn Gln Leu Gly Leu Thr Gln Ser Gln Gly  
 65 70 75 80  
 Arg Val Lys Asn Ile Gln Ser Gly Thr Ile Ser Arg  
 85 90

<210> 561  
 <211> 477  
 <212> DNA  
 <213> Homo sapiens

<400> 561  
 ngcgcgcccc ctccctccgat ggcggcggag atccagccca agcctctgac ccgcaagccg  
 60  
 atcctgctgc agcggatgga ggggtcccag gaggtggtga atatggccgt gatcgtgcc  
 120  
 aaagaggagg gcgtcatcag cgtctccgag gacaggacag ttcgtgtttg gttaaagaga  
 180  
 gacagtggac agtattggcc aagcgtatac catgcaatgc cttgagttta tattgtcaga  
 240  
 agattataac aagatgactc ctgtgaaaaa ctatcaagcg catcagagca gagtgacgat  
 300

gacccctgttt gtcctggagc tggagtgggt gctgagcaca ggacaggaca agcaatttgc  
 360  
 ctggcactgc tctgagagtg ggcagcgcct gggagggttat cggaccagtg ctgtggcctc  
 420  
 aggccctgcaa tttgatgttg aaacccggca tgtgtttatc ggtgaccact caggcca  
 477

<210> 562  
 <211> 74  
 <212> PRT  
 <213> Homo sapiens

<400> 562  
 Xaa Ala Pro Pro Pro Pro Met Ala Ala Glu Ile Gln Pro Lys Pro Leu  
 1 5 10 15  
 Thr Arg Lys Pro Ile Leu Leu Gln Arg Met Glu Gly Ser Gln Glu Val  
 20 25 30  
 Val Asn Met Ala Val Ile Val Pro Lys Glu Glu Gly Val Ile Ser Val  
 35 40 45  
 Ser Glu Asp Arg Thr Val Arg Val Trp Leu Lys Arg Asp Ser Gly Gln  
 50 55 60  
 Tyr Trp Pro Ser Val Tyr His Ala Met Pro  
 65 70

<210> 563  
 <211> 403  
 <212> DNA  
 <213> Homo sapiens

<400> 563  
 ccatggcaga cagggagctg agcggcctgc ggacccaggt gcaccagagc atggtgcccc  
 60  
 tgctcctaca cctgaaggac caatgcccaa ctgtcgccac gggcaatgcc caccceaaga  
 120  
 aaaggaaggg aaaaggcctc aaccttggcc agggctggaa cccacaggag gccagggtac  
 180  
 ggggcagacg gatggcagca gcactgcctg agagttgggg gagctccac ggggcagcaa  
 240  
 gtggcgggca gagggctctg ccatctgcac tggtttctgt gaccacagtt ggctgccccg  
 300  
 ctccccact gcaccactga cgaagcgaga ccctgcctca aaaaaaaaaa caaaaacaaa  
 360  
 aacaaaaaca aaactcaaac ttcacactgg agatctgtgc aat  
 403

<210> 564  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 564  
 Met Ala Asp Arg Glu Leu Ser Gly Leu Arg Thr Gln Val His Gln Ser  
 1 5 10 15  
 Met Val Pro Leu Leu Leu His Leu Lys Asp Gln Cys Pro Thr Val Ala



```

      20      25      30
Thr Gly Asn Ala His Pro Lys Lys Arg Lys Gly Lys Gly Leu Asn Leu
      35      40      45
Gly Gln Gly Trp Asn Pro Gln Glu Ala Arg Val Arg Gly Arg Arg Met
      50      55      60
Ala Ala Ala Leu Pro Glu Ser Trp Gly Ser Ser His Gly Ala Ala Ser
      65      70      75      80
Gly Gly Gln Arg Val Trp Pro Ser Ala Leu Val Ser Val Thr Thr Val
      85      90      95
Gly Leu Pro Ala Pro Pro Leu His His
      100      105

```

&lt;210&gt; 565

&lt;211&gt; 311

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 565

```

ncctctccat ggagcagccc catcttcact cttcacctgg ggccaggcct tccacagcag
60
ccaccaccca gcgaccacag agaggctgcg cggaggacac aggagagagg gagcccacgg
120
gcacgatctc caccggcttt cccagctccc tgggtcagcc ccacgggacc tctctctctc
180
tctcccatat ctccaagcca gccttgcata tagtaagagc tgtgatcagg atggaaagag
240
gcttgggccc cacagacctg gacaatgtcc cagtgagggc tggaggtgct agaagggcac
300
aggaggcccc n
311

```

&lt;210&gt; 566

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 566

```

Met Glu Gln Pro His Leu His Ser Ser Pro Gly Ala Arg Pro Ser Thr
  1      5      10      15
Ala Ala Thr Thr Gln Arg Pro Gln Arg Gly Cys Ala Glu Asp Thr Gly
      20      25      30
Glu Arg Glu Pro Thr Gly Thr Ile Ser Thr Gly Phe Pro Ser Ser Leu
      35      40      45
Gly Gln Pro His Gly Thr Ser Pro Pro Leu Ser His Ile Ser Lys Pro
      50      55      60
Ala Leu His Ile Val Arg Ala Val Ile Arg Met Glu Arg Gly Leu Gly
      65      70      75      80
Arg Thr Asp Leu Asp Asn Val Pro Val Arg Ala Gly Gly Ala Arg Arg
      85      90      95
Ala Gln Glu Ala Pro
      100

```

&lt;210&gt; 567

&lt;211&gt; 929

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 567

atcacatcgg tcgctgaacc ccgacgagcc tcacctgtgc gaaatattca tccttgagat  
 60  
 cagcccacgt gccgtcgacc tctacctcgg tgaggggtcgc gggcgggtac caacagccga  
 120  
 cctcgtcctc gggtccactc atggcggcaa gttccgctgc cagtccgggg atcgtcgggg  
 180  
 catgggcat gatgagcagg ttatccacat cgtcgtcgat ttctccgatg cgccgacgca  
 240  
 cggatatcagt gccgcagtaa tagagggctc gcatgaattc gaccggacaa tccagttgga  
 300  
 ggcagtccca ggtctggcgg gtgcgtaggg catcggagac cagagcatgt ccaacattgc  
 360  
 gcagtcctaa acgcgtgccg acctcacggg cctgacggcg cccacgtcg gtgagcggac  
 420  
 gctcccgatc ccgcccggga gcatgggatg cgggctgtgc atgtctcatg aggaacagag  
 480  
 tgtgcatgga tccatcgttg cacttcgcgg tcgccgcggg tctacgatgt tggcatgccg  
 540  
 ttgacggatt tgggcattga tgaggcgcgt acctaccgcc cgaacgtccc tgaacccgat  
 600  
 ggtttcgact ctttttgggc cgagaccctc gatgagtatt ccggcgttcc ccaagatctg  
 660  
 acggcgggtgc ctttcgataa ccgtcaggct ctgatagata cctgggattt gtcgtgggtg  
 720  
 gggatcacca actctcgggt gagcgggtga ttacatgcc cagccgctgt gaacggccca  
 780  
 ttcccccttg tcatcgagta cctcgggtac tcgagttcgc gtggtgtgcc gattggatca  
 840  
 gtcttcgctg ctgctggcta tgcacatc gtcgtcgatc cacgtggtca ggggtggggc  
 900  
 caccacaacct tgacggaaaa ctgtccgga  
 929

&lt;210&gt; 568

&lt;211&gt; 71

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 568

Met Pro Leu Thr Asp Leu Gly Ile Asp Glu Ala Arg Thr Tyr Arg Pro  
 1 5 10 15  
 Asn Val Pro Glu Pro Asp Gly Phe Asp Ser Phe Trp Ala Glu Thr Leu  
 20 25 30  
 Asp Glu Tyr Ser Gly Val Pro Gln Asp Leu Thr Ala Val Pro Phe Asp  
 35 40 45  
 Asn Arg Gln Ala Leu Ile Asp Thr Trp Asp Leu Ser Trp Val Gly Tyr  
 50 55 60  
 His Asn Ser Arg Val Ser Gly  
 65 70

<210> 569  
 <211> 371  
 <212> DNA  
 <213> Homo sapiens

<400> 569  
 ncgcaaactt caacgggtgcc atctgccata ttccagggat gccagatttg gatggaaaat  
 60  
 accatatcac tctcgattca gaattcgtac ttgatttagt ggcctttaac aaaacgctac  
 120  
 ctgtcgatta cttaatggtc gaaggaacgg aacttggtga ttcaaactg gaagaactac  
 180  
 ctgaatgccc atattatcca aaagatcaaa agccaatcgt gattgggaaa aacacaaaac  
 240  
 tcaaggaaca accaacagcc gttgctctct tctcgatgt tgataaacgg ccagagatta  
 300  
 aatcaaaaat cttagaccgc tatgataatg atattgaaat ccgtacttgg ggcggtactt  
 360  
 cccatgtcta n  
 371

<210> 570  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 570  
 Met Pro Asp Leu Asp Gly Lys Tyr His Ile Thr Leu Asp Ser Glu Phe  
 1 5 10 15  
 Val Leu Asp Leu Val Ala Phe Asn Lys Thr Leu Pro Val Asp Tyr Leu  
 20 25 30  
 Met Val Glu Gly Thr Glu Leu Val Tyr Ser Asn Met Glu Glu Leu Pro  
 35 40 45  
 Glu Cys Pro Tyr Tyr Pro Lys Asp Gln Lys Pro Ile Val Ile Gly Lys  
 50 55 60  
 Asn Thr Lys Leu Lys Glu Gln Pro Thr Ala Val Ala Leu Phe Ser Asp  
 65 70 75 80  
 Val Asp Lys Arg Pro Glu Ile Lys Ser Lys Ile Leu Asp Arg Tyr Asp  
 85 90 95  
 Asn Asp Ile Glu Ile Arg Thr Trp Gly Gly Thr Ser His Val Xaa  
 100 105 110

<210> 571  
 <211> 407  
 <212> DNA  
 <213> Homo sapiens

<400> 571  
 nacgcgtatc ttcgctggtc cacaccagac gtggcattaa acgacgtcac aagaacgaca  
 60  
 ccgggacctg acgggcccac gcacgaagag gccaagacac tgaccgagac tactgtttcc  
 120  
 gttcccacct ccttcgccga cctcggcgtc cgagaagata tctgccaggc gctggaaggg  
 180

gtgggaattg tctccccgtt cccgatccag gccatgtcga tcccgattgc cgtcgagggc  
 240  
 acggatctta ttgggcaggc gcgtactggc actggcaaaa cactcgcctt cggcatcacc  
 300  
 atcttcgagc gcatcaccct gcccggtgac gaaggttggg aagaactcac caccaaaggc  
 360  
 aagcccccaa gcactcgtga tgtgcccta cccgggagct aggtcgg  
 407

<210> 572

<211> 100

<212> PRT

<213> Homo sapiens

<400> 572

Leu	Thr	Glu	Thr	Thr	Val	Ser	Val	Pro	Thr	Ser	Phe	Ala	Asp	Leu	Gly
1				5				10						15	
Val	Arg	Glu	Asp	Ile	Cys	Gln	Ala	Leu	Glu	Gly	Val	Gly	Ile	Val	Ser
			20					25					30		
Pro	Phe	Pro	Ile	Gln	Ala	Met	Ser	Ile	Pro	Ile	Ala	Val	Glu	Gly	Thr
		35					40					45			
Asp	Leu	Ile	Gly	Gln	Ala	Arg	Thr	Gly	Thr	Gly	Lys	Thr	Leu	Ala	Phe
	50					55				60					
Gly	Ile	Thr	Ile	Leu	Gln	Arg	Ile	Thr	Leu	Pro	Gly	Asp	Glu	Gly	Trp
65					70					75				80	
Glu	Glu	Leu	Thr	Thr	Lys	Gly	Lys	Pro	Pro	Ser	Thr	Arg	Asp	Val	Pro
				85					90					95	
Leu	Pro	Gly	Ser												
			100												

<210> 573

<211> 393

<212> DNA

<213> Homo sapiens

<400> 573

acgcgtctac cgtaggatcc atgaccttcc gcaagaccga ccaccacaag aacgccattg  
 60  
 actacgaggt cgccggacta atgtggctcg ctgctgcccg gccagatggg gccggcatcg  
 120  
 tcgaggtgct cgaccacggc aagggatggc tcaccgaacc cgaattgtcc actgggcacc  
 180  
 ccacccgcga ggcagccgag gactttggcc gccgactggc tcacaccac gcagccgggg  
 240  
 cctcacacct gggggctgca cctgacgggt ttgttcccga cgatgggtat atcggccgtg  
 300  
 ctccccctgcc actgccgtcc gaaccaatct ctcctgggg agagttttac gctcagtgcc  
 360  
 gcatcgaacc atatatggac agtctcgacg ctg  
 393

<210> 574

<211> 124

<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 574

```

Met Thr Phe Arg Lys Thr Asp His His Lys Asn Ala Ile Asp Tyr Glu
 1           5           10           15
Val Ala Gly Leu Met Trp Leu Ala Ala Ala Arg Pro Asp Gly Ala Gly
          20           25           30
Ile Val Glu Val Leu Asp His Gly Lys Gly Trp Leu Thr Glu Pro Glu
          35           40           45
Leu Ser Thr Gly His Pro Thr Arg Glu Ala Ala Glu Asp Phe Gly Arg
          50           55           60
Arg Leu Ala His Thr His Ala Ala Gly Ala Ser His Leu Gly Ala Ala
65           70           75           80
Pro Asp Gly Phe Val Pro Asp Asp Gly Tyr Ile Gly Arg Ala Pro Leu
          85           90           95
Pro Leu Pro Ser Glu Pro Ile Ser Ser Trp Gly Glu Phe Tyr Ala Gln
          100          105          110
Cys Arg Ile Glu Pro Tyr Met Asp Ser Leu Asp Ala
          115          120

```

&lt;210&gt; 575

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 575

```

nntatccatg cagacatggg accaggggtct ctgagggcag gaagcaaagt gggtaggggg
60
gatgggacaa gatgccctgg tgctaaggcc tctggagctg gagctgggta tagggatgat
120
accaggcacc ctgagtcact cgcacctcac aatggggccg cttctgggag ccagtgggct
180
tatggggctg gcaatgtgct gggttatgag gatggatcag aacttcagg gcctcagggg
240
actgggggtca gaacagccta tggagaaagg tcaaggggcc ttgggcctag gagtacaggg
300
ccagggggtg aggcaggctt tagagatggt tcaggaggcc tccaaggaat gggatcagca
360
gatggggccc gt
372

```

&lt;210&gt; 576

&lt;211&gt; 124

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 576

```

Xaa Ile His Ala Asp Met Gly Pro Gly Ser Leu Arg Ala Gly Ser Lys
 1           5           10           15
Val Gly Glu Gly Asp Gly Thr Arg Cys Pro Gly Ala Lys Ala Ser Gly
          20           25           30
Ala Gly Ala Gly Tyr Arg Asp Asp Thr Arg His Pro Glu Ser Leu Ala
          35           40           45
Pro His Asn Gly Ala Ala Ser Gly Ser Gln Trp Ala Tyr Gly Ala Gly

```

```

      50              55              60
Asn Val Leu Gly Tyr Glu Asp Gly Ser Glu Leu Pro Gly Pro Gln Gly
65              70              75              80
Thr Gly Val Arg Thr Ala Tyr Gly Glu Arg Ser Arg Gly Leu Gly Pro
      85              90              95
Arg Ser Thr Gly Pro Gly Gly Glu Ala Gly Phe Arg Asp Gly Ser Gly
      100              105              110
Gly Leu Gln Gly Met Gly Ser Ala Asp Gly Pro Gly
      115              120

```

&lt;210&gt; 577

&lt;211&gt; 432

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 577

```

nagcgcaatg tcatgatgtc ggatttgtca atgtcggatt tctcatccca gccatcaccc
60
ccgcagcgcc gggcgcggat gaccagcggc cagcgccgtg aacagctcat cagcgtggcc
120
cgtcgcctct tcgcagacaa tggcatggca gggacctccg tcgaggagat cgccgctacc
180
gcgggagtct ccaaaccctg catctacgag catttcgggt ccaaggatgg gctgtacgcc
240
gtcgtcgtag accgcgaggt acgccacctt caagattccc tcaacgcgcg catgaccgcg
300
ccaaagcaag gcccgaacg caccctggag tcagcggtag tggccctgct ggactacatc
360
gacgaccgtc cagacggttt tcggatcatc tcgcgagact cctcgggtcgg ttcagccacc
420
ggttcgtacg cg
432

```

&lt;210&gt; 578

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 578

```

Met Thr Ser Gly Gln Arg Arg Glu Gln Leu Ile Ser Val Ala Arg Arg
1              5              10              15
Leu Phe Ala Asp Asn Gly Met Ala Gly Thr Ser Val Glu Glu Ile Ala
      20              25              30
Ala Thr Ala Gly Val Ser Lys Pro Val Ile Tyr Glu His Phe Gly Ser
      35              40              45
Lys Asp Gly Leu Tyr Ala Val Val Val Asp Arg Glu Val Arg His Leu
      50              55              60
Gln Asp Ser Leu Asn Ala Ala Met Thr Arg Pro Lys Gln Gly Pro Lys
65              70              75              80
Arg Thr Leu Glu Ser Ala Val Leu Ala Leu Leu Asp Tyr Ile Asp Asp
      85              90              95
Arg Pro Asp Gly Phe Arg Ile Ile Ser Arg Asp Ser Ser Val Gly Ser
      100              105              110
Ala Thr Gly Ser Tyr Ala

```

115

<210> 579  
 <211> 320  
 <212> DNA  
 <213> Homo sapiens

<400> 579  
 ggcccaaac actccgacct cagctgggtcc agcatgctgg gcaccgtgct gctgctggcc  
 60  
 ctgctcccag ggatcaccac cttaccacagc gggccacctg ctcccccggt ccccgcggcg  
 120  
 cccggcccct ggctgcgagc acccctcttc agcctgaagc tgtccgacac agaggacgtc  
 180  
 ttctctcgcc gcgcgggggc gctcgaggtc ccggccgaca gccgcgtgtt cgtgcaggcg  
 240  
 gccttggccc gtccctcccc gcgctggggc ctggccctgc accgctgctc agtgacgccg  
 300  
 tcctcacgcc cggccccggg  
 320

<210> 580  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 580  
 Met Leu Gly Thr Val Leu Leu Leu Ala Leu Leu Pro Gly Ile Thr Thr  
 1 5 10 15  
 Leu Pro Ser Gly Pro Pro Ala Pro Pro Phe Pro Ala Ala Pro Gly Pro  
 20 25 30  
 Trp Leu Arg Arg Pro Leu Phe Ser Leu Lys Leu Ser Asp Thr Glu Asp  
 35 40 45  
 Val Phe Pro Arg Arg Ala Gly Pro Leu Glu Val Pro Ala Asp Ser Arg  
 50 55 60  
 Val Phe Val Gln Ala Ala Leu Ala Arg Pro Ser Pro Arg Trp Gly Leu  
 65 70 75 80  
 Ala Leu His Arg Cys Ser Val Thr Pro Ser Ser Arg Pro Ala Pro  
 85 90 95

<210> 581  
 <211> 419  
 <212> DNA  
 <213> Homo sapiens

<400> 581  
 nacgacggca accattcgct gtggaaggag ctgaacggcc agctcgacgt gcagtttttc  
 60  
 cacgtcggca tgggcttcaa gacgccagta cgcattgaca gcgtcgaccc caagaccgcg  
 120  
 gaagcccgcg aggtgcattt ccgcccgtcg ctgttcaact atgccaagac cacgggtggac  
 180  
 accaagcagc tgaccggcga cctgggtttc tccggtttca agctgttcaa ggcgcgggaa  
 240

ctggatcgcc atgacgtgct gtcgtttctc ggcgccagtt acttccgtgc ggtggacgca  
 300  
 acccgccagt acggcctctc cgcacgcggc ctggcgattg atacctacgc gaaaaaacgc  
 360  
 gaggaattcc ccgacttcac gcagttctgg ttcgaaaccc cgagcaagga cccacgcgt  
 419

<210> 582

<211> 139

<212> PRT

<213> Homo sapiens

<400> 582

Xaa	Asp	Gly	Asn	His	Ser	Leu	Trp	Lys	Glu	Leu	Asn	Gly	Gln	Leu	Asp
1			5					10					15		
Val	Gln	Phe	Phe	His	Val	Gly	Met	Gly	Phe	Lys	Thr	Pro	Val	Arg	Met
			20					25					30		
His	Ser	Val	Asp	Pro	Lys	Thr	Arg	Glu	Ala	Arg	Glu	Val	His	Phe	Arg
			35				40					45			
Pro	Ser	Leu	Phe	Asn	Tyr	Ala	Lys	Thr	Thr	Val	Asp	Thr	Lys	Gln	Leu
			50				55				60				
Thr	Gly	Asp	Leu	Gly	Phe	Ser	Gly	Phe	Lys	Leu	Phe	Lys	Ala	Pro	Glu
65					70					75				80	
Leu	Asp	Arg	His	Asp	Val	Leu	Ser	Phe	Leu	Gly	Ala	Ser	Tyr	Phe	Arg
			85						90					95	
Ala	Val	Asp	Ala	Thr	Arg	Gln	Tyr	Gly	Leu	Ser	Ala	Arg	Gly	Leu	Ala
			100						105					110	
Ile	Asp	Thr	Tyr	Ala	Lys	Lys	Arg	Glu	Glu	Phe	Pro	Asp	Phe	Thr	Gln
			115				120						125		
Phe	Trp	Phe	Glu	Thr	Pro	Ser	Lys	Asp	Pro	Arg					
			130				135								

<210> 583

<211> 407

<212> DNA

<213> Homo sapiens

<400> 583

cttttgatca atgctgatgg cacgaagcta tcgaaaaggt cgggtgatgt ccgcgtagct  
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 gattatatgg agcagggatg ggagccggag acgctgggtga acctagttgc cctcacgggc  
 120  
 tatagctatg cgaatttgga gcatgctgat catgatgtca agacgatgaa cgaactcatc  
 180  
 cgtgactttg agcttactcg tatctcccat acgcgagcca cactcccat ggacaagctt  
 240  
 gtgtttttga acaagcatca cttgacaaat aagctggcgc tcgccacgac gtgtgagcag  
 300  
 accaaacaag acctattgtc gcgtatccgg ccgatcacta cctcgtggta cggcgattat  
 360  
 tcagatgatt atatcctgcg cgtcgttaaca ctgggacccc aacgcgt  
 407

<210> 584



<211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 584  
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 Val Arg Val Ala Asp Tyr Met Glu Gln Gly Trp Glu Pro Glu Thr Leu  
                   20                  25                  30  
 Val Asn Leu Val Ala Leu Thr Gly Tyr Ser Tyr Ala Asn Leu Glu His  
           35                  40                  45  
 Ala Asp His Asp Val Lys Thr Met Asn Glu Leu Ile Arg Asp Phe Glu  
   50                  55                  60  
 Leu Thr Arg Ile Ser His Thr Arg Ala Thr Leu Pro Met Asp Lys Leu  
  65                  70                  75                  80  
 Val Phe Leu Asn Lys His His Leu Thr Asn Lys Leu Ala Leu Ala Thr  
                   85                  90                  95  
 Thr Cys Glu Gln Thr Lys Gln Asp Leu Leu Ser Arg Ile Arg Pro Ile  
                   100                  105                  110  
 Thr Thr Ser Trp Tyr Gly Asp Tyr Ser Asp Asp Tyr Ile Leu Arg Val  
           115                  120                  125  
 Val Thr Leu Gly Pro Gln Arg  
       130                  135

<210> 585  
 <211> 502  
 <212> DNA  
 <213> Homo sapiens

<400> 585  
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  60  
 gatattttgt tgtgcgcggt gggattgttg gttcagcacc gtgacatcac tgaggagatt  
  120  
 cgggctcggg accgacattt cgttgctgac gaataccagg acgtttctcc gctgcagcat  
  180  
 aggttgcttg aactgtgggt tggcgatcga aatgatgtat gcgtcgtggg agatccgcac  
  240  
 caggccattc actcttatgc aggcgcacga gctgactacc tcctcgactt cgttgccgat  
  300  
 catcctggcg ctaaacgcat cgatttggtt cgcaactacc gctccactcc cgagatcggt  
  360  
 cagttggcca atgaagttct tgtcaaccgt atgactocag aggaggcttt ggaacatggc  
  420  
 aggggagtca cattggtttc gcggggtcga tccgggtccc agcccatcta tcaggctctc  
  480  
 ggggacgatg cctccgaagc tt  
  502

<210> 586  
 <211> 167  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 586

Xaa Arg Val Leu Ala Gly Tyr Glu Ala Val Lys Arg Glu Arg Cys Val  
 1 5 10 15  
 Ile Asp Leu Asp Asp Ile Leu Leu Cys Ala Val Gly Leu Leu Val Gln  
 20 25 30  
 His Arg Asp Ile Thr Glu Glu Ile Arg Ala Arg Tyr Arg His Phe Val  
 35 40 45  
 Val Asp Glu Tyr Gln Asp Val Ser Pro Leu Gln His Arg Leu Leu Glu  
 50 55 60  
 Leu Trp Phe Gly Asp Arg Asn Asp Val Cys Val Val Gly Asp Pro His  
 65 70 75 80  
 Gln Ala Ile His Ser Tyr Ala Gly Ala Arg Ala Asp Tyr Leu Leu Asp  
 85 90 95  
 Phe Val Ala Asp His Pro Gly Ala Lys Arg Ile Asp Leu Val Arg Asn  
 100 105 110  
 Tyr Arg Ser Thr Pro Glu Ile Val Gln Leu Ala Asn Glu Val Leu Val  
 115 120 125  
 Asn Arg Met Thr Pro Glu Glu Ala Leu Glu His Gly Arg Gly Val Thr  
 130 135 140  
 Leu Val Ser Arg Gly Arg Ser Gly Pro Glu Pro Ile Tyr Gln Ala Leu  
 145 150 155 160  
 Gly Asp Asp Ala Ser Glu Ala  
 165

&lt;210&gt; 587

&lt;211&gt; 746

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 587

gcgtcctgcc tcgagggcct cgggagcttc cgctgcctct gttggccagg ctacagcggc  
 60  
 gagctgtgcg aggtggacga ggacgagtgt gcatcgagcc cctgccagca tgggggcccga  
 120  
 tgcctgcagc gctctgacct ggccctctac ggggggtgtcc aggccgcctt ccctggcgcc  
 180  
 ttcagcttcc gccatgctgc gggtttctctg tgccactgcc ctcttggett tgaggagacc  
 240  
 gactgcggtg tggaggtgga cgagtgtgcc tcacggccat gcctcaatgg aggccactgc  
 300  
 caggacctgc ccaatggctt ccagtgtcac tgcccagatg gctacgcagg gccgacatgt  
 360  
 gaggaagatg tggatgaatg cctgtccgat ccctgcctgc acggcggaac ctgcagtgc  
 420  
 actgtggcag gctatatctg caggtgcccc gagacctggg gtgggcgcga ctgttctgtg  
 480  
 cagctcactg gctgccaggg ccacacctgc ccgctggctg ccacctgcat ccctatcttc  
 540  
 gagtctgggg tccacagtta cgtctgccac tgcccacctg gtacctatgg accgttctgt  
 600  
 ggccagaata ccaccttctc tgtgatggct gggagcccca ttcaggcatc agtgccagct  
 660  
 ggtggccccc tgggtctggc actgaggttt cgcaccacac tgcccgtctg gacctggcc  
 720

actcgcaatg acaccaagga aagctt  
746

<210> 588  
<211> 248  
<212> PRT  
<213> Homo sapiens

<400> 588  
Ala Ser Cys Leu Glu Gly Leu Gly Ser Phe Arg Cys Leu Cys Trp Pro  
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Gly Tyr Ser Gly Glu Leu Cys Glu Val Asp Glu Asp Glu Cys Ala Ser  
20 25 30  
Ser Pro Cys Gln His Gly Gly Arg Cys Leu Gln Arg Ser Asp Pro Ala  
35 40 45  
Leu Tyr Gly Gly Val Gln Ala Ala Phe Pro Gly Ala Phe Ser Phe Arg  
50 55 60  
His Ala Ala Gly Phe Leu Cys His Cys Pro Pro Gly Phe Glu Gly Ala  
65 70 75 80  
Asp Cys Gly Val Glu Val Asp Glu Cys Ala Ser Arg Pro Cys Leu Asn  
85 90 95  
Gly Gly His Cys Gln Asp Leu Pro Asn Gly Phe Gln Cys His Cys Pro  
100 105 110  
Asp Gly Tyr Ala Gly Pro Thr Cys Glu Glu Asp Val Asp Glu Cys Leu  
115 120 125  
Ser Asp Pro Cys Leu His Gly Gly Thr Cys Ser Asp Thr Val Ala Gly  
130 135 140  
Tyr Ile Cys Arg Cys Pro Glu Thr Trp Gly Gly Arg Asp Cys Ser Val  
145 150 155 160  
Gln Leu Thr Gly Cys Gln Gly His Thr Cys Pro Leu Ala Ala Thr Cys  
165 170 175  
Ile Pro Ile Phe Glu Ser Gly Val His Ser Tyr Val Cys His Cys Pro  
180 185 190  
Pro Gly Thr His Gly Pro Phe Cys Gly Gln Asn Thr Thr Phe Ser Val  
195 200 205  
Met Ala Gly Ser Pro Ile Gln Ala Ser Val Pro Ala Gly Gly Pro Leu  
210 215 220  
Gly Leu Ala Leu Arg Phe Arg Thr Thr Leu Pro Ala Gly Thr Leu Ala  
225 230 235 240  
Thr Arg Asn Asp Thr Lys Glu Ser  
245

<210> 589  
<211> 381  
<212> DNA  
<213> Homo sapiens

<400> 589  
atctcacaag tacaattaca gtctcaagaa ctgagctatc agcaaaagca aggtcttcag  
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ccagtacctc tgcaagccac tatgagtgtc gcaactggta tccagccatc gcctgtaaat  
120  
gtggttggtg taacttcagc tttaggtcag cagccttcca tttccagttt ggctcaaccc  
180

cagctaccat attctcaggc ggctcctcca gtgcaaactc cccttcaggc ggcaccacca  
 240  
 cccaacagt tacagtatgg acaacagcaa ccaatgggtt ctacacagat ggccccaggc  
 300  
 catgtcaaat cagtgactca aaatcctgct tcagagtatg tacaacagca gccaatctt  
 360  
 caaacagcaa tgcctccgg a  
 381

<210> 590

<211> 127

<212> PRT

<213> Homo sapiens

<400> 590

Ile	Ser	Gln	Val	Gln	Leu	Gln	Ser	Gln	Glu	Leu	Ser	Tyr	Gln	Gln	Lys
1				5					10					15	
Gln	Gly	Leu	Gln	Pro	Val	Pro	Leu	Gln	Ala	Thr	Met	Ser	Ala	Ala	Thr
		20						25					30		
Gly	Ile	Gln	Pro	Ser	Pro	Val	Asn	Val	Val	Gly	Val	Thr	Ser	Ala	Leu
	35					40						45			
Gly	Gln	Gln	Pro	Ser	Ile	Ser	Ser	Leu	Ala	Gln	Pro	Gln	Leu	Pro	Tyr
	50					55					60				
Ser	Gln	Ala	Ala	Pro	Pro	Val	Gln	Thr	Pro	Leu	Pro	Gly	Ala	Pro	Pro
65					70					75				80	
Pro	Gln	Gln	Leu	Gln	Tyr	Gly	Gln	Gln	Gln	Pro	Met	Val	Ser	Thr	Gln
			85					90					95		
Met	Ala	Pro	Gly	His	Val	Lys	Ser	Val	Thr	Gln	Asn	Pro	Ala	Ser	Glu
	100							105				110			
Tyr	Val	Gln	Gln	Gln	Pro	Ile	Leu	Gln	Thr	Ala	Met	Ser	Ser	Gly	
	115						120					125			

<210> 591

<211> 684

<212> DNA

<213> Homo sapiens

<400> 591

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 aagcaggaat acaagcgcgga gtcgttcacc ctgttctccg agctgctgga ctgatcaag  
 120  
 cgcgattcga ttcgggtcct cttccacgtc caggggcccgg gggaaaaatc cgtatcgaaa  
 180  
 naaaaagcgc gcctgcgtca ggaagccgaa gccctggccc agcgcgatgca gttcgagcac  
 240  
 gctgaagccc caggcctgga cgcgcccggaa atcctcggtg aagaagtcga tgcgcacctg  
 300  
 gccaccgcgc cggtagcga cagcagaag ctgggcccgt acgaactgtg ctactgcggt  
 360  
 tcgggcaaga agtacaagca ctgccacggt cagatcagct aaggtcttta ccggatactg  
 420  
 aaatacctgc gccgcgaccg gcattagccg tcgcggcggt tttccatttg aaacactgcc  
 480

cttgtgacgg cagtgcagat atcacattaa aaggagggca ttcattgggtg ttggttctgg  
 540  
 gtccttggcc tacgttgacac ccggttgccg gttttgaact cggatcgcgc tcggccggta  
 600  
 tcaagcgccc tgggcgcaag gatgtggtgg cgatgcgctg cgccgaaggt tccacgggtg  
 660  
 cgggggtggt taccctcaac gcgt  
 684

<210> 592  
 <211> 133  
 <212> PRT  
 <213> Homo sapiens

<400> 592  
 Ser Thr Met Asp His Leu Arg His Gly Ile His Leu Arg Gly Tyr Ala  
 1 5 10 15  
 Gln Lys Asn Pro Lys Gln Glu Tyr Lys Arg Glu Ser Phe Thr Leu Phe  
 20 25 30  
 Ser Glu Leu Leu Asp Ser Ile Lys Arg Asp Ser Ile Arg Val Leu Phe  
 35 40 45  
 His Val Gln Gly Pro Gly Glu Lys Ser Val Ser Lys Xaa Lys Ala Arg  
 50 55 60  
 Leu Arg Gln Glu Ala Glu Ala Leu Ala Gln Arg Met Gln Phe Glu His  
 65 70 75 80  
 Ala Glu Ala Pro Gly Leu Asp Ala Pro Glu Ile Leu Gly Glu Glu Val  
 85 90 95  
 Asp Val Ala Leu Ala Thr Ala Pro Val Arg Asn Glu Gln Lys Leu Gly  
 100 105 110  
 Arg Asn Glu Leu Cys Tyr Cys Gly Ser Gly Lys Lys Tyr Lys His Cys  
 115 120 125  
 His Gly Gln Ile Ser  
 130

<210> 593  
 <211> 615  
 <212> DNA  
 <213> Homo sapiens

<400> 593  
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 tgtgaaaccg tcacggtaga gcgtcgtggc gggctaccac ttagagcggc ccgattcacc  
 120  
 gataccatcc ccgcgccgct aggccagcca cgatggtcga cggccaccat ccagacccca  
 180  
 gtcataccta ctacacgtgg tcgattcgtg atcgccccg tcatgatgcg caccatcgac  
 240  
 ccgtttggca tggcccgcca tcacaccgat ctcggtcagg ttgccgaagt cattgtcacg  
 300  
 ccaaggatcg tcgatttggg cgcctccggg gagctcgggg gtcagggatt cgacacaagg  
 360  
 tcctcagcga tccatgccgg acgacgtggt cccgacgat ccattggtgcg cgattggcac  
 420

accggagact cgggtgcgacg cattcactgg cgctccaccg ctcaccgcgg ggacctcatg  
 480  
 gtccgatgcg aggagcaggc ctggaaccca tccgtcgtca tcgtgttgga ttctcgggct  
 540  
 cggcgctcacg ctggaactgg ccccgacgca tcctttgaat gggccgtcaa cgcggtggca  
 600  
 tccatctcga cgcgt  
 615

<210> 594

<211> 205

<212> PRT

<213> Homo sapiens

<400> 594

Xaa	Arg	Val	Gln	Thr	Ala	Arg	Ser	Leu	Ala	Pro	Val	Arg	Ile	Ala	Leu
1				5					10					15	
Gly	Ser	Gln	Thr	Cys	Glu	Thr	Val	Thr	Val	Glu	Arg	Arg	Gly	Gly	Leu
		20					25						30		
Pro	Leu	Arg	Ala	Ala	Arg	Phe	Thr	Asp	Thr	Ile	Pro	Ala	Pro	Leu	Gly
	35					40					45				
Gln	Pro	Arg	Trp	Ser	Thr	Ala	Thr	Ile	Gln	Thr	Pro	Val	Ile	Pro	Thr
	50				55					60					
Thr	Arg	Gly	Arg	Phe	Val	Ile	Gly	Pro	Val	Met	Met	Arg	Thr	Ile	Asp
65				70					75					80	
Pro	Phe	Gly	Met	Ala	Arg	His	His	Thr	Asp	Leu	Gly	Gln	Val	Ala	Glu
				85				90					95		
Val	Ile	Val	Thr	Pro	Arg	Ile	Val	Asp	Leu	Gly	Ala	Ser	Gly	Glu	Leu
		100					105					110			
Gly	Gly	Gln	Gly	Phe	Asp	Thr	Arg	Ser	Ser	Ala	Ile	His	Ala	Gly	Arg
	115					120						125			
Arg	Gly	Pro	Asp	Asp	Ala	Met	Val	Arg	Asp	Trp	His	Thr	Gly	Asp	Ser
	130					135					140				
Val	Arg	Arg	Ile	His	Trp	Arg	Ser	Thr	Ala	His	Arg	Gly	Asp	Leu	Met
145				150					155					160	
Val	Arg	Cys	Glu	Glu	Gln	Ala	Trp	Asn	Pro	Ser	Val	Val	Ile	Val	Leu
			165					170					175		
Asp	Ser	Arg	Ala	Arg	Arg	His	Ala	Gly	Thr	Gly	Pro	Asp	Ala	Ser	Phe
		180					185					190			
Glu	Trp	Ala	Val	Asn	Ala	Val	Ala	Ser	Ile	Ser	Thr	Arg			
	195					200					205				

<210> 595

<211> 303

<212> DNA

<213> Homo sapiens

<400> 595

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 cccatggggc catcggaccg cgccgcgcgg gggcggttcgc cagggcctcc gcagaagccc  
 120  
 gcctgtgccc gcaaccgccc cgaaattctc tcctggcac cgtgtccgct ttacggagcc  
 180

cggagcaagg ctcagaaaaa tgtcccagcc aaaaacatgg tacatgctg tcatcaggca  
 240  
 agtcttcaaa gagcggctgg gaccaggggc cgagggacct cgttttagagg cggcttaggg  
 300  
 gga  
 303

<210> 596  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<400> 596  
 Met Leu Leu Asn Pro Gly Asp Leu Thr Val Glu Gly Arg Pro His Gly  
 1 5 10 15  
 Ala Ile Gly Pro Arg Arg Ala Gly Ala Phe Ala Arg Ala Ser Ala Glu  
 20 25 30  
 Ala Arg Leu Cys Pro Gln Pro Pro Arg Asn Ser Leu Pro Gly Thr Val  
 35 40 45  
 Ser Ala Leu Arg Ser Pro Glu Gln Gly Ser Glu Lys Cys Pro Ser Gln  
 50 55 60  
 Lys His Gly Thr Cys Leu Ser Ser Gly Lys Ser Ser Lys Ser Gly Trp  
 65 70 75 80  
 Asp Gln Gly Pro Arg Asp Leu Val  
 85

<210> 597  
 <211> 2709  
 <212> DNA  
 <213> Homo sapiens

<400> 597  
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 60  
 aagaaccaca tggaggagaa gacctacgaa tgtaaagaat ggggaaatc ctttggcgat  
 120  
 ctcgtgtccc ggaggaaaca catgaggatt cacatcgtca agaaaccgt ggaatgtcgg  
 180  
 cagtgcggga agaccttccg aaaccagtcc atccttaaga ctcacatgaa ctctcacact  
 240  
 ggagagaaac catacgggtg cgatctctgc gggaaagctt tcagcgcgag ttcaaacctc  
 300  
 accgcacaca ggaagataca cagcaagag agacgctacg aatgcgccgc ctgcgggaaa  
 360  
 gtcttcgggtg actatattatc ccggcggagg cacatgagcg ttcaccttgt aaagaaacga  
 420  
 gttgagtgtg ggcattgtgg caaggccttc aggaaccagt caacgctgaa gacgcacatg  
 480  
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 540  
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 600  
 gtctgcggga aagccttcag cgaccactca tccctcagga gccacgtgaa aatcaccgg  
 660

ggagagaagc tcttttngtg tcatccgtgt ggaaaaggct ccagtgaagc cgccntgctt  
720  
tagagacaca ggatgattca gaccggaaac agacctcgtg ggtgtaagag gaagcctctg  
780  
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840  
gtaaaaactg ggaagacgag gcgttctcat cccataggag gtttgtgaga actcacgccg  
900  
ggggtgaaaa tgtacgtctg tagcatggag aagccttcag gtacattcag ctcttaacaa  
960  
acacaggaag acttaatggc agcttggcat ttaatgtcaa aatccaagcc gtggcattta  
1020  
atgtcaaaat gacttcagac cacttctagc cttctgggcc catgagtaat aatgagcaca  
1080  
ctaggagca tctctgtaaa cacagtggct ggggaaaccc ttcctagtct cacttgattc  
1140  
ctcatgacgg aaatcacact aaagagagaa atcagtgaag taaggacgt ggaaggctcat  
1200  
gaatgggccc caaaccacgg ccagctgctt gtctttgtat ggcttgccag ctaacaatag  
1260  
tggttccatc ttttaaggaag aagaatgttt gatggagaaa atttgtggcc aatgaagtct  
1320  
gaaatacttc ctgtcatctg cccctttcca gaaaaacttg gccgaccctt ggtctacagc  
1380  
acgggttctc agtcgggcga cgatttggct gtctaggcgt catttggaac tgtctagaga  
1440  
catttttggg agttagaatg gggggaagat actcctgact tgtaataaga agacatcaga  
1500  
gatgctgcta agtcggctcc agcacacagg agccccccac aacgaagagt tagtgcccc  
1560  
aaacgtcact gttgctgagg ttgaaaataa tcatgcagtc attcctcaat tactgcctgc  
1620  
agcaattcct ccatttttat gaatcttctg agcacttacg ctaggagaaa tttcttttac  
1680  
aaaactttta aaatacaatt agtgctgata attcctatgt ggaaatgatt ccagccatgg  
1740  
tcccctcact tgagcatgtg aatattctca cggagagaag ccccgagag attttccggt  
1800  
gaatacggga ttgcacttac tctttcatca cggaaacaga ccccccagaga gaagccccaa  
1860  
cgagattttc cgggtgaatac gggactgcac gtactctctc atcatgaaaa cagagccccg  
1920  
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1980  
atcaagaaag gtttgtttat agtattttta ctatagcttc atccttgata acgtccta  
2040  
ttccttctgg acaacctcct tgaccaatgg catattgaga tctatgtgac atgaggatat  
2100  
ttctcagtac cactttgtta ctggtacctg atgcacacgg attgagacca gagcatgatg  
2160  
cctccatcaa gtggtaatat gtttgcagcc tgctgtccag ccaagagtga cagatacttc  
2220  
tagtgacttc ccgggtatcc actctcatct tcttccaata tcaagagaat ccaggttctg  
2280



tcagattagt aagggtgtgct aatctaaatt ttaaaaaaatc tcttacagggt tttcttgtag  
 2340  
 ctggtaccat ccatgtctca cagccctggc cactgacaga tcagcagatg tcaccacgtg  
 2400  
 ggcttctgag aaagctcttg aatggggatc gttcttaaac atgaattcct ccctgtatgt  
 2460  
 tttgttcttt gctttacttt tcaccttgca aagagatcca gtacctagta ttggaagatc  
 2520  
 caccttaacg accgtgcata tgaaaaccac agtctaagga agtgactgca gaaagctcac  
 2580  
 agcgaccctg gcctcccctg tggcctcttt gagtgtctgc agcagccctg gacttccaga  
 2640  
 cttctatcac atgagaaaaa ataaaactga ttattggttt aagctgcaaa aaaaaaaaaa  
 2700  
 aaaaaaaaaa  
 2709

<210> 598

<211> 240

<212> PRT

<213> Homo sapiens

<400> 598

Xaa	Ala	Cys	Thr	Gln	Cys	Gly	Lys	Ala	Phe	Arg	Trp	Lys	Ser	Asn	Phe
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Asn	Leu	His	Lys	Asn	His	Met	Val	Glu	Lys	Thr	Tyr	Glu	Cys	Lys	
	20						25				30				
Glu	Cys	Gly	Lys	Ser	Phe	Gly	Asp	Leu	Val	Ser	Arg	Arg	Lys	His	Met
	35					40					45				
Arg	Ile	His	Ile	Val	Lys	Lys	Pro	Val	Glu	Cys	Arg	Gln	Cys	Gly	Lys
	50					55					60				
Thr	Phe	Arg	Asn	Gln	Ser	Ile	Leu	Lys	Thr	His	Met	Asn	Ser	His	Thr
	65			70					75					80	
Gly	Glu	Lys	Pro	Tyr	Gly	Cys	Asp	Leu	Cys	Gly	Lys	Ala	Phe	Ser	Ala
			85					90						95	
Ser	Ser	Asn	Leu	Thr	Ala	His	Arg	Lys	Ile	His	Thr	Gln	Glu	Arg	Arg
		100						105				110			
Tyr	Glu	Cys	Ala	Ala	Cys	Gly	Lys	Val	Phe	Gly	Asp	Tyr	Leu	Ser	Arg
	115					120					125				
Arg	Arg	His	Met	Ser	Val	His	Leu	Val	Lys	Lys	Arg	Val	Glu	Cys	Arg
	130					135					140				
His	Cys	Gly	Lys	Ala	Phe	Arg	Asn	Gln	Ser	Thr	Leu	Lys	Thr	His	Met
	145			150					155					160	
Arg	Ser	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asp	His	Cys	Gly	Lys
			165					170						175	
Ala	Phe	Ser	Ile	Gly	Ser	Asn	Leu	Asn	Val	His	Arg	Arg	Ile	His	Thr
		180					185						190		
Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Leu	Val	Cys	Gly	Lys	Ala	Phe	Ser	Asp
	195					200					205				
His	Ser	Ser	Leu	Arg	Ser	His	Val	Lys	Thr	His	Arg	Gly	Glu	Lys	Leu
	210					215					220				
Phe	Xaa	Cys	His	Pro	Cys	Gly	Lys	Gly	Ser	Ser	Glu	Arg	Ala	Xaa	Leu
225					230					235					240

<210> 599  
 <211> 340  
 <212> DNA  
 <213> Homo sapiens

<400> 599  
 acgcgtgcct cgcgactctt gacgtcgtgg tggctgcgct cggtcgtgtc actcctcttg  
 60  
 ttcggcggtca tggcgaggt gctaggcgtg gccgtgcatc tgagtctgca ccgctttgcc  
 120  
 caggcatgtt tgccggggcg catcccttgc acttgcatgc cgtggcctat cggccgaggc  
 180  
 gcaggcctgc agttggagcc gtgcgtgggt gtcccgcgcg aggagcgtgt tggcagacta  
 240  
 tggggctcgt cggaggacga ggatgtgagt ggcatggct ttgcgcgact gggcgatttc  
 300  
 caccggcgga tgggtctcca gatcgtccag ggcgatgatca  
 340

<210> 600  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 600  
 Met Pro Trp Thr Ile Trp Ser Thr Ile Ala Gly Trp Asn Thr Pro Ser  
 1 5 10 15  
 Arg Ala Lys Pro Ser Pro Leu Thr Ser Ser Ser Ser Asp Glu Pro His  
 20 25 30  
 Ser Leu Pro Thr Arg Ser Ser Arg Gly Thr Pro Thr His Gly Ser Asn  
 35 40 45  
 Cys Arg Pro Ala Pro Arg Pro Ile Gly His Gly Leu Gln Val Gln Gly  
 50 55 60  
 Met Arg Pro Gly Lys His Ala Trp Ala Lys Arg Cys Arg Leu Arg Cys  
 65 70 75 80  
 Thr Ala Thr Pro Ser Thr Cys Ala Met Thr Pro Asn Lys Arg Ser Asp  
 85 90 95  
 Thr Thr Glu Arg Ser His His Asp Val Lys Ser Arg Glu Ala Arg  
 100 105 110

<210> 601  
 <211> 421  
 <212> DNA  
 <213> Homo sapiens

<400> 601  
 gccggcggca ggcacatctc gctcaacgtc ggcggtgcgcg gcctgacttc gcgtctttct  
 60  
 ccgcgctcca ccattttgat ggacggcgtc ccgctggcgg tcgcgcctta cggccagccg  
 120  
 cagctgtcga tggccccgct gtctatcgggt aatctgcaat cgggtggacgt ggtgcgcggc  
 180  
 ggcggcgcgg tgcgctacgg gccgcagaac gtcggcggcg tgatcaactt cgttaccgga  
 240

gacattccca aaacgtttgg cgggtgccgc agcgtacaaa cccaggggtgc cagccacggc  
 300  
 ggccctgaaga ccctgaccag cgcctccgtg ggcggcaccg cagacaacgg cctcggcgcc  
 360  
 gagctgctct actccggcct gcacggccag ggctaccgag acaacaacga caacaccgac  
 420  
 n  
 421

<210> 602  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 602  
 Ala Gly Gly Ser Asp Ile Ser Leu Asn Val Gly Val Arg Gly Leu Thr  
 1 5 10 15  
 Ser Arg Leu Ser Pro Arg Ser Thr Ile Leu Met Asp Gly Val Pro Leu  
 20 25 30  
 Ala Val Ala Pro Tyr Gly Gln Pro Gln Leu Ser Met Ala Pro Leu Ser  
 35 40 45  
 Ile Gly Asn Leu Gln Ser Val Asp Val Val Arg Gly Gly Gly Ala Val  
 50 55 60  
 Arg Tyr Gly Pro Gln Asn Val Gly Gly Val Ile Asn Phe Val Thr Arg  
 65 70 75 80  
 Asp Ile Pro Lys Thr Phe Gly Gly Ala Ala Ser Val Gln Thr Gln Gly  
 85 90 95  
 Ala Ser His Gly Gly Leu Lys Thr Leu Thr Ser Ala Ser Val Gly Gly  
 100 105 110  
 Thr Ala Asp Asn Gly Leu Gly Ala Glu Leu Leu Tyr Ser Gly Leu His  
 115 120 125  
 Gly Gln Gly Tyr Arg Asp Asn Asn Asp Asn Thr Asp  
 130 135 140

<210> 603  
 <211> 309  
 <212> DNA  
 <213> Homo sapiens

<400> 603  
 nagggcggca tgcacgaaag cttgcgcaaa cgctcgctgg aaggcttgga caagatcggc  
 60  
 ttcgacggcc tggccatcgg cggctctgtcg gtgggcgagc ccaagcacga gatgatcaag  
 120  
 gtgctggatt acctgccggg cctgatgccg gctgacaaac ctcgttacct tatgggcgtt  
 180  
 ggcaaaccgg aagacctcgt agagggtgtg cgccgcggtg tggacatgtt cgattgcgtg  
 240  
 atgccaaacc gtaatgcccg caatgggcat ctgttcacg atacaggcgt gctgaagatc  
 300  
 cgtaacgag  
 309

<210> 604

<211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 604  
 Xaa Gly Gly Met His Glu Ser Leu Arg Lys Arg Ser Leu Glu Gly Leu  
 1 5 10 15  
 Asp Lys Ile Gly Phe Asp Gly Leu Ala Ile Gly Gly Leu Ser Val Gly  
 20 25 30  
 Glu Pro Lys His Glu Met Ile Lys Val Leu Asp Tyr Leu Pro Gly Leu  
 35 40 45  
 Met Pro Ala Asp Lys Pro Arg Tyr Leu Met Gly Val Gly Lys Pro Glu  
 50 55 60  
 Asp Leu Val Glu Gly Val Arg Arg Gly Val Asp Met Phe Asp Cys Val  
 65 70 75 80  
 Met Pro Thr Arg Asn Ala Arg Asn Gly His Leu Phe Ile Asp Thr Gly  
 85 90 95  
 Val Leu Lys Ile Arg Asn Ala  
 100

<210> 605  
 <211> 428  
 <212> DNA  
 <213> Homo sapiens

<400> 605  
 acgcgttcac gatagggtag ttgcctatct caacgcggtc ggtattttcc tgcacaacaa  
 60  
 actggcccaa ggctgggcta tagtcaggtg catagtactt ggtgaagtag cgtacgtccg  
 120  
 caccacatc acatttcagt accttggtta tcttcaatcg gaaaaaaga ttggagtaaa  
 180  
 tgttgagttt tggtaatggc aacgccgttt gactggaaga gttttggaag gtaatgaccg  
 240  
 attcccagtg caaagggtccc catgctacat cctgcgacaa tgaggccggt agcacgttta  
 300  
 ttgcctcgct gctttgccga acgccaacct ctgtaccgat acgtgatac tgattgttga  
 360  
 tggatataggc ttgcgccagg taggtataat tggtaattc gtccatggca atgcgcagtg  
 420  
 aagtcttg  
 428

<210> 606  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 606  
 Met Asp Glu Leu Thr Asn Tyr Thr Tyr Leu Ala Gln Ala Tyr Thr Ile  
 1 5 10 15  
 Asn Asn Gln Tyr Gln Arg Ile Gly Thr Glu Val Gly Val Arg Gln Ser  
 20 25 30  
 Ser Glu Ala Ile Asn Val Leu Thr Ala Ser Leu Ser Gln Asp Val Ala

```

      35              40              45
Trp Gly Pro Leu His Trp Glu Ser Val Ile Thr Phe Gln Asn Ser Ser
  50              55              60
Ser Gln Thr Ala Leu Pro Leu Pro Lys Leu Asn Ile Tyr Ser Asn Leu
65              70              75              80
Phe Phe Arg Leu Lys Ile Ala Lys Val Leu Lys Cys Asp Val Gly Ala
      85              90              95
Asp Val Arg Tyr Phe Thr Lys Tyr Tyr Ala Pro Asp Tyr Ser Pro Ala
      100              105              110
Leu Gly Gln Phe Val Val Gln Glu Asn Thr Asp Arg Val Glu Ile Gly
      115              120              125
Asn Tyr Pro Ile Val Asn Ala
      130              135

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<210> 607  
 <211> 366  
 <212> DNA  
 <213> Homo sapiens

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<400> 607
gatcacgatg aattgtgggc gtacacgtac gagaatgtga tggcgctaaa cttgccgcct
60
gacattgtgt gtaaaggatt ctttagaaaa ttggaaaacg tagtgaccgg agtcaatttg
120
gttttcaacg gcaaacatta tcaaattgta aagaaagagg atgacctatt caaattgacc
180
aaaagcaatt gttacaagtt gagcaacata aaatttaaca attggaaata cttgtacttg
240
acaacgcacg gtgtgtacaa cgtgttcacc aacagctttc attcgagctg tccatttttg
300
ttgggcacca cgttgccgca gacattcaag aagcccaccg acgaaaagta tttgcccag
360
gacgcg
366

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<210> 608  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

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<400> 608
Asp His Asp Glu Leu Trp Ala Tyr Thr Tyr Glu Asn Val Met Ala Leu
1              5              10              15
Asn Leu Pro Pro Asp Ile Val Cys Lys Gly Phe Phe Arg Lys Leu Glu
      20              25              30
Asn Val Val Thr Gly Val Asn Leu Val Phe Asn Gly Lys His Tyr Gln
      35              40              45
Ile Val Lys Lys Glu Asp Asp Leu Phe Lys Leu Thr Lys Ser Asn Cys
      50              55              60
Tyr Lys Leu Ser Asn Ile Lys Phe Asn Asn Trp Lys Tyr Leu Tyr Leu
65              70              75              80
Thr Thr His Gly Val Tyr Asn Val Phe Thr Asn Ser Phe His Ser Ser
      85              90              95
Cys Pro Phe Leu Leu Gly Thr Thr Leu Pro Gln Thr Phe Lys Lys Pro

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100 105 110  
 Thr Asp Glu Lys Tyr Leu Pro Glu Asp Ala  
 115 120

<210> 609  
 <211> 291  
 <212> DNA  
 <213> Homo sapiens

<400> 609  
 nacgcgttat gacacggcct cctccaaggt cagtgtcatc gagtcacgta actcgtcggg  
 60  
 tgggtcgggtt ggaacgagtc cgtcatgagc cgggtcgcca tggacgactc cagcagtcgg  
 120  
 taccacgcct ggaagcagga ccccccacgcg acggaatcgc cggcttccaa gtcgtcgccc  
 180  
 ccgaagcctc aaacttcccc cgccccgtac gccgggcccgg ctccgaagac accggccaca  
 240  
 cctggaccat ctggggcggg ggcgcgcggc tgggtggtggc ggggtggagcc g  
 291

<210> 610  
 <211> 69  
 <212> PRT  
 <213> Homo sapiens

<400> 610  
 Met Ser Pro Val Ala Met Asp Asp Ser Ser Ser Pro Tyr Pro Ala Trp  
 1 5 10 15  
 Lys Gln Asp Pro His Ala Thr Glu Ser Pro Ala Ser Lys Ser Ser Pro  
 20 25 30  
 Pro Lys Pro Gln Thr Ser Pro Ala Pro Tyr Ala Gly Pro Ala Pro Lys  
 35 40 45  
 Thr Pro Ala Thr Pro Gly Pro Ser Gly Ala Gly Ala Pro Pro Trp Trp  
 50 55 60  
 Trp Arg Val Glu Pro  
 65

<210> 611  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<400> 611  
 nnnatcttgt gtcgattttc ggtcgcatac actatggggg agtattgtat aatgcggcgg  
 60  
 tgtacccaag tagagaggtg ttcgatgcca cacagtccgg aagaaaagaa gcaagcactg  
 120  
 acgcgcacaa ggcgcaccaa aggtcaggta ggcactcttg agcaagcgct tgatgcaggc  
 180  
 gcgaaatgtc ctgcaattct tcagcagctt gcggccgttc gtggcgagc caacggattg  
 240  
 atggcaacgg ttctggagag ctatctgcgg gaagagtctt ccagtagcga aatcaggagc  
 300

gattcgcaga acaagtccat tgacgagacc atctctatcg tccgctccta tctgcggtag  
 360  
 aggcaccagg gtgtcctcgg tgagggcaaa ttt  
 393

<210> 612  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 612  
 Xaa Ile Leu Cys Arg Phe Ser Val Ala Tyr Thr Met Gly Glu Tyr Cys  
 1 5 10 15  
 Ile Met Arg Arg Cys Thr Gln Val Glu Arg Cys Ser Met Pro His Ser  
 20 25 30  
 Pro Glu Glu Lys Lys Gln Ala Leu Thr Arg Ile Arg Arg Ile Lys Gly  
 35 40 45  
 Gln Val Ala Thr Leu Glu Gln Ala Leu Asp Ala Gly Ala Lys Cys Pro  
 50 55 60  
 Ala Ile Leu Gln Gln Leu Ala Ala Val Arg Gly Ala Val Asn Gly Leu  
 65 70 75 80  
 Met Ala Thr Val Leu Glu Ser Tyr Leu Arg Glu Glu Phe Pro Ser Ser  
 85 90 95  
 Glu Ile Arg Ser Asp Ser Gln Asn Lys Ser Ile Asp Glu Thr Ile Ser  
 100 105 110  
 Ile Val Arg Ser Tyr Leu Arg  
 115

<210> 613  
 <211> 567  
 <212> DNA  
 <213> Homo sapiens

<400> 613  
 gaaaatgctc ctggcgccctc agggaaggctc cttctcaaag aaaaggatgg ggctgaatcg  
 60  
 ctggaaacgg ttcaacaagga agccgagctcc caagcctact tttggtcctg acagtgtgga  
 120  
 aacttgata aagagagtgg agaaagcctc agagtttgca gtgtcaaatg cattttttac  
 180  
 tagaaattca gatttaccta gaagtccttg gggccaaatc acagatttga aaacatctga  
 240  
 gcaaatagag gatcatgatg aaatctatgc agaagctcag gagctgggtca atgactgggt  
 300  
 agacacaaaa cttaagcaag aattagcaag tgaggaagaa ggtgatgcta aaaacactgt  
 360  
 gtcaagtgtc actattatgc cggaagccaa tggccatttg aaatatgaca agttttagta  
 420  
 tttatgtggc tatttggagg aagaagagga aagtaccacc gttcaaaaat ttatagacca  
 480  
 tctgctccat aaaaatgtgg tagattctgc aatgatggaa gatcttggaa ggaagggaaa  
 540  
 ccaagacaag aagcagcaga aggatcc  
 567

<210> 614  
 <211> 187  
 <212> PRT  
 <213> Homo sapiens

<400> 614  
 Met Leu Leu Ala Pro Gln Gly Arg Ser Phe Ser Lys Lys Arg Met Gly  
 1 5 10 15  
 Leu Asn Arg Trp Lys Arg Phe Thr Arg Lys Pro Ser Pro Lys Pro Thr  
 20 25 30  
 Phe Gly Pro Asp Ser Val Glu His Trp Ile Lys Arg Val Glu Lys Ala  
 35 40 45  
 Ser Glu Phe Ala Val Ser Asn Ala Phe Phe Thr Arg Asn Ser Asp Leu  
 50 55 60  
 Pro Arg Ser Pro Trp Gly Gln Ile Thr Asp Leu Lys Thr Ser Glu Gln  
 65 70 75 80  
 Ile Glu Asp His Asp Glu Ile Tyr Ala Glu Ala Gln Glu Leu Val Asn  
 85 90 95  
 Asp Trp Leu Asp Thr Lys Leu Lys Gln Glu Leu Ala Ser Glu Glu Glu  
 100 105 110  
 Gly Asp Ala Lys Asn Thr Val Ser Ser Val Thr Ile Met Pro Glu Ala  
 115 120 125  
 Asn Gly His Leu Lys Tyr Asp Lys Phe Asp Asp Leu Cys Gly Tyr Leu  
 130 135 140  
 Glu Glu Glu Glu Glu Ser Thr Thr Val Gln Lys Phe Ile Asp His Leu  
 145 150 155 160  
 Leu His Lys Asn Val Val Asp Ser Ala Met Met Glu Asp Leu Gly Arg  
 165 170 175  
 Lys Glu Asn Gln Asp Lys Lys Gln Gln Lys Asp  
 180 185

<210> 615  
 <211> 685  
 <212> DNA  
 <213> Homo sapiens

<400> 615  
 nnacgcgtgc tgcctaagt gacggattcc atgtcgggtgc gagtcgggtc ggggccgatg  
 60  
 ggccatgaac gggccctagc gagggccgga ctgcggccccg tggccggatg cgacgaggcg  
 120  
 gggcgggggcg cgtgtgcagg gccattggtg gccgcagctg tcattcttga tgatcgcaga  
 180  
 tccggcagga ttgcggggct agcagattcc aagacactat ctgcggccaa gagagaggcc  
 240  
 ctgtttaacg tcatcatgga taaagctttg gcagtgtcgt ggggtacgtgt agaagccgac  
 300  
 gaatgcgatc gggtggggat gcaggaggca gatatcagcg gcttgaggcg tgccgtggtg  
 360  
 aggctgggag ttgaaccggg ctacgtgctg tcggacgggt tcccggtcga cggactgacg  
 420  
 gttccccgatc tgggaatgtg gaagggcgat tcagtgtgtg cgtgtgtggc agctgcctcc  
 480



atcgtggcca aagtggccag ggatcgcatc atgatcgcta tggacgccga gattcctggt  
 540  
 tacgattttg cgggtgcacaa ggggtacgag acagccttac accagcgctcg tctgaaggag  
 600  
 ttaggaccgt ctcgtcagca ccggatgagc tacgccaatg tgcgacgagc ggctaggctt  
 660  
 cattcatcat gagtgccgaa gatct  
 685

<210> 616  
 <211> 213  
 <212> PRT  
 <213> Homo sapiens

<400> 616  
 Met Ser Val Arg Val Gly Ser Gly Pro Met Gly His Glu Arg Ala Leu  
 1 5 10 15  
 Ala Arg Ala Gly Leu Gly Pro Val Ala Gly Cys Asp Glu Ala Gly Arg  
 20 25 30  
 Gly Ala Cys Ala Gly Pro Leu Val Ala Ala Ala Val Ile Leu Asp Asp  
 35 40 45  
 Arg Arg Ser Gly Arg Ile Ala Gly Leu Ala Asp Ser Lys Thr Leu Ser  
 50 55 60  
 Ala Ala Lys Arg Glu Ala Leu Phe Asn Val Ile Met Asp Lys Ala Leu  
 65 70 75 80  
 Ala Val Ser Trp Val Arg Val Glu Ala Asp Glu Cys Asp Arg Leu Gly  
 85 90 95  
 Met Gln Glu Ala Asp Ile Ser Gly Leu Arg Arg Ala Val Val Arg Leu  
 100 105 110  
 Gly Val Glu Pro Gly Tyr Val Leu Ser Asp Gly Phe Pro Val Asp Gly  
 115 120 125  
 Leu Thr Val Pro Asp Leu Gly Met Trp Lys Gly Asp Ser Val Cys Ala  
 130 135 140  
 Cys Val Ala Ala Ala Ser Ile Val Ala Lys Val Ala Arg Asp Arg Ile  
 145 150 155 160  
 Met Ile Ala Met Asp Ala Glu Ile Pro Gly Tyr Asp Phe Ala Val His  
 165 170 175  
 Lys Gly Tyr Ala Thr Ala Leu His Gln Arg Arg Leu Lys Glu Leu Gly  
 180 185 190  
 Pro Ser Arg Gln His Arg Met Ser Tyr Ala Asn Val Arg Arg Ala Ala  
 195 200 205  
 Arg Leu His Ser Ser  
 210

<210> 617  
 <211> 337  
 <212> DNA  
 <213> Homo sapiens

<400> 617  
 nncacctgtt tggctcgggg cactcgcgga tcattggtcga ggaaatgtgg ccgcgctacg  
 60  
 gctcgtttcc cggttcaac cccatcgctg agctgctgct gtcgttccac aacctcgctg  
 120

tcggcgccaa cggccagcgc caggccatgt tcttcgaaaa cgtttcgggc cttcccggag  
 180  
 cgaatcctcc gaaacttcga cctgtcccaa caagactctg cactcgtgat ttcacaaagc  
 240  
 gctgcaacgt cgtgccaatc gagatggcgc aggagttcca gcgtcgcggc gtccgcgtcg  
 300  
 tctcgatcat ctgcgtggcg cactcgcagg cgtcgac  
 337

<210> 618

<211> 112

<212> PRT

<213> Homo sapiens

<400> 618

Xaa	Thr	Cys	Leu	Ala	Arg	Gly	Thr	Arg	Gly	Ser	Trp	Ser	Arg	Lys	Cys
1				5					10					15	
Gly	Arg	Ala	Thr	Ala	Arg	Phe	Pro	Ala	Ser	Thr	Pro	Ser	Ser	Ser	Cys
			20					25					30		
Arg	Cys	Arg	Ser	Thr	Thr	Ser	Ser	Ser	Ala	Pro	Thr	Ala	Ser	Ala	Arg
			35				40					45			
Pro	Cys	Ser	Ser	Lys	Thr	Phe	Pro	Ala	Phe	Pro	Glu	Arg	Ile	Leu	Arg
			50			55					60				
Asn	Phe	Asp	Leu	Ser	Gln	Gln	Asp	Ser	Ala	Leu	Val	Ile	Ser	Ser	Ser
65					70					75				80	
Ala	Ala	Thr	Ser	Cys	Gln	Ser	Arg	Trp	Pro	Arg	Ser	Ser	Ser	Val	Ala
				85					90				95		
Ala	Ser	Ala	Ser	Ser	Arg	Ser	Ser	Arg	Trp	Arg	Thr	Arg	Arg	Arg	Arg
			100					105					110		

<210> 619

<211> 425

<212> DNA

<213> Homo sapiens

<400> 619

acgcgttttt tatgccgatc ttatgctcta acctagaaac aatatcagct acaaacctaa  
 60  
 tagctataag ataatatctg aaagcatcaa taggagtttt gatcatttcc gcatacctaa  
 120  
 gttttatagc atctttgtca gaaggcaaac ctgccaaacc agatgaatcg atgccactct  
 180  
 caaacttgct caaatgttca attaaatcat ccaagttgtg gccatgctta ccgcttccag  
 240  
 attttgaatg aatcattact ttaattgatt tttcaatcgc taaatggaat tcccagcaag  
 300  
 caatagaagc ccgctcattt ttaaagctca gtatgtcact aatgcctttt tcgaagtggc  
 360  
 tccatattcc ctgcgccata ttagaagctg actgggttga atggcttgcc atgttcaa  
 420  
 ctaga  
 425

<210> 620

<211> 137  
 <212> PRT  
 <213> Homo sapiens

<400> 620  
 Met Ala Ser His Ser Asn Gln Ser Ala Ser Asn Met Ala Gln Gly Ile  
   1                  5                  10                  15  
 Trp Ser His Phe Glu Lys Gly Ile Ser Asp Ile Leu Ser Phe Lys Asn  
                   20                  25                  30  
 Glu Arg Ala Ser Ile Ala Cys Trp Glu Phe His Leu Ala Ile Glu Lys  
                   35                  40                  45  
 Ser Ile Lys Val Met Ile His Ser Lys Ser Gly Ser Gly Lys His Gly  
                   50                  55                  60  
 His Asn Leu Asp Asp Leu Ile Glu His Leu Ser Lys Phe Glu Ser Gly  
 65                  70                  75                  80  
 Ile Asp Ser Ser Gly Leu Ala Gly Leu Pro Ser Asp Lys Asp Ala Ile  
                   85                  90                  95  
 Lys Leu Arg Tyr Ala Glu Met Ile Lys Thr Pro Ile Asp Ala Phe Glu  
                   100                  105                  110  
 Tyr Tyr Leu Ile Ala Ile Arg Phe Val Ala Asp Ile Val Ser Arg Leu  
                   115                  120                  125  
 Glu His Lys Ile Gly Ile Lys Asn Ala  
                   130                  135

<210> 621  
 <211> 453  
 <212> DNA  
 <213> Homo sapiens

<400> 621  
 cccggcaagg gagccatctt gacgaatatg tccttggtggt ggttcgacca attggccgac  
 60  
 atcgctcgata accatctcgt gagcgtggat gtccccgccg aggtcgcagg gcgcgccatg  
 120  
 gtcgttgagg aactcgacat gttccccggtc gaatgcgtcg tgcgggggcta cctcaccggt  
 180  
 tcagggtggg ccgaatatca gcgcaaccag gccgtgtgcy gaatccgcct tcccaggggg  
 240  
 ctgcagaatg ggtccccggt cgaagagccc attttcaccc cggcaattaa ggccccgcag  
 300  
 ggagaacatg acgagaacat cgactatcta cgcttgtag aactcgtcgg tccngatgn  
 360  
 tcagcgcagc tgcgtgacct ttcgctgcgg gtctaccagc gtgcagagga gatcgtcgg  
 420  
 aagcgaggca tcctcctggc ggataccaag ctt  
 453

<210> 622  
 <211> 151  
 <212> PRT  
 <213> Homo sapiens

<400> 622  
 Pro Gly Lys Gly Ala Ile Leu Thr Asn Met Ser Leu Trp Trp Phe Asp

```

      1           5           10           15
Gln Leu Ala Asp Ile Val Asp Asn His Leu Val Ser Val Asp Val Pro
      20           25           30
Ala Glu Val Ala Gly Arg Ala Met Val Val Glu Glu Leu Asp Met Phe
      35           40           45
Pro Val Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Trp Ala
      50           55           60
Glu Tyr Gln Arg Asn Gln Ala Val Cys Gly Ile Arg Leu Pro Glu Gly
65           70           75           80
Leu Gln Asn Gly Ser Arg Leu Glu Glu Pro Ile Phe Thr Pro Ala Ile
      85           90           95
Lys Ala Pro Gln Gly Glu His Asp Glu Asn Ile Asp Tyr Leu Arg Leu
      100          105          110
Val Glu Leu Val Gly Pro Xaa Xaa Ser Ala Gln Leu His Asp Leu Ser
      115          120          125
Leu Arg Val Tyr Gln Arg Ala Glu Glu Ile Ala Arg Lys Arg Gly Ile
      130          135          140
Leu Leu Ala Asp Thr Lys Leu
145          150

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<210> 623  
 <211> 345  
 <212> DNA  
 <213> Homo sapiens

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<400> 623
acgcgtccag tatgtccacg gaggacatgc ttgacctcga ctcgaacgtc tcctactacg
60
cgaggaacta tcaggccgcg caatcagttg tggcgaaatt cgacgcgggc accattgccc
120
aagccgaaga cctgccacct gacgacaccc acacgggggc ggaactggta aagagcgtgg
180
tcaacagcat cacctgtgtg tcaccctgtg acatcgaaga tttcaccacc atagagatcc
240
aggggctggg actgcaactgt gtcaggctct gggcgctgg gctgctcgcc ctgtcactgc
300
ccagcgcacc catgcgggca caccctcgct acgccgcata tggcg
345

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<210> 624  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

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<400> 624
Met Ser Thr Glu Asp Met Leu Asp Leu Asp Ser Asn Val Ser Tyr Tyr
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Leu Asp Ser Lys Ile Leu Ala Leu His Asn Met Val Gln Phe Ser His
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Ser Lys Asp Phe Gln Lys Val Asn Arg Ser Val Phe Ser Gly Val Leu
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Cys Pro Phe Cys Pro Arg Gly Leu Cys Ser Pro Glu Lys His Leu Gly
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Val Leu Leu Phe His Tyr Glu Ser Val His Glu Ser Gln Ala Ser Asp
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Val Lys Gln Glu Ala Asn His Leu Gln Gly Ser Asp Gly Gln Gln Ser

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      35           40           45
Thr Leu Pro Gly Arg Asn Trp Ile Asn Leu Gly Leu Leu Val Val Ile
      50           55           60
Ile Ala Cys Gly Ile Trp Phe Ser Asn Val Ser Gly Gly Ile Ala Trp
      65           70           75           80
Leu Pro Leu Ala Leu Leu Thr Leu Ala Ser Leu Phe Leu Gly Phe His
      85           90           95
Phe Val Ala Ala Ile Gly Gly Ala Asp Met Pro Val Val Ile Ser Met
      100           105           110
Leu Asn Ser Tyr Ser Gly Trp Ala Ala Ala Phe Ser Gly Phe Ser Leu
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His Ile Pro Val Leu Ile Val Thr Gly
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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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Glu Arg Asp Gln Tyr Lys Leu Met Ala Asn Gln Leu Arg Glu Arg His
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5340  
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5520  
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5640  
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5700  
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5760  
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5820  
cagcgatggc ggcccctatt agagaccagg tttgttaaaa caccaaata tgcgtgccac  
5880  
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6000  
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6600  
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6660

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 6780  
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 6900  
 aaaaaaaaaa aaaaaaag  
 6918

<210> 636

<211> 619

<212> PRT

<213> Homo sapiens

<400> 636

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Val	Val	Leu	Asp	Phe	Ser	Ala	Asp	Ala	Thr	Glu	Gly	Pro	Ile	Arg	Ala
		20					25					30			
Tyr	Leu	Leu	Asp	Val	Val	Asp	Ser	Glu	Glu	Gln	Asp	Met	Ala	Leu	Asn
		35				40					45				
Ile	His	Ala	Phe	Ser	Ala	Gly	Leu	Gly	Gly	Ala	Ile	Gly	Tyr	Val	Leu
	50					55				60					
Gly	Gly	Leu	Asp	Trp	Thr	Gln	Thr	Phe	Leu	Gly	Ser	Trp	Phe	Arg	Thr
65				70					75					80	
Gln	Asn	Gln	Val	Leu	Phe	Phe	Phe	Ala	Ala	Ile	Ile	Phe	Thr	Val	Ser
			85					90						95	
Val	Ala	Leu	His	Leu	Phe	Ser	Ile	Asp	Glu	Glu	Gln	Tyr	Ser	Pro	Gln
			100					105					110		
Gln	Glu	Arg	Ser	Ala	Glu	Glu	Pro	Gly	Ala	Leu	Asp	Gly	Gly	Glu	Pro
		115					120					125			
His	Gly	Val	Pro	Ala	Phe	Pro	Asp	Glu	Val	Gln	Ser	Glu	His	Glu	Leu
	130					135						140			
Ala	Leu	Asp	Tyr	Pro	Asp	Val	Asp	Ile	Met	Arg	Ser	Lys	Ser	Asp	Ser
145				150						155				160	
Ala	Leu	His	Val	Pro	Asp	Thr	Ala	Leu	Asp	Leu	Glu	Pro	Glu	Leu	Leu
			165						170					175	
Phe	Leu	His	Asp	Ile	Glu	Pro	Ser	Ile	Phe	His	Asp	Ala	Ser	Tyr	Pro
		180						185					190		
Ala	Thr	Pro	Arg	Ser	Thr	Ser	Gln	Glu	Leu	Ala	Lys	Thr	Lys	Leu	Pro
		195					200						205		
Arg	Leu	Ala	Thr	Phe	Leu	Lys	Glu	Ala	Ala	Lys	Glu	Asp	Glu	Thr	Leu
	210					215						220			
Leu	Asp	Asn	His	Leu	Asn	Glu	Ala	Lys	Val	Pro	Asn	Gly	Ser	Gly	Ser
225				230						235				240	
Pro	Thr	Lys	Asp	Ala	Leu	Gly	Gly	Tyr	Thr	Arg	Val	Asp	Thr	Lys	Pro
			245						250					255	
Ser	Ala	Thr	Ser	Ser	Met	Arg	Arg	Arg	Arg	His	Ala	Phe	Arg	Arg	
		260					265						270		
Gln	Ala	Ser	Ser	Thr	Phe	Ser	Tyr	Tyr	Gly	Lys	Leu	Gly	Ser	His	Cys
	275						280					285			
Tyr	Arg	Tyr	Arg	Arg	Ala	Asn	Ala	Val	Val	Leu	Ile	Lys	Pro	Ser	Arg

```

      290              295              300
Ser Met Ser Asp Leu Tyr Asp Met Gln Lys Arg Gln Arg Gln His Arg
305              310              315              320
His Arg Asn Gln Ser Gly Ala Thr Thr Ser Ser Gly Asp Thr Glu Ser
      325              330              335
Glu Glu Gly Glu Gly Glu Thr Thr Val Arg Leu Leu Trp Leu Ser Met
      340              345              350
Leu Lys Met Pro Arg Glu Leu Met Arg Leu Cys Leu Cys His Leu Leu
      355              360              365
Thr Trp Phe Ser Val Ile Ala Glu Ala Val Phe Tyr Thr Asp Phe Met
      370              375              380
Gly Gln Val Ile Phe Glu Gly Asp Pro Lys Ala Pro Ser Asn Ser Thr
385              390              395              400
Ala Trp Gln Ala Tyr Asn Ala Gly Val Lys Met Gly Cys Trp Gly Leu
      405              410              415
Val Ile Tyr Ala Ala Thr Gly Ala Ile Cys Ser Ala Leu Leu Gln Lys
      420              425              430
Tyr Leu Asp Asn Tyr Asp Leu Ser Val Arg Val Ile Tyr Val Leu Gly
      435              440              445
Thr Leu Gly Phe Ser Val Gly Thr Ala Val Met Ala Met Phe Pro Asn
      450              455              460
Val Tyr Val Ala Met Val Thr Ile Ser Thr Met Gly Ile Val Ser Met
465              470              475              480
Ser Ile Ser Tyr Cys Pro Tyr Ala Leu Leu Gly Gln Tyr His Asp Ile
      485              490              495
Lys Gln Tyr Ile His His Ser Pro Gly Asn Ser Lys Arg Gly Phe Gly
      500              505              510
Ile Asp Cys Ala Ile Leu Ser Cys Gln Val Tyr Ile Ser Gln Ile Leu
      515              520              525
Val Ala Ser Ala Leu Gly Gly Val Val Asp Ala Val Gly Thr Val Arg
      530              535              540
Val Ile Pro Met Val Ala Ser Val Gly Ser Phe Leu Gly Phe Leu Thr
545              550              555              560
Ala Thr Phe Leu Val Ile Tyr Pro Asp Val Ser Glu Glu Ala Lys Glu
      565              570              575
Glu Gln Lys Gly Leu Ser Ser Pro Leu Ala Gly Glu Gly Arg Ala Gly
      580              585              590
Gly Asn Ser Glu Lys Pro Thr Val Leu Lys Leu Thr Arg Lys Glu Gly
      595              600              605
Leu Gln Gly Pro Val Glu Thr Glu Ser Val Val
      610              615

```

&lt;210&gt; 637

&lt;211&gt; 370

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 637

```

ngaaaaacag gatgaatccc gtatcattct taagcccgaa aagtactgaa tgtcgtcttc
60
tctcgatcgg tgatgatctg gaaaggaaaa atcatcgtga ctactacatc acccgctact
120
acgcaaagac cgtcagttgg caggaaagtt gggttctggt cccttaatcc atggtggttt
180

```

tgtaggcctt tattatTTTT cggaatgggt cggtttattg cgattccagt attcctcact  
 240  
 gtgccgaata tcattaatat cggaatccaa gccgcgggtg tggcgattat ggccttcggt  
 300  
 atgaccttcg tcacgttac ctccggcatt gatttgtctg tgggttcggt cgcagctctt  
 360  
 tcagccatgg  
 370

<210> 638  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 638  
 Met Ile Trp Lys Gly Lys Ile Ile Val Thr Thr Thr Ser Pro Ala Thr  
 1 5 10 15  
 Thr Gln Arg Pro Ser Val Gly Arg Lys Val Gly Ser Trp Ser Leu Asn  
 20 25 30  
 Pro Trp Cys Phe Cys Arg Pro Leu Leu Phe Phe Gly Met Val Arg Phe  
 35 40 45  
 Ile Ala Ile Pro Val Phe Leu Thr Val Pro Asn Ile Ile Asn Ile Gly  
 50 55 60  
 Ile Gln Ala Ala Val Val Ala Ile Met Ala Phe Gly Met Thr Phe Val  
 65 70 75 80  
 Ile Val Thr Ser Gly Ile Asp Leu Ser Val Gly Ser Val Ala Ala Leu  
 85 90 95  
 Ser Ala Met

<210> 639  
 <211> 330  
 <212> DNA  
 <213> Homo sapiens

<400> 639  
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 gactcccagt ccgctgagtc gcgtcatgac atgggtggcg acatcatccc gagattcgtc  
 120  
 gaggccgggg acgcgcaggt ctacgacttc tgtgacaacc aggtgcccg aaccaccgag  
 180  
 aaggatcggg actactggcg ggacgtggga actatcgatg cctaccacga cgcgcacatg  
 240  
 gacctcgtgt cgggtggaacc ggagttcaac ctctacaacc ccgactggcc gatctggagc  
 300  
 atccaggaac aggcaccggg agcgaaattt  
 330

<210> 640  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens



&lt;400&gt; 640

Xaa Ala Ser Met Gly Asn Tyr Ile Phe Ser Arg Asp Ala Leu Val Glu  
 1 5 10 15  
 Ala Leu Phe Ala Asp Ser Gln Ser Ala Glu Ser Arg His Asp Met Gly  
 20 25 30  
 Gly Asp Ile Ile Pro Arg Phe Val Glu Ala Gly Asp Ala Gln Val Tyr  
 35 40 45  
 Asp Phe Cys Asp Asn Gln Val Pro Gly Thr Thr Glu Lys Asp Arg Asp  
 50 55 60  
 Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Tyr His Asp Ala His Met  
 65 70 75 80  
 Asp Leu Val Ser Val Glu Pro Glu Phe Asn Leu Tyr Asn Pro Asp Trp  
 85 90 95  
 Pro Ile Trp Ser Ile Gln Glu Gln Ala Pro Gly Ala Lys Phe  
 100 105 110

&lt;210&gt; 641

&lt;211&gt; 491

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 641

cgcgtgaccg gcgcggagaa cgtgcgcaag atcctcatgg gcgagcacca cctcgtgagc  
 60  
 accgagtggc ctgcagcac ccgcatgttg ctgggccccca acacggtgtc caattccatt  
 120  
 ggcgacatcc accgcaacaa gcgcaaggctc ttctccaaga tcttcagcca cgaggccctg  
 180  
 gagagttacc tgcccaagat ccagctgggtg atccaggaca cactgcgcgc ctggagcagc  
 240  
 caccgaggg ccataacgt gtaccaggag gcgcagaagc tgaccttccg catggccatc  
 300  
 cgggtgctgc tgggcttcag catccctgag gaggaccttg ggcacctctt tgaggtctac  
 360  
 cagcagtttg tggacaatgt cttctccctg cctgtcgacc tgcccttcag tggctaccgg  
 420  
 cggggcattc aggctcggca gatcctgcag aaggggctgg agaaggccat ccgggagaag  
 480  
 ctgcagtga c  
 491

&lt;210&gt; 642

&lt;211&gt; 163

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 642

Arg Val Thr Gly Ala Glu Asn Val Arg Lys Ile Leu Met Gly Glu His  
 1 5 10 15  
 His Leu Val Ser Thr Glu Trp Pro Arg Ser Thr Arg Met Leu Leu Gly  
 20 25 30  
 Pro Asn Thr Val Ser Asn Ser Ile Gly Asp Ile His Arg Asn Lys Arg  
 35 40 45  
 Lys Val Phe Ser Lys Ile Phe Ser His Glu Ala Leu Glu Ser Tyr Leu

```

      50              55              60
Pro Lys Ile Gln Leu Val Ile Gln Asp Thr Leu Arg Ala Trp Ser Ser
65              70              75              80
His Pro Glu Ala Ile Asn Val Tyr Gln Glu Ala Gln Lys Leu Thr Phe
      85              90              95
Arg Met Ala Ile Arg Val Leu Leu Gly Phe Ser Ile Pro Glu Glu Asp
      100              105              110
Leu Gly His Leu Phe Glu Val Tyr Gln Gln Phe Val Asp Asn Val Phe
      115              120              125
Ser Leu Pro Val Asp Leu Pro Phe Ser Gly Tyr Arg Arg Gly Ile Gln
      130              135              140
Ala Arg Gln Ile Leu Gln Lys Gly Leu Glu Lys Ala Ile Arg Glu Lys
145              150              155              160
Leu Gln Cys

```

<210> 643  
 <211> 628  
 <212> DNA  
 <213> Homo sapiens

```

<400> 643
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gccatcacgc tgcgggaagg ccagtatgtg gaggtcctgg atgcagccca cccactgcgc
120
tggcttgtec gcaccaagcc caccaagtcc agcccctcac ggcagggctg ggtgtcacca
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gcctacctgg acaggaggct caagctgtca cctgagtggg gggccgctga ggcccctgag
240
ttccctgggg aggctgtgtc tgaagacgaa tacaaggcaa ggctgagctc tgtgatccag
300
gagctgctga gttctgagca ggccttcgtg gaggagctgc agttcctgca gagccaccac
360
ctgcagcacc tggagcgctg cccccacgtg cccatagctg tggccggcca gaaggcagtc
420
atcttccgca atgtgcggga catcgccgc ttccacagca gcttctgca ggagttgcag
480
cagtgcgaca cggacgacga cgtggccatg tgcttcatca agaaccaggc ggcctttgag
540
cagtacctgg agttcctggt gggacgtgtg caggctgagt cggtggtcgt cagcacggcc
600
atccaggagt tctacaagaa atacgct
628

```

<210> 644  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

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<400> 644
Xaa Ile Phe Asp Ile Tyr Val Val Thr Ala Asp Tyr Leu Pro Leu Gly
1              5              10              15
Ala Glu Gln Asp Ala Ile Thr Leu Arg Glu Gly Gln Tyr Val Glu Val

```



```

      1           5           10           15
Arg Ser Leu Cys His Pro Phe Trp Asn Pro Leu Ile Trp Lys Ile Trp
      20           25           30
Gly Ser Val Leu Phe Arg Arg Tyr Trp Arg His Trp Leu Asp Ile Leu
      35           40           45
Gln Pro Ser Gln Glu Ala Gln Lys Val Asp Val Ile Thr Thr Pro Ile
      50           55           60
Phe Gln Met Lys Lys Leu Ser Leu Trp Asp Leu Arg Lys Leu Pro Glu
      65           70           75           80
Leu Glu Gln Leu Val Pro Gly Pro Tyr Thr His Ser Thr Val Ser
      85           90           95

```

&lt;210&gt; 647

&lt;211&gt; 421

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 647

```

acgcgttttcg gttcttgagc gcttccacca attcagcggg ggtgagcggc ccctgtgcat
60
cgcgacgacg ggtgatcaga taggcgatat cgcctcgtt cagttgcacg gtgtcggtat
120
cggtagccat gcgtggcgaa ctcctttggc atgggaaaat cgggtgaggc caacgggcac
180
agcaacagga cgtgtccctt gcggcacgtg gcaacacgtc agtatagcgc gtttccgccg
240
ggatttccgt tgaatgaagg caagaagtcg ggcacgcac cactgtctac cgctcggtgg
300
tacgatagcc gcggcgccac caggttggtt acattccaaa cgcaacgcag gaaccgcac
360
gaacagcgtt ttctgcaaca aacccttat gacgttggtt ctcgggcatt tcagtgtcga
420

```

c

421

&lt;210&gt; 648

&lt;211&gt; 90

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 648

```

Met Gly Lys Ser Gly Glu Ala Asn Gly His Ser Asn Arg Thr Cys Pro
      1           5           10           15
Leu Arg His Val Ala Thr Arg Gln Tyr Ser Ala Phe Pro Pro Gly Phe
      20           25           30
Pro Leu Asn Glu Gly Lys Lys Ser Gly Thr His Pro Pro Ala Thr Ala
      35           40           45
Arg Trp Tyr Asp Ser Arg Gly Ala Thr Arg Leu Ala Thr Phe Gln Thr
      50           55           60
Gln Arg Arg Asn Pro His Glu Gln Arg Phe Ser Gln Gln Thr Pro Tyr
      65           70           75           80
Asp Ala Gly Ser Arg Ala Phe Gln Cys Arg
      85           90

```

<210> 649  
 <211> 563  
 <212> DNA  
 <213> Homo sapiens

<400> 649  
 cgcaacatgc ataaacacat gtgctcctcc gagactcagc tacttccttt gccctctctg  
 60  
 gacctcagtg tccaggcttg tgcatttagg ggctcagggt tgggctctgt gcctatgagc  
 120  
 cagtctatgt gtgcactgtc tgtctgtctg tccgtctgcc agcaaccttc aaggccccag  
 180  
 gaggggaagg caccaatgga aggtgggggc agggaaggag gtagcgttga caagttccaa  
 240  
 tgtctggctt tccctcctgg aaaccccgag ctggggctgg ccccccttc ccttcctgtc  
 300  
 tctctcgtc aagcacgtcc cttctaagag cccctctctg cagacgcccc cagtgaacc  
 360  
 aagcctagat tcgctgccaa gaaggccgac attttttaga cttgccacgt taaaggggac  
 420  
 tgacacaggca cgcactcaaa tccccccctc catgtcctcc gcctgtgcac attcaggcaa  
 480  
 cccgaaacac acaaagacac ggttggacac agcggccacc tgtgcacaca ggaggtagca  
 540  
 catggagcgc atctgacccc ggg  
 563

<210> 650  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 650  
 Met His Lys His Met Cys Ser Ser Glu Thr Gln Leu Leu Pro Leu Pro  
 1 5 10 15  
 Ser Leu Asp Leu Ser Val Gln Ala Cys Ala Phe Arg Gly Ser Gly Leu  
 20 25 30  
 Gly Ser Val Pro Met Ser Gln Ser Met Cys Ala Leu Ser Val Cys Leu  
 35 40 45  
 Ser Val Cys Gln Gln Pro Ser Arg Pro Gln Glu Gly Lys Ala Pro Met  
 50 55 60  
 Glu Gly Gly Gly Arg Glu Gly Gly Ser Val Asp Lys Phe Gln Cys Leu  
 65 70 75 80  
 Ala Phe Pro Pro Gly Asn Pro Glu Leu Gly Leu Ala Pro Pro Ser Leu  
 85 90 95  
 Pro Val Ser Leu Ala Gln Ala Arg Pro Phe  
 100 105

<210> 651  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 651

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 cataatggag tccatgggggt caaagttatc tcttgagct cagcagttga tggatatggt  
 120  
 taggtgtcag cagcggaatt gtattcccat tggagagcag cttcagtcgg tgttggggcaa  
 180  
 ttctggatac aagcatatga ttggactaca atcctcatct accttaggaa ccttaaacia  
 240  
 gtcgtcctcc acaccttttc cttttagaac tggattgaca tctgggaacg tgactgaaaa  
 300  
 cttacaagcg tacattgata aaagtacaca actgcctggg ggagagaatt c  
 351

<210> 652  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 652  
 Met Glu Ser Met Gly Ser Lys Leu Ser Pro Gly Ala Gln Gln Leu Met  
 1 5 10 15  
 Asp Met Val Arg Cys Gln Gln Arg Asn Cys Ile Pro Ile Gly Glu Gln  
 20 25 30  
 Leu Gln Ser Val Leu Gly Asn Ser Gly Tyr Lys His Met Ile Gly Leu  
 35 40 45  
 Gln Ser Ser Ser Thr Leu Gly Thr Leu Asn Lys Ser Ser Ser Thr Pro  
 50 55 60  
 Phe Pro Phe Arg Thr Gly Leu Thr Ser Gly Asn Val Thr Glu Asn Leu  
 65 70 75 80  
 Gln Ala Tyr Ile Asp Lys Ser Thr Gln Leu Pro Gly Gly Glu Asn  
 85 90 95

<210> 653  
 <211> 399  
 <212> DNA  
 <213> Homo sapiens

<400> 653  
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 60  
 caccggcgga aagctgttgc tatggcaact ctgtaccgca gcatggagac cacctgctca  
 120  
 cactcttctc ctggagaggg agcgagcccc caaatgttcc aactgtgtc ccaggggccc  
 180  
 cctctgccc gccctccctg tcgagtctct cctacaactc cacttaatgg gggtcctggc  
 240  
 tcccttcccc cagaaccacc ctcagtttcc caggcctttc ccactctagc aggccctggg  
 300  
 gggcttttcc cccaaggt tgetgaccca gtcccttctg ggggcagtag cagccccgt  
 360  
 ttctcccaa ggggcaatgc cccctctcca gccccacct  
 399

<210> 654

<211> 133  
 <212> PRT  
 <213> Homo sapiens

<400> 654  
 Xaa Pro Gly Gly Ala Gly Val Gly Pro Ala Ser Glu Glu Asp Met Thr  
 1 5 10 15  
 Lys Leu Cys Asn His Arg Arg Lys Ala Val Ala Met Ala Thr Leu Tyr  
 20 25 30  
 Arg Ser Met Glu Thr Thr Cys Ser His Ser Ser Pro Gly Glu Gly Ala  
 35 40 45  
 Ser Pro Gln Met Phe His Thr Val Ser Pro Gly Pro Pro Ser Ala Arg  
 50 55 60  
 Pro Pro Cys Arg Val Pro Pro Thr Thr Pro Leu Asn Gly Gly Pro Gly  
 65 70 75 80  
 Ser Leu Pro Pro Glu Pro Pro Ser Val Ser Gln Ala Phe Pro Thr Leu  
 85 90 95  
 Ala Gly Pro Gly Gly Leu Phe Pro Pro Arg Leu Ala Asp Pro Val Pro  
 100 105 110  
 Ser Gly Gly Ser Ser Ser Pro Arg Phe Leu Pro Arg Gly Asn Ala Pro  
 115 120 125  
 Ser Pro Ala Pro Pro  
 130

<210> 655  
 <211> 368  
 <212> DNA  
 <213> Homo sapiens

<400> 655  
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 60  
 gatgaggtgg gaagtgcact gggatctggg ggaagaagcc cggggttcaa gactcagcta  
 120  
 ctgactgcat ggtgtcaaag gattcgggca tcctctctga ggctgagtct tcagatgaca  
 180  
 gtgagaacag ggacacctgc cctgcccttc tcacggggcg tgtgggcacc catgagcatg  
 240  
 cttgacaaat gcaaggtgcc atacaaacag gaactgcaca atctcaccgc ccggcctact  
 300  
 cagcattggt atttttacct ttacatctat atgaagatgt agttccattc cttttaactg  
 360  
 ttgttttc  
 368

<210> 656  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 656  
 Met Ala Cys Val His His Val Glu Gln Pro Met Arg Arg Ile Gly Asp  
 1 5 10 15  
 Glu Val Gly Ser Ala Leu Gly Ser Gly Gly Arg Ser Pro Gly Phe Lys

```

                20                25                30
Thr  Gln  Leu  Leu  Thr  Ala  Trp  Cys  Gln  Arg  Ile  Arg  Ala  Ser  Ser  Leu
      35                40                45
Arg  Leu  Ser  Leu  Gln  Met  Thr  Val  Arg  Thr  Gly  Thr  Pro  Ala  Leu  Pro
      50                55                60
Phe  Ser  Arg  Gly  Val  Trp  Ala  Pro  Met  Ser  Met  Leu  Asp  Lys  Cys  Lys
65                70                75                80
Val  Pro  Tyr  Lys  Gln  Glu  Leu  His  Asn  Leu  Thr  Ala  Arg  Pro  Thr  Gln
      85                90                95
His  Cys  Tyr  Phe  Tyr  Leu  Tyr  Ile  Tyr  Met  Lys  Met
      100                105

```

&lt;210&gt; 657

&lt;211&gt; 330

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 657

```

gtcgaccacg gcatgaaaaa gccgggggatg atcctcatca acaaccctg gggcgagtc
60
aacgaggcgg gcttcaagcg cgccctcgaa gagcgtggca tggccaacgc cgggtgctgag
120
cgtattcagg acagcgacct ggacgtggtg ccgcaattga ccccgctga aaaacgccc
180
tgccgacacc ttgctgatgg tcggcaacgt cgcccttcg gcacaggtgg tcaagtcct
240
ggaccgcatg ggttgggacg tgctgtggt gtctcactgg gggccggccg gnggtcgctt
300
tggcgagctg gcggggccta acgcttctcg
330

```

&lt;210&gt; 658

&lt;211&gt; 102

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 658

```

Met  Lys  Lys  Pro  Gly  Met  Ile  Leu  Ile  Asn  Asn  Pro  Trp  Gly  Glu  Ser
  1                5                10                15
Asn  Glu  Ala  Gly  Phe  Lys  Arg  Ala  Leu  Glu  Glu  Arg  Gly  Met  Ala  Asn
      20                25                30
Ala  Gly  Val  Glu  Arg  Ile  Gln  Asp  Ser  Asp  Leu  Asp  Val  Val  Pro  Gln
      35                40                45
Leu  Thr  Pro  Pro  Glu  Lys  Arg  Arg  Cys  Arg  His  Leu  Ala  Asp  Gly  Arg
      50                55                60
Gln  Arg  Arg  Pro  Phe  Gly  Thr  Gly  Gly  Gln  Val  Pro  Gly  Pro  His  Gly
65                70                75                80
Leu  Gly  Arg  Ala  Cys  Gly  Val  Ser  Leu  Gly  Ala  Gly  Arg  Xaa  Ser  Leu
      85                90                95
Trp  Arg  Ala  Gly  Gly  Ala
      100

```

&lt;210&gt; 659

&lt;211&gt; 1505



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 659

```
gccaggatca tgtccaccac cacatgccaa gtggtggcgt tcctcctgtc catcctgggg
60
ctggccgget gcatecgggc caccgggatg gacatgtgga gcaccagga cctgtacgac
120
aaccctgtca cctccgtgtt ccagtacgaa gggctctgga ggagctgctg gaggcagagt
180
tcaggcttca ccgaatgcag gccctatttc accatcctgg gacttccagc catgctgcag
240
gcagtgcgag ccctgatgat cgtaggcatc gtctctgggtg ccattggcct cctggatatcc
300
atctttgccc tgaaatgcat ccgcattggc agcatggagg actctgccaa agccaacatg
360
acactgacct ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct
420
gtgtttgcc aatgctggt gactaacttc tggatgtcca cagctaacat gtacaccggc
480
atgggtggga tggtcagac tgttcagacc aggtacacat ttggtgcggc tctgttcgtg
540
ggctgggtcg ctggaggcct cacactaatt ggggtgtga tgatgtgcat cgctgccgg
600
ggcctggcac cagaagaaac caactacaaa gccgtttctt atcatgcctc aggccacagt
660
gttgccctaca agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaa
720
aagaagatat acgatggagg tgccgcaca gaggacgagg tacaatctta tccttccaag
780
cacgactatg tgtaatgtc taagacctc cagcacgggc ggaagaaact cccggagagc
840
tcacccaaaa aacaaggaga tccatctag atttcttctt gcttttgact cacagctgga
900
agttagaaaa gcctcgattt catctttgga gaggccaagt ggtcttagcc tcagtctctg
960
tctctaaata ttccaccata aaacagctga gttatttatg aattagaagc tatagctcac
1020
attttcaatc ctctatttct ttttttaaat ataactttct actctgatga gagaatgtgg
1080
ttttaatctc tctctcacat tttgatgatt tagacagact cccctcttc ctctagtca
1140
ataaacccat tgatgatcta tttccagct tatccccaag aaaacttttg aaaggaaaga
1200
gtagacccaa agatgttatt ttctgctgtt tgaattttgt ctccccaccc ccaacttggc
1260
tagtaataaa cacttactga agaagaagca ataagagaaa gatatttgta atctctccag
1320
ccatgatct cggttttctt aactgtgat cttaaaagt accaaaccaa agtcattttc
1380
agtttgaggc aaccaaactt ttctactgct gttgacatct tcttattaca gcaacaccat
1440
tctaggagtt tctgagctc tccactggag tcctccctct ctgctgtctt ctgcagcgg
1500
```

taccc  
1505

<210> 660  
<211> 261  
<212> PRT  
<213> Homo sapiens

<400> 660  
Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu  
1 5 10 15  
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr  
20 25 30  
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly  
35 40 45  
Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg  
50 55 60  
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg  
65 70 75 80  
Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val  
85 90 95  
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser  
100 105 110  
Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser  
115 120 125  
Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val  
130 135 140  
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly  
145 150 155 160  
Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe  
165 170 175  
Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met  
180 185 190  
Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala  
195 200 205  
Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly  
210 215 220  
Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile  
225 230 235 240  
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser  
245 250 255  
Lys His Asp Tyr Val  
260

<210> 661  
<211> 451  
<212> DNA  
<213> Homo sapiens

<400> 661  
nnacgcgtgt agtttgtgta tcggcgcgga actcgccgcg tctgatctcg aggagcttcc  
60  
cccatggacg agattttaac cttgcttgcc ggaggcggtg acgacgagcc agagtggcat  
120

gacaaggcat tatgtgcccc gactgatccg gaggcattct tccctgaaaa ggggtggatcc  
 180  
 acccgtgagg ccaagcgcac ctgtgagtc tgtgaggtcc gccaggagtg cttggagtac  
 240  
 gcccttgcca atgacgagag gttcgggaatc tggggcggat tgtccgagat ggagaggcgt  
 300  
 cggctgcgca agcggggcgtg acctgacgtc ggagcgcggg tattgacacg gcccggtaaa  
 360  
 atgccctgtc tgcccgggat ggctgtctgc acgatgcggc atatgcgatg atcgacagacg  
 420  
 tgggtgtgcat cccgtgtctc atgacgtcga c  
 451

<210> 662

<211> 85

<212> PRT

<213> Homo sapiens

<400> 662

Met	Asp	Glu	Ile	Leu	Thr	Leu	Leu	Ala	Gly	Gly	Gly	Asp	Asp	Glu	Pro
1				5					10					15	
Glu	Trp	His	Asp	Lys	Ala	Leu	Cys	Ala	Gln	Thr	Asp	Pro	Glu	Ala	Phe
			20					25					30		
Phe	Pro	Glu	Lys	Gly	Gly	Ser	Thr	Arg	Glu	Ala	Lys	Arg	Ile	Cys	Glu
		35					40					45			
Ser	Cys	Glu	Val	Arg	Gln	Glu	Cys	Leu	Glu	Tyr	Ala	Leu	Ala	Asn	Asp
	50					55				60					
Glu	Arg	Phe	Gly	Ile	Trp	Gly	Gly	Leu	Ser	Glu	Met	Glu	Arg	Arg	Arg
65					70				75					80	
Leu	Arg	Lys	Arg	Ala											
					85										

<210> 663

<211> 552

<212> DNA

<213> Homo sapiens

<400> 663

ctcgagcgtc tcgacgccga cgccgcccag ggagccaagg aagacctctc gcagcgcgac  
 60  
 ccctacgacg tgctcgtcgt agggggcgggt cccgccgggt ccgcggccgc cgtgtacgcg  
 120  
 gctcgtaagg gcattcgac cgccatggtc ggggtctcga tcggcggcca ggtactcgat  
 180  
 accgaggcca tcgacaacct catctcgggt ccgcacacca ccggtccgcg tctggccgac  
 240  
 gccctccgca gccacgtcaa cgactacaac attgacgtta ttgagcgtca gaccgccagc  
 300  
 gccatagaga ccaccggcgg tatgaccacc gtgcatctga ccgacggcga cctgcgggcg  
 360  
 cgctcagtca tcgtggccac cgggtgccgc tggcgcaacc ttggcgtaac tggcgaggag  
 420  
 gaataccgca ccaagggtgt gacctactgc ccgcaactgc atggcccgtc attcacaggc  
 480

aaaaagggtgg ccgtcgtcgg aggtggaac tccggtattg aggccgctat cgacctcgcc  
 540  
 ggcgtcgtcg ac  
 552

<210> 664  
 <211> 184  
 <212> PRT  
 <213> Homo sapiens

<400> 664  
 Leu Glu Arg Leu Asp Ala Asp Ala Ala Gln Gly Ala Lys Glu Asp Leu  
 1 5 10 15  
 Ser Gln Arg Asp Pro Tyr Asp Val Leu Val Val Gly Ala Gly Pro Ala  
 20 25 30  
 Gly Ala Ala Ala Val Tyr Ala Ala Arg Lys Gly Ile Arg Thr Ala  
 35 40 45  
 Met Val Gly Ser Arg Ile Gly Gly Gln Val Leu Asp Thr Glu Ala Ile  
 50 55 60  
 Asp Asn Leu Ile Ser Val Pro His Thr Thr Gly Pro Arg Leu Ala Asp  
 65 70 75 80  
 Ala Leu Arg Ser His Val Asn Asp Tyr Asn Ile Asp Val Ile Glu Arg  
 85 90 95  
 Gln Thr Ala Ser Ala Ile Glu Thr Thr Gly Gly Met Thr Thr Val His  
 100 105 110  
 Leu Thr Asp Gly Asp Leu Arg Ala Arg Ser Val Ile Val Ala Thr Gly  
 115 120 125  
 Ala Arg Trp Arg Asn Leu Gly Val Pro Gly Glu Glu Glu Tyr Arg Thr  
 130 135 140  
 Lys Gly Val Thr Tyr Cys Pro His Cys Asp Gly Pro Leu Phe Thr Gly  
 145 150 155 160  
 Lys Lys Val Ala Val Val Gly Gly Gly Asn Ser Gly Ile Glu Ala Ala  
 165 170 175  
 Ile Asp Leu Ala Gly Val Val Asp  
 180

<210> 665  
 <211> 352  
 <212> DNA  
 <213> Homo sapiens

<400> 665  
 acgcgtacag ttcgccgtcg aggttgaaca ccacgatcgg tgtaccggtc acttcgtcga  
 60  
 acacgtcttt catttcgccc ggcagcagtt cggcgccggc gcagacaaag gtccaggcct  
 120  
 cgctcacgcg gtggccccgg ccagcggctt ttccaggatc tcgaaacgca ggtcgtcgcg  
 180  
 cttgggggatg ccgaatcggt cgtcgccata cgggaacggc ttcttgatgc cggtgcgacg  
 240  
 gtagccgcgg cgctcgtaga agcgatcaga tcgcgcgcac gtcgatcact gtcattctgca  
 300  
 ttaccggcac gttccattcg cgcgcggcgt gggcttcggc ggcgtccatc aa  
 352

<210> 666  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 666  
 Met Glu Arg Ala Gly Asn Ala Asp Asp Ser Asp Arg Arg Ala Arg Asp  
 1 5 10 15  
 Leu Ile Ala Ser Thr Ser Ala Ala Ala Thr Cys Ala Pro Ala Ser Arg  
 20 25 30  
 Ser Arg Ser Arg Met Ala Thr Asn Asp Ser Ala Ser Pro Ser Ala Thr  
 35 40 45  
 Thr Cys Val Ser Arg Ser Trp Lys Ser Arg Trp Pro Gly Pro Pro Arg  
 50 55 60  
 Glu Arg Gly Leu Asp Leu Cys Leu Arg Arg Arg Arg Thr Ala Ala Gly  
 65 70 75 80  
 Arg Asn Glu Glu Arg Val Arg Arg Ser Asp Arg Tyr Thr Asp Arg Gly  
 85 90 95  
 Val Gln Pro Arg Arg Arg Thr Val Arg  
 100 105

<210> 667  
 <211> 391  
 <212> DNA  
 <213> Homo sapiens

<400> 667  
 nacgcgtacg aatcggtgtt gcgtcgcaac ccaggggagg ccgagttcca ccaggctgtg  
 60  
 cgggagatct ttgaatctct cggcccggtg ctcgacaaga atccgcagta cgtggaggca  
 120  
 gccgtgttgt cgcgcattctg cgaaccggaa cgccagatca ttttccgggt gccgtgggtt  
 180  
 gaccagcagg gcaagatccg tatcaaccgt ggcttccgcg ttgaatattc gtcggtactg  
 240  
 gggccgtata aggggtggatt gcgattccac cctcgggtgt acttaggaac gattaagtgc  
 300  
 cttgggttttg agcagatctt caaaaatgct ctgactggca tgccgatcgg tggcgcggaag  
 360  
 ggtgggtcgg actttgatcc ccatgacgcg t  
 391

<210> 668  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 668  
 Xaa Ala Tyr Glu Ser Val Leu Arg Arg Asn Pro Gly Glu Ala Glu Phe  
 1 5 10 15  
 His Gln Ala Val Arg Glu Ile Phe Glu Ser Leu Gly Pro Val Leu Asp  
 20 25 30  
 Lys Asn Pro Gln Tyr Val Glu Ala Ala Val Leu Ser Arg Ile Cys Glu

```

      35              40              45
Pro Glu Arg Gln Ile Ile Phe Arg Val Pro Trp Val Asp Asp Glu Gly
  50              55              60
Lys Ile Arg Ile Asn Arg Gly Phe Arg Val Glu Tyr Ser Ser Val Leu
  65              70              75              80
Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Tyr Leu Gly
      85              90              95
Thr Ile Lys Phe Leu Gly Phe Glu Gln Ile Phe Lys Asn Ala Leu Thr
      100              105              110
Gly Met Pro Ile Gly Gly Ala Lys Gly Gly Ser Asp Phe Asp Pro His
      115              120              125
Asp Ala
      130

```

<210> 669  
 <211> 707  
 <212> DNA  
 <213> Homo sapiens

```

<400> 669
nngagtccgt tccccgtcta agtcatcgt ggtggtgctg gcatggccgt caacaaggga
  60
attgagaaca cccttgctgc cttcgccac gcggtcgagg tgggatgcac ctacctgaa
  120
actgacgttc acgcgaccag cgacggggtg ctagtggcct tccacgatcc gatactcgat
  180
cgcgctactg aatcaggcgg agtcatcgcc gccatgccgt ggcacaaggc caaacaagcc
  240
aaggttggtg gcgaaccgat cccacctta gatgagattt tcgacgcctt tcccgcgcg
  300
ttcatcaata tcgacatcaa gcatgatggc gccaccatgc cgctcatcga cgttctttcc
  360
cgtcaccggg cttggagtcg ggtttgcgtc gggtcgttca gcagtaaacy catccagacc
  420
ttcgtcgcc tggttcaggg acgcactgcg actgcagtgg ggtcggtggg agtcnnggct
  480
gggctgtcat cagccctcat agcatgcaga tggcacagtc ccatgggaat gcgtaccagg
  540
tgccgcaccg cttgaccggg tnatggggtg ccccttgtga caccgacctt cattaaagct
  600
gcccacgtc aggggcgagc tgttcatgtc tggacgggta atgagatctc tgagggtcga
  660
gaactgatgg atatgggggt cgacggcatc gtcacagatc gtccgga
  707

```

<210> 670  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

```

<400> 670
Met Ala Val Asn Lys Gly Ile Glu Asn Thr Leu Ala Ala Phe Gly His
  1              5              10              15
Ala Val Glu Val Gly Cys Thr Tyr Leu Glu Thr Asp Val His Ala Thr

```

```

      20      25      30
Ser Asp Gly Val Leu Val Ala Phe His Asp Pro Ile Leu Asp Arg Val
      35      40      45
Thr Glu Ser Gly Gly Val Ile Ala Ala Met Pro Trp His Lys Val Lys
      50      55      60
Gln Ala Lys Val Gly Gly Glu Pro Ile Pro Thr Leu Asp Glu Ile Phe
      65      70      75      80
Asp Ala Phe Pro Asp Ala Phe Ile Asn Ile Asp Ile Lys His Asp Gly
      85      90      95
Ala Thr Met Pro Leu Ile Asp Val Leu Ser Arg His Arg Ala Trp Ser
      100      105      110
Arg Val Cys Val Gly Ser Phe Ser Ser Lys Arg Ile Gln Thr Phe Arg
      115      120      125
Arg Leu Val Gln Gly Arg Thr Ala Thr Ala Val Gly Ser Val Gly Val
      130      135      140
Xaa Ala Gly Leu Ser Ser Ala Leu Ile Ala Cys Arg Trp His Ser Pro
      145      150      155      160
Met Gly Met Arg Thr Arg Cys Arg Thr Ala
      165      170

```

&lt;210&gt; 671

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 671

```

acgcgtgggc cttcgggttg atgggatcag aaggggacgg gacctgtaga aaggggcctg
60
cagctcagag catggggcgg ccttggtcca ctacgcctgc agctgtgaat tcgttctccg
120
gtgctggaga gggatctggt tatctccatt ctctgtctc cacgtggaaa ggaaggacgt
180
gcgctctcat cctacgtgtt ttgagaaatc gcattgtccc cagctctgcg ggaggatctg
240
gggacgcagt ggggaaccag acaggcagtt ggaggtctag tgcgcgccag aagccagttc
300
ccacccaggg tgccatttgc tgggcgccct agggagctgc gtgggcatcc agaggagtga
360
gtcgcgccct gctctgtcca gtgccactt ccccgggcag ggcaggcggt attaacgtag
420
agggagaaca cccatgcaca caac
444

```

&lt;210&gt; 672

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 672

```

Met Gly Ser Glu Gly Asp Gly Thr Cys Arg Lys Gly Pro Ala Ala Gln
1      5      10      15
Ser Met Gly Arg Pro Trp Leu Thr Thr Pro Ala Ala Val Asn Ser Phe
      20      25      30
Ser Gly Ala Gly Glu Gly Ser Gly Tyr Leu His Ser Leu Val Ser Thr

```

```

          35          40          45
Trp Lys Gly Arg Thr Cys Ala Leu Ile Leu Arg Val Leu Arg Asn Arg
          50          55          60
Ile Val Pro Ser Ser Ala Gly Gly Ser Gly Asp Ala Val Gly Asn Gln
65          70          75          80
Thr Gly Ser Trp Arg Ser Ser Ala Arg Gln Lys Pro Val Pro Thr Gln
          85          90          95
Gly Ala Ile Cys Trp Ala Pro
          100

```

&lt;210&gt; 673

&lt;211&gt; 452

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 673

```

acgcgtccct gcagaaatcc tctcggccta ggatcatccgc aagatgtggc agggcatgca
60
ccgtgaaaagc cttcaagtct gccgcagcaa gaccgcacgc ctgctgaaat tcgcagttgt
120
gccgcggtcc ctgatgcgga caaactcggc caccacgatc agcctgacgc ttgcggacca
180
acgttcaaact actgtgcact tgaaacgtcc gggccgcac acctgggtga ctttgtgcga
240
ccgacattac ttatgttcac gctctttcag ttcttgtcaa taccgtatatt ttcgtcgacg
300
tctccatcag aaaaatgtcg gtgttacgc accgcagacg atgcgtaccc ttgcgctgac
360
gatggaggcc ttgaaaagtg cattagccac tactgggcga atctacggca aaaagctgtt
420
actaggcggt gattggggag gcccgtagtg gc
452

```

&lt;210&gt; 674

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 674

```

Met Trp Gln Gly Met His Arg Glu Ser Leu Gln Val Cys Arg Ser Lys
1          5          10          15
Thr Ala Arg Leu Leu Lys Phe Ala Val Val Pro Arg Ser Leu Met Arg
          20          25          30
Thr Asn Ser Ala Thr Thr Ile Ser Leu Thr Leu Ala Asp Gln Arg Ser
          35          40          45
Asn Thr Val His Leu Lys Arg Pro Gly Arg Ile Thr Trp Val Thr Leu
          50          55          60
Cys Asp Arg His Tyr Leu Cys Ser Arg Ser Phe Ser Ser Cys Gln Tyr
65          70          75          80
Arg Ile Phe Arg Arg Arg Leu His Gln Lys Asn Val Gly Val Thr Ala
          85          90          95
Pro Gln Thr Met Arg Thr Leu Ala Leu Thr Met Glu Ala Leu Lys Ser
          100          105          110
Ala Leu Ala Thr Thr Gly Arg Ile Tyr Gly Lys Lys Leu Leu Leu Gly

```



115  
Gly Asp Trp Gly Gly Pro  
130

120

125

&lt;210&gt; 675

&lt;211&gt; 8564

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 675

atgtcgggct ccacacagct tgtggcacag acgtggaggg ccactgagcc ccgctacccg  
60  
ccccacagcc ttctctaccc agtgcagatc gcccggacgc acacggacgt cgggctcctg  
120  
gagtaccagc accactcccg cgactatgcc tcccacctgt cgccgggctc catcatccag  
180  
ccccagcggc ggaggccctc cctgctgtct gagttccagc ccgggaatga acggtcccag  
240  
gagctccacc tgcggccaga gtcccaactca tacctgcccg agctggggaa gtcagagatg  
300  
gagttcattg aaagcaagcg ccctcggtta gagctgctgc ctgacccctt gctgcgaccg  
360  
tcacccctgc tggccacggg ccagcctgcg ggatctgaag acctcaccaa ggaccgtagc  
420  
ctgacgggca agctggaacc ggtgtctccc ccagccccc cgcacactga ccctgagctg  
480  
gagctggtgc cgccacggct gtccaaggag gagctgatcc agaacaatga ccgcgtggac  
540  
cgagagatca ccatggtaga gcagcagatc tctaagctga agaagaagca gcaacagctg  
600  
gaggaggagg ctgccaagcc gcccgagcct gagaagcccg tgtcaccgcc gccatcgag  
660  
tcgaagcacc gcagcctggt gcagatcatc tacgacgaga accggaagaa ggctgaagct  
720  
gcacatcgga ttctggaagg cctggggccc cagggtggagc tgccgctgta caaccagccc  
780  
tcgacacccc ggcagtatca tgagaacatc aaaataaacc aggcgatgcy gaagaagcta  
840  
atcttgctact tcaagaggag gaatcacgct cggaacaat gggagcagaa gttctgccag  
900  
cgctatgacc agctcatgga ggcctgggaa aaaaagggtg agcgcatcga gaacaacccc  
960  
cggcggcggg ccaaggagag caaggtgcgc gactactacg aaaagcagtt ccctgagatc  
1020  
cgcaagcagc gcgagctgca ggagcgcatg cagggcaggg tgggcccagc gggcagtggg  
1080  
ctgtccatgt cgcccgcccc cagcgagcac gaggtgtcag agatcatcga tggcctctca  
1140  
gagcaggaga acctggagaa gcagatgcgc cagctggccg tgatcccgcc catgctgtac  
1200  
gacgctgacc agcagcgcat caagttcatc aacatgaacg ggcttatggc cgaccccatg  
1260  
aaggtgtaca aagaccgcca ggtcatgaac atgtggagtg agcaggagaa ggagaccttc  
1320

cgaggagaagt tcatgcagca tcccaagaac tttggcctga tcgcatcatt cctggagagg  
1380  
aagacagtgg ctgagtgcgt cctctattac tacctgacta agaagaatga gaactataag  
1440  
agcctgggtga gacggagcta tcggcgccgc ggcaagagcc agcagcagca acaacagcag  
1500  
cagcagcagc agcagcagca gcagcagcag cagcccatgc cccgcagcag ccaggaggag  
1560  
aaagatgaga aggagaagga aaaggaggcg gagaaggagg aggagaagcc ggaggtggag  
1620  
aacgacaagg aagacctcct caaggagaag acagacgaca cctcagggga ggacaacgac  
1680  
gagaaggagg ctgtggcctc caaaggccgc aaaactgcc aagccaggg aagacgcaa  
1740  
ggccgcatca cccgctcaat ggctaagtgc gccaacagcg aggaggccat cccccccag  
1800  
cagacgccc agctggcctc catggagctg aatgagagtt ctgctggac agaagaagaa  
1860  
atggaacag ccaagaaagg tctcctggaa cagggccgc actggtcggc catcgcccg  
1920  
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<213> Homo sapiens

<400> 676

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			20					25					30		
Thr	His	Thr	Asp	Val	Gly	Leu	Leu	Glu	Tyr	Gln	His	His	Ser	Arg	Asp
		35				40					45				
Tyr	Ala	Ser	His	Leu	Ser	Pro	Gly	Ser	Ile	Ile	Gln	Pro	Gln	Arg	Arg
	50				55					60					
Arg	Pro	Ser	Leu	Leu	Ser	Glu	Phe	Gln	Pro	Gly	Asn	Glu	Arg	Ser	Gln
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Glu	Leu	His	Leu	Arg	Pro	Glu	Ser	His	Ser	Tyr	Leu	Pro	Glu	Leu	Gly
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Lys	Ser	Glu	Met	Glu	Phe	Ile	Glu	Ser	Lys	Arg	Pro	Arg	Leu	Glu	Leu
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Leu	Pro	Asp	Pro	Leu	Leu	Arg	Pro	Ser	Pro	Leu	Leu	Ala	Thr	Gly	Gln
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Pro	Ala	Gly	Ser	Glu	Asp	Leu	Thr	Lys	Asp	Arg	Ser	Leu	Thr	Gly	Lys
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Leu	Glu	Pro	Val	Ser	Pro	Ser	Pro	Pro	His	Thr	Asp	Pro	Glu	Leu	
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Glu	Leu	Val	Pro	Pro	Arg	Leu	Ser	Lys	Glu	Glu	Leu	Ile	Gln	Asn	Met

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      290      295      300
Leu Met Glu Ala Trp Glu Lys Lys Val Glu Arg Ile Glu Asn Asn Pro
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Phe Pro Glu Ile Arg Lys Gln Arg Glu Leu Gln Glu Arg Met Gln Gly
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Ser Glu Glu Ala Ile Thr Pro Gln Gln Ser Ala Glu Leu Ala Ser Met

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  705              710              715              720
Glu Ala Glu Ala Leu His Ala Ser Gly Asn Glu Val Pro Arg Gly Glu
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Cys Ser Gly Pro Ala Thr Val Asn Asn Ser Ser Asp Thr Glu Ser Ile
      740              745              750
Pro Ser Pro His Thr Glu Ala Ala Lys Asp Thr Gly Gln Asn Gly Pro
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Lys Pro Pro Ala Thr Leu Gly Ala Asp Gly Pro Pro Pro Gly Pro Pro
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  785              790              795              800
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Lys Glu Gly Gly Ser Gly Arg Ala Thr Thr Ala Lys Ser Ser Gly Ala
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Pro Gln Asp Ser Asp Ser Ser Ala Thr Cys Ser Ala Asp Glu Val Asp
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Pro Arg Gly Ile Ile Asp Leu Ser Gln Val Pro His Leu Pro Val Leu		
1730	1735	1740
Val Pro Pro Thr Pro Gly Thr Pro Ala Thr Ala Met Asp Arg Leu Ala		
1745	1750	1755
Tyr Leu Pro Thr Ala Pro Gln Pro Phe Ser Ser Arg His Ser Ser Ser		
1765	1770	1775
Pro Leu Ser Pro Gly Gly Pro Thr His Leu Thr Lys Pro Thr Thr Thr		
1780	1785	1790
Ser Ser Ser Glu Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp		
1795	1800	1805
Arg Glu Arg Glu Lys Ser Ile Leu Thr Ser Thr Thr Val Glu His		
1810	1815	1820
Ala Pro Ile Trp Arg Pro Gly Thr Glu Gln Ser Ser Gly Ser Ser Gly		
1825	1830	1835
Ser Ser Gly Gly Gly Gly Gly Ser Ser Ser Arg Pro Ala Ser His Ser		
1845	1850	1855
His Ala His Gln His Ser Pro Ile Ser Pro Arg Thr Gln Asp Ala Leu		
1860	1865	1870
Gln Gln Arg Pro Ser Val Leu His Asn Thr Gly Met Lys Gly Ile Ile		
1875	1880	1885
Thr Ala Val Glu Pro Ser Thr Pro Thr Val Leu Arg Ser Thr Ser Thr		

1890	1895	1900
Ser Ser Pro Val Arg	Pro Ala Ala Thr Phe	Pro Pro Ala Thr His Cys
1905	1910	1915
Pro Leu Gly Gly Thr	Leu Asp Gly Val Tyr	Pro Thr Leu Met Glu Pro
1925	1930	1935
Val Leu Leu Pro Lys	Glu Ala Pro Arg Val Ala Arg	Pro Glu Arg Pro
1940	1945	1950
Arg Ala Asp Thr Gly	His Ala Phe Leu Ala Lys	Pro Pro Ala Arg Ser
1955	1960	1965
Gly Leu Glu Pro Ala	Ser Ser Pro Ser Lys Gly	Ser Glu Pro Arg Pro
1970	1975	1980
Leu Val Pro Pro Val	Ser Gly His Ala Thr Ile	Ala Arg Thr Pro Ala
1985	1990	1995
Lys Asn Leu Ala Pro	His His Ala Ser Pro Asp	Pro Pro Ala Pro Pro
2005	2010	2015
Ala Ser Ala Ser Asp	Pro His Arg Glu Lys	Thr Gln Ser Lys Pro Phe
2020	2025	2030
Ser Ile Gln Glu Leu	Glu Leu Arg Ser Leu Gly	Tyr His Gly Ser Ser
2035	2040	2045
Tyr Ser Pro Glu Gly	Val Glu Pro Val Ser	Pro Val Ser Ser Pro Ser
2050	2055	2060
Leu Thr His Asp Lys	Gly Leu Pro Lys His	Leu Glu Glu Leu Asp Lys
2065	2070	2075
Ser His Leu Glu Gly	Glu Leu Arg Pro Lys	Gln Pro Gly Pro Val Lys
2085	2090	2095
Leu Gly Gly Glu Ala	Ala His Leu Pro His	Leu Arg Pro Leu Pro Glu
2100	2105	2110
Ser Gln Pro Ser Ser	Ser Pro Leu Leu Gln	Thr Ala Pro Gly Val Lys
2115	2120	2125
Gly His Gln Arg Val	Val Thr Leu Ala Gln	His Ile Ser Glu Val Ile
2130	2135	2140
Thr Gln Asp Tyr Thr	Arg His His Pro Gln	Gln Leu Ser Ala Pro Leu
2145	2150	2155
Pro Ala Pro Leu Tyr	Ser Phe Pro Gly Ala	Ser Cys Pro Val Leu Asp
2165	2170	2175
Leu Arg Arg Pro Pro	Ser Asp Leu Tyr Leu	Pro Pro Asp His Gly
2180	2185	2190
Ala Pro Ala Arg Gly	Ser Pro His Ser Glu	Gly Gly Lys Arg Ser Pro
2195	2200	2205
Glu Pro Asn Lys Thr	Ser Val Leu Gly Gly	Gly Glu Asp Gly Ile Glu
2210	2215	2220
Pro Val Ser Pro Pro	Glu Gly Met Thr Glu	Pro Gly His Ser Arg Ser
2225	2230	2235
Ala Val Tyr Pro Leu	Leu Tyr Arg Asp Gly	Glu Gln Thr Glu Pro Ser
2245	2250	2255
Arg Met Gly Ser Lys	Ser Pro Gly Asn Thr	Ser Gln Pro Pro Ala Phe
2260	2265	2270
Phe Ser Lys Leu Thr	Glu Ser Asn Ser Ala	Met Val Lys Ser Lys Lys
2275	2280	2285
Gln Glu Ile Asn Lys	Lys Leu Asn Thr His	Asn Arg Asn Glu Pro Glu
2290	2295	2300
Tyr Asn Ile Ser Gln	Pro Gly Thr Glu Ile	Phe Asn Met Pro Ala Ile
2305	2310	2315
Thr Gly Thr Gly Leu	Met Thr Tyr Arg Ser	Gln Ala Val Gln Glu His

2325 2330 2335  
 Ala Ser Thr Asn Met Gly Leu Glu Ala Ile Ile Arg Lys Ala Leu Met  
 2340 2345 2350  
 Gly Lys Tyr Asp Gln Trp Glu Glu Ser Pro Pro Leu Ser Ala Asn Ala  
 2355 2360 2365  
 Phe Asn Pro Leu Asn Ala Ser Ala Ser Leu Pro Ala Ala Met Pro Ile  
 2370 2375 2380  
 Thr Ala Ala Asp Gly Arg Ser Asp His Thr Leu Thr Ser Pro Gly Gly  
 2385 2390 2395 2400  
 Gly Gly Lys Ala Lys Val Ser Gly Arg Pro Ser Ser Arg Lys Ala Lys  
 2405 2410 2415  
 Ser Pro Ala Pro Gly Leu Ala Ser Gly Asp Arg Pro Pro Ser Val Ser  
 2420 2425 2430  
 Ser Val His Ser Glu Gly Asp Cys Asn Arg Arg Thr Pro Leu Thr Asn  
 2435 2440 2445  
 Arg Val Trp Glu Asp Arg Pro Ser Ser Ala Gly Ser Thr Pro Phe Pro  
 2450 2455 2460  
 Tyr Asn Pro Leu Ile Met Arg Leu Gln Ala Gly Val Met Ala Ser Pro  
 2465 2470 2475 2480  
 Pro Pro Pro Gly Leu Pro Ala Gly Ser Gly Pro Leu Ala Gly Pro His  
 2485 2490 2495  
 His Ala Trp Asp Glu Glu Pro Lys Pro Leu Leu Cys Ser Gln Tyr Glu  
 2500 2505 2510  
 Thr Leu Ser Asp Ser Glu  
 2515

<210> 677  
 <211> 345  
 <212> DNA  
 <213> Homo sapiens

<400> 677  
 gtaatgcaag gtgaacgccc aatggctgcg cagaacaaga gcattggtca gttcaccctt  
 60  
 gagggatatag ctccggcagc cgtggtgtt ccacagattg aagttacttt cgatatcgat  
 120  
 gccaacggta tcttgaatgt gagcgcaaag gataaggcta ccggttaagga acagaagatt  
 180  
 cgcacgcaag cttcaagtgg tttagtcag gaagaaatcg acagaatgaa agctgaggca  
 240  
 gaacagaatg cagcagcagg caaggctgaa cgcgaaaaga ttgataagct gaaccaagct  
 300  
 gactcaatga tttccccccc cgaaaactcc tgaaagacaa cgatn  
 345

<210> 678  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 678  
 Val Met Gln Gly Glu Arg Pro Met Ala Ala Gln Asn Lys Ser Ile Gly  
 1 5 10 15  
 Gln Phe Thr Leu Glu Gly Ile Ala Pro Ala Arg Arg Gly Val Pro Gln

```

      20      25      30
Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Ser
      35      40      45
Ala Lys Asp Lys Ala Thr Gly Lys Glu Gln Lys Ile Arg Ile Glu Ala
      50      55      60
Ser Ser Gly Leu Ser Gln Glu Glu Ile Asp Arg Met Lys Ala Glu Ala
      65      70      75      80
Glu Gln Asn Ala Ala Ala Gly Lys Ala Glu Arg Glu Lys Ile Asp Lys
      85      90      95
Leu Asn Gln Ala Asp Ser Met Ile Ser Pro Pro Glu Asn Ser
      100      105      110

```

&lt;210&gt; 679

&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 679

```

acgcgtgacg tcaccgctcc atggggaaga tgacgactat ccctgtgaaa gtaaagcata
60
atgggaaaaa tgtacgttaa atgtgctaac gcgcagtatg atgtatctat gaatcttgag
120
ggtacaggcc tggatttcaa gcgtgccatt gctgacgtca cgcattgtgcc acccgaacgc
180
caaaaagtac tcatcaaggg aggattgcta aaagacgata cccattagg taaagtgggt
240
gcgcgtgcag gacagcagtt catggtgctg ggtgctgtgg gtgagctgcc caaggcccca
300
gaaaaacctg tgctgttctt ggaggatttg ccggaagacg agctcaacaa ggctaaggat
360
cc
362

```

&lt;210&gt; 680

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 680

```

Met Gly Lys Met Tyr Val Lys Cys Ala Asn Ala Gln Tyr Asp Val Ser
  1      5      10      15
Met Asn Leu Glu Gly Thr Gly Leu Asp Phe Lys Arg Ala Ile Ala Asp
      20      25      30
Val Thr His Val Pro Pro Glu Arg Gln Lys Val Leu Ile Lys Gly Gly
      35      40      45
Leu Leu Lys Asp Asp Thr Pro Leu Gly Lys Val Gly Ala Arg Ala Gly
      50      55      60
Gln Gln Phe Met Val Leu Gly Ala Val Gly Glu Leu Pro Lys Ala Pro
      65      70      75      80
Glu Lys Pro Val Leu Phe Leu Glu Asp Leu Pro Glu Asp Glu Leu Asn
      85      90      95
Lys Ala Lys Asp
      100

```

<210> 681  
 <211> 357  
 <212> DNA  
 <213> Homo sapiens

<400> 681  
 acgcgtccaa atggacaaac gcttgatgat ttctaccatg aaattagagc aaaatatcca  
 60  
 gaacaattac tgatggcaga ctgttcaaca gtagaagaaa tgattcacgc tgatgaactc  
 120  
 ggttttgatt ttatcggaag tacttttagta ggatatacaa aacaaagtaa aggtgacaaa  
 180  
 atcgaagaaa atgactttga aatcttgaga acagtttttag aacgaattaa acatccacta  
 240  
 attgcagaag gcaatatcga tacacctgaa aagggtgaaac gtgtgcttga gttaggcgcg  
 300  
 tatagtgtcg ttgtagggtc agcgattact cgtccacaac tcatcacgaa aaaattt  
 357

<210> 682  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 682  
 Thr Arg Pro Asn Gly Gln Thr Leu Asp Asp Phe Tyr His Glu Ile Arg  
 1 5 10 15  
 Ala Lys Tyr Pro Glu Gln Leu Leu Met Ala Asp Cys Ser Thr Val Glu  
 20 25 30  
 Glu Met Ile His Ala Asp Glu Leu Gly Phe Asp Phe Ile Gly Ser Thr  
 35 40 45  
 Leu Val Gly Tyr Thr Lys Gln Ser Lys Gly Asp Lys Ile Glu Glu Asn  
 50 55 60  
 Asp Phe Glu Ile Leu Arg Thr Val Leu Glu Arg Ile Lys His Pro Leu  
 65 70 75 80  
 Ile Ala Glu Gly Asn Ile Asp Thr Pro Glu Lys Val Lys Arg Val Leu  
 85 90 95  
 Glu Leu Gly Ala Tyr Ser Val Val Val Gly Ser Ala Ile Thr Arg Pro  
 100 105 110  
 Gln Leu Ile Thr Lys Lys Phe  
 115

<210> 683  
 <211> 411  
 <212> DNA  
 <213> Homo sapiens

<400> 683  
 ntctccgacc gcgtggtaaa actggcgacc ttaattgctg aagatgagca agctgaaatg  
 60  
 aatattgttt tgcccgcagc gtggttgcatt gattgcgtca gttaccctaa aaaccatgta  
 120  
 ttaagagcac aaagtgcatt acatgcagca gataaagcga ttgtattttt gcgcagtatt  
 180

aattacccca aacaatactt attagcaatt catcatgcaa tttcagcgca cagtgtcagt  
 240  
 ggtaaaatac aggcaatgag tttagaagct caaatagtg c aagatgcaga tagattggat  
 300  
 gcgctagggg caattggcgt ggctcgttgc attcaagtaa gtagccagtt acagcgccca  
 360  
 ctatattctg aagttgaccc cttcagcgag acacgatctc tagtctgcat g  
 411

<210> 684

<211> 137

<212> PRT

<213> Homo sapiens

<400> 684

Xaa	Ser	Asp	Arg	Val	Val	Lys	Leu	Ala	Thr	Leu	Ile	Ala	Glu	Asp	Glu
1				5					10					15	
Gln	Ala	Glu	Met	Asn	Ile	Val	Leu	Pro	Ala	Ala	Trp	Leu	His	Asp	Cys
			20					25					30		
Val	Ser	Tyr	Pro	Lys	Asn	His	Val	Leu	Arg	Ala	Gln	Ser	Ala	Leu	His
		35				40						45			
Ala	Ala	Asp	Lys	Ala	Ile	Val	Phe	Leu	Arg	Ser	Ile	Asn	Tyr	Pro	Lys
	50					55					60				
Gln	Tyr	Leu	Leu	Ala	Ile	His	His	Ala	Ile	Ser	Ala	His	Ser	Val	Ser
65					70				75					80	
Gly	Lys	Ile	Gln	Ala	Met	Ser	Leu	Glu	Ala	Gln	Ile	Val	Gln	Asp	Ala
			85					90					95		
Asp	Arg	Leu	Asp	Ala	Leu	Gly	Ala	Ile	Gly	Val	Ala	Arg	Cys	Ile	Gln
			100				105						110		
Val	Ser	Ser	Gln	Leu	Gln	Arg	Pro	Leu	Tyr	Ser	Glu	Val	Asp	Pro	Phe
		115				120						125			
Ser	Glu	Thr	Arg	Ser	Leu	Val	Cys	Met							
		130				135									

<210> 685

<211> 417

<212> DNA

<213> Homo sapiens

<400> 685

acgcgttgcg ttgcggagtg aacccggaac gatggatgga ttgacactat tcggcctgtt  
 60  
 cgccgtcact gcgatgctgg tctgctatgc catggaggac cgcagccact ggttcgtgct  
 120  
 gctgttcgcg gccgcttggc gctcgggttcg gcctacggct tcctccaagg cgcttgccg  
 180  
 ttcggcttcg tcgaggcgat atgggcgctc gttgcctgcg gcgtggtgga cgatcaggcc  
 240  
 gcgatgaccg catcgtccgg cttaagcccc gaaacgaaac cgaccagtgc gctggtttga  
 300  
 tggggcgcg gtcgctggat gcacagcgtc tcgacgcgag cgtgatgatg gcctcagcgc  
 360  
 gtgcatgccg acgctgtcgc tcatcgcgct acgctcgacc acggcgcgcg gcaatag  
 417

<210> 686  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 686  
 Met Pro Trp Arg Thr Ala Ala Thr Gly Ser Cys Cys Cys Ser Arg Pro  
 1 5 10 15  
 Leu Gly Ala Arg Phe Gly Leu Arg Leu Pro Pro Arg Arg Leu Ala Val  
 20 25 30  
 Arg Leu Arg Arg Gly Asp Met Gly Ala Arg Cys Leu Arg Arg Gly Gly  
 35 40 45  
 Arg Ser Gly Arg Asp Asp Arg Ile Val Arg Leu Lys Pro Gly Asn Glu  
 50 55 60  
 Thr Asp Gln Cys Ala Gly Leu Met Gly Gly Ala Ser Leu Asp Ala Gln  
 65 70 75 80  
 Arg Leu Asp Ala Ser Val Met Met Ala Ser Ala Arg Ala Cys Arg Arg  
 85 90 95  
 Cys Arg Ser Ser Arg Tyr Ala Arg Pro Arg Arg Ala Ala Ile  
 100 105 110

<210> 687  
 <211> 412  
 <212> DNA  
 <213> Homo sapiens

<400> 687  
 nnacgcgtga ccgaccaact gcgagccacc ctgctcgcca tggctgctat ggggttgac  
 60  
 gacggcatcg atattccgtc tggggcgatt attgaaagct gccgcacctt atcagccgtt  
 120  
 ctcgatgaaa cccacgggtg tgcgacgac gagcttcggg taccacctgc gtgcgcggtt  
 180  
 caattggcgg ccattgagtc gggccccaac caccaccggg gcaactccgcc caatgtggcc  
 240  
 gagaccgacc ctgtcacctt cctgcagttg gcaactggct tctcactctg gccagaaatg  
 300  
 cgctcagcag gacgggttca ggcgtctgga tcccacgtcg acgacgttgc tggcgtgttc  
 360  
 ccagtcgttg atatggcgg ggttttccgc gacatttttg ccgacgacta ga  
 412

<210> 688  
 <211> 136  
 <212> PRT  
 <213> Homo sapiens

<400> 688  
 Xaa Arg Val Thr Asp Gln Leu Arg Ala Thr Leu Leu Ala Met Ala Ala  
 1 5 10 15  
 Met Gly Leu His Asp Gly Ile Asp Ile Pro Ser Gly Ala Ile Ile Glu  
 20 25 30  
 Ser Cys Arg Thr Leu Ser Ala Val Leu Asp Glu Thr His Gly Gly Arg



```

      35              40              45
Thr Ile Glu Leu Arg Val Pro Pro Ala Cys Ala Val Gln Leu Ala Ala
      50              55              60
Ile Glu Ser Gly Pro Asn His His Arg Gly Thr Pro Pro Asn Val Ala
65              70              75              80
Glu Thr Asp Pro Val Thr Phe Leu Gln Leu Ala Thr Gly Phe Ser His
      85              90              95
Trp Pro Glu Met Arg Ser Ala Gly Arg Val Gln Ala Ser Gly Ser His
      100             105             110
Val Asp Asp Val Ala Gly Val Phe Pro Val Val Asp Met Ala Gly Val
      115             120             125
Phe Arg Asp Ile Phe Ala Asp Asp
      130             135

```

<210> 689  
 <211> 499  
 <212> DNA  
 <213> Homo sapiens

```

<400> 689
cgcgtcgcgg tactcgacgt cgattttcat cacggtaacg gcacccagaa cattttttac
60
ccgcgcaatg acgtgatgtt catatcgctg caggcgagc cggccgtgtc ctatccctac
120
tattcgggggt tcagcgatga agtcggcgca ggtggtggcg aagggttcaa cctcaactac
180
ccgctgccga aaaacaccgc ctgggatacc taccgcgacg ccctgctgca tgcttgcagg
240
aaactccagc aattctcgcc gcaggatttg gtgatctcac tgggggtcga caccttcaag
300
gacgaccoga tcagtcactt cctgctggaa ggcgaggatt tcatcgggat cggcgagctg
360
atagcgagtg tgggttgccc caccctgttt gtgatggaag gcggctatat ggtcgatgaa
420
atcggaatca acgcggtgaa cgtactgcat ggcttcgaga gcaagcgcgc ttgagcatcc
480
gcccgaaagac ggcgtgata
499

```

<210> 690  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

```

<400> 690
Arg Val Ala Val Leu Asp Val Asp Phe His His Gly Asn Gly Thr Gln
1              5              10              15
Asn Ile Phe Tyr Pro Arg Asn Asp Val Met Phe Ile Ser Leu His Gly
      20              25              30
Glu Pro Ala Val Ser Tyr Pro Tyr Tyr Ser Gly Phe Ser Asp Glu Val
      35              40              45
Gly Ala Gly Val Gly Glu Gly Phe Asn Leu Asn Tyr Pro Leu Pro Lys
      50              55              60
Asn Thr Ala Trp Asp Thr Tyr Arg Asp Ala Leu Leu His Ala Cys Arg

```

```

65          70          75          80
Lys Leu Gln Gln Phe Ser Pro Gln Val Leu Val Ile Ser Leu Gly Val
          85          90          95
Asp Thr Phe Lys Asp Asp Pro Ile Ser His Phe Leu Leu Glu Gly Glu
          100          105          110
Asp Phe Ile Gly Ile Gly Glu Leu Ile Ala Ser Val Gly Cys Pro Thr
          115          120          125
Leu Phe Val Met Glu Gly Gly Tyr Met Val Asp Glu Ile Gly Ile Asn
          130          135          140
Ala Val Asn Val Leu His Gly Phe Glu Ser Lys Arg Ala
145          150          155

```

<210> 691  
 <211> 336  
 <212> DNA  
 <213> Homo sapiens

```

<400> 691
ntgctgctg aaaacgtgca ggcgcgcgca tcagcgactg gcgagcgctt tggctggagt
60
tcgcaaaggc aaggccctg ggagttggcc tgcgacatcg cgctgccgtg cgccaccag
120
aacgaactgg acgccgacgc cgcccgacgc ctgctgcgca acggctgcct ttgctgggt
180
ggagcgcgca atatgccgcc cgcgcttgag gctgtggata tctttatcga ggcgggcatt
240
ctgttcgcgc cgggcaaggc atccaatgcc ggcggcgctg ccgtgagtg cctggaaatg
300
tcgcagaacg ccatgcgcct gctgtggacc gccggc
336

```

<210> 692  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

```

<400> 692
Xaa Leu Arg Glu Asn Val Gln Arg Gly Ala Ser Ala Thr Gly Glu Arg
1          5          10          15
Phe Gly Trp Ser Ser Gln Arg Gln Gly Pro Trp Glu Leu Ala Cys Asp
          20          25          30
Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu Leu Asp Ala Asp Ala Ala
          35          40          45
Arg Thr Leu Leu Arg Asn Gly Cys Leu Cys Val Ala Gly Gly Ala Asn
          50          55          60
Met Pro Pro Ala Leu Glu Ala Val Asp Ile Phe Ile Glu Ala Gly Ile
65          70          75          80
Leu Phe Ala Pro Gly Lys Ala Ser Asn Ala Gly Gly Val Ala Val Ser
          85          90          95
Gly Leu Glu Met Ser Gln Asn Ala Met Arg Leu Leu Trp Thr Ala Gly
          100          105          110

```

<210> 693  
 <211> 580

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 693

```

ngggcaaccc ggaaggtccg gcgtcccgagc cgcctacctc gctgggaccc tgggtcttgct
60
gtcccccgcgt ggcttcctgc ccaagcgact gcggccagga tgggccggaa ggtgaccgtg
120
gccacctgcg cactcaacca gtgggccctg gacttcgagg gcaatttgca aagaatttta
180
aagagtattg aaattgccaa aaacagagga gcaagataca ggcttgacc agagctggaa
240
atatgcggct gcggatgttg ggatcattat tacgagtcgg acaccctctt gcactcgttt
300
caagtcctag cggcccttgt ggagtcctcc gtcactcagg acatcatctg cgacgtgggg
360
atacctgtaa tgcaccgaaa cgtccgctac aactgcagag tgatattcct caacaggaag
420
atcctgctca tcagacccaa gatggccttg gccaatgaag gcaactaccg cgagctgcgc
480
tggttcaccc cgtggtcgag gagtcggtga gtcgggtgcc tgaccactcc tgggatgtgc
540
gttaagcacc tccgctgtgt gtagccttgg gtctgatca
580

```

&lt;210&gt; 694

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 694

```

Met Gly Arg Lys Val Thr Val Ala Thr Cys Ala Leu Asn Gln Trp Ala
1      5      10      15
Leu Asp Phe Glu Gly Asn Leu Gln Arg Ile Leu Lys Ser Ile Glu Ile
20     25     30
Ala Lys Asn Arg Gly Ala Arg Tyr Arg Leu Gly Pro Glu Leu Glu Ile
35     40     45
Cys Gly Cys Gly Cys Trp Asp His Tyr Tyr Glu Ser Asp Thr Leu Leu
50     55     60
His Ser Phe Gln Val Leu Ala Ala Leu Val Glu Ser Pro Val Thr Gln
65     70     75     80
Asp Ile Ile Cys Asp Val Gly Ile Pro Val Met His Arg Asn Val Arg
85     90     95
Tyr Asn Cys Arg Val Ile Phe Leu Asn Arg Lys Ile Leu Leu Ile Arg
100    105    110
Pro Lys Met Ala Leu Ala Asn Glu Gly Asn Tyr Arg Glu Leu Arg Trp
115    120    125
Phe Thr Pro Trp Ser Arg Ser Arg
130    135

```

&lt;210&gt; 695

&lt;211&gt; 439

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 695

ntggtgactc aggcgtccaa tggcacgatg gctgacgtcg tcaatatgcc gtcctcgacc  
 60  
 atcatggctc tgtcgagggc tgattacctg ctcgatatcg agacttcggt gcccgggtatc  
 120  
 ggcgacaagt tcgtcccga cgtctggggc aaactcaaac tcggcaagga caacgagcac  
 180  
 accgctctgc cctgggtactt cggcccgttc gtcgtgacgt acaacaagga cattttcaag  
 240  
 gatgttggcc tcgatcccga aatcccgcg aagacgatga ccgagtacct cgacttcgcc  
 300  
 aagaaaatca ccgctgccgg caagcaggcg gtctatggca acacgtcgtg gtacatgctc  
 360  
 gcggaatggc gtgccctcgg cgtcaaggtc atgaatgacg acttcaccaa gttcactttt  
 420  
 gcctcggaat ccaacgcgt  
 439

&lt;210&gt; 696

&lt;211&gt; 146

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 696

Xaa	Val	Thr	Gln	Ala	Ser	Asn	Gly	Thr	Met	Ala	Asp	Val	Val	Asn	Met
1				5					10					15	
Pro	Ser	Ser	Thr	Ile	Met	Ala	Leu	Ser	Arg	Ala	Asp	Tyr	Leu	Leu	Asp
			20					25					30		
Ile	Glu	Thr	Ser	Val	Pro	Gly	Ile	Gly	Asp	Lys	Phe	Val	Pro	Asp	Val
			35				40					45			
Trp	Gly	Lys	Leu	Lys	Leu	Gly	Lys	Asp	Asn	Glu	His	Thr	Ala	Leu	Pro
	50					55				60					
Trp	Tyr	Phe	Gly	Pro	Phe	Val	Val	Thr	Tyr	Asn	Lys	Asp	Ile	Phe	Lys
65					70					75				80	
Asp	Val	Gly	Leu	Asp	Pro	Glu	Ile	Pro	Pro	Lys	Thr	Met	Thr	Glu	Tyr
				85					90					95	
Leu	Asp	Phe	Ala	Lys	Lys	Ile	Thr	Ala	Ala	Gly	Lys	Gln	Ala	Val	Tyr
			100					105					110		
Gly	Asn	Thr	Ser	Trp	Tyr	Met	Leu	Ala	Glu	Trp	Arg	Ala	Leu	Gly	Val
	115					120						125			
Lys	Val	Met	Asn	Asp	Asp	Phe	Thr	Lys	Phe	Thr	Phe	Ala	Ser	Glu	Ser
	130					135					140				
Asn	Ala														
145															

&lt;210&gt; 697

&lt;211&gt; 368

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 697

nggcaataac gccgtcgtcg aaatccgttc ccttgatctc gaacatgccg atgaagcggg  
 60

tgtcggatgat ggggtcggag atgtcgccct ccacaaactt gaacttgatc ggaccaaccc  
 120  
 tttccaccct ggagagactc gcctgccttg aaagtcttct tgcccttctt gggcaactga  
 180  
 tcgccctccc gaacgagata atccaagctc aagcgaccgc ccaccttgtc gcgcgcctcc  
 240  
 acaccgacgg aatgcgatgc cgggatcgca tcgatgctag cggcgggtgcg tgcaatgaca  
 300  
 atcttgtctt cacgcagcga tacgggccccg ccgttggaaat cgaacacaaa caccttgaag  
 360  
 gcgttgtn  
 368

<210> 698  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 698  
 Met Pro Met Lys Arg Leu Ser Val Met Gly Ser Glu Met Ser Pro Ser  
 1 5 10 15  
 His Asn Leu Asn Leu Ile Gly Pro Thr Leu Ser Thr Leu Glu Arg Leu  
 20 25 30  
 Ala Cys Leu Glu Ser Leu Leu Ala Leu Leu Gly Gln Leu Ile Ala Leu  
 35 40 45  
 Pro Asn Glu Ile Ile Gln Ala Gln Ala Thr Ala His Leu Val Ala Arg  
 50 55 60  
 Leu His Thr Asp Gly Met Arg Cys Arg Asp Arg Ile Asp Ala Ser Gly  
 65 70 75 80  
 Gly Ala Cys Asn Asp Asn Leu Val Phe Thr Gln Arg Tyr Gly Pro Ala  
 85 90 95  
 Val Gly Ile Glu His Lys His Leu Glu Gly Val Val  
 100 105

<210> 699  
 <211> 363  
 <212> DNA  
 <213> Homo sapiens

<400> 699  
 nacgcgtaca caaatagtat cggaatcatt tcctatcatg ctgctatgac gagatttctc  
 60  
 cacacctcag attggcaact ggggatgact cggcactacc tgtcgaagcg cggcgacgac  
 120  
 gaccacaggg cacggtttac tgccgatcga atcgagacgg tgcgcaggct gggcgacggt  
 180  
 gcccggaagg agggctgcga gtttgtcgtc gtcgccggag atgtcttcga aaccacaaat  
 240  
 gtctccactc agatcattgc ccgcgcgtgt gagcgatag cctccattga tctccccgtg  
 300  
 tacctgctgc ccggaaatca cgacagctta gagccgggggt gtctctggga tgggccagaa  
 360  
 ttc  
 363

<210> 700  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 700  
 Xaa Ala Tyr Thr Asn Ser Ile Gly Ile Ile Ser Tyr His Ala Ala Met  
 1 5 10 15  
 Thr Arg Phe Leu His Thr Ser Asp Trp Gln Leu Gly Met Thr Arg His  
 20 25 30  
 Tyr Leu Ser Lys Arg Gly Asp Asp Asp Pro Gln Ala Arg Phe Thr Ala  
 35 40 45  
 Asp Arg Ile Glu Thr Val Arg Arg Leu Gly Asp Val Ala Arg Lys Glu  
 50 55 60  
 Gly Cys Glu Phe Val Val Val Ala Gly Asp Val Phe Glu Thr His Asn  
 65 70 75 80  
 Val Ser Thr Gln Ile Ile Ala Arg Ala Cys Glu Ala Ile Ala Ser Ile  
 85 90 95  
 Asp Leu Pro Val Tyr Leu Leu Pro Gly Asn His Asp Ser Leu Glu Pro  
 100 105 110  
 Gly Cys Leu Trp Asp Gly Pro Glu Phe  
 115 120

<210> 701  
 <211> 585  
 <212> DNA  
 <213> Homo sapiens

<400> 701  
 nacgcgtccg ggcacaccgt caccgaggcg acgttccacg gccacccac gctgatctat  
 60  
 ttccggtacg tccattgcg cggatgtctgc ccgctgacac tgggcaacat ggtctcggcc  
 120  
 ctccgatcgcc tgggctcccg ggcggacggc atcgttccga tcttcatctc cgtcgatccg  
 180  
 gcccgcgaca caccgcgct ggtcggacag tatgtcgcgc atttctcgcc gcggatcgtc  
 240  
 gggctgaccg gcaccgcagc gcagctggcg ccggtactgg cggagttcca catcaccgcg  
 300  
 cgcgcgaac ctgcggcaca cgacatggcc gccgacatgt atgccgtcga ccacagcgcc  
 360  
 ctctctatc tgatggacgg caacaaccgc ctgttgcggg tgatggcggt cagcgccgac  
 420  
 gctgcctcgc tgacgcacca gctggcgggc ggccctggccg gggcaagaat gagaccatga  
 480  
 aagcgatcgg accgacggac gccccgaac aggcagcgcc gggtggtcg ttcggcatca  
 540  
 tctgtctgct cggcatcgcc ggcgtgctcg atttcgtcga ccggt  
 585

<210> 702  
 <211> 159  
 <212> PRT

<213> Homo sapiens

<400> 702

```

Xaa Ala Ser Gly His Thr Val Thr Glu Ala Thr Phe His Gly His Pro
 1           5           10           15
Thr Leu Ile Tyr Phe Gly Tyr Val His Cys Ala Asp Val Cys Pro Leu
 20           25           30
Thr Leu Gly Asn Met Val Ser Ala Leu Asp Arg Leu Gly Ser Arg Ala
 35           40           45
Asp Gly Ile Val Pro Ile Phe Ile Ser Val Asp Pro Ala Arg Asp Thr
 50           55           60
Pro Ala Leu Val Gly Gln Tyr Val Ala His Phe Ser Pro Arg Ile Val
 65           70           75           80
Gly Leu Thr Gly Thr Ala Ala Gln Leu Ala Pro Val Leu Ala Glu Phe
 85           90           95
His Ile Thr Ala Arg Ala Glu Pro Ala Ala His Asp Met Ala Ala Asp
 100          105          110
Met Tyr Ala Val Asp His Ser Ala Leu Leu Tyr Leu Met Asp Gly Asn
 115          120          125
Asn Arg Leu Leu Arg Val Met Ala Val Ser Ala Asp Ala Ala Ser Leu
 130          135          140
Thr His Gln Leu Ala Ala Gly Leu Ala Gly Ala Arg Met Arg Pro
 145          150          155

```

<210> 703

<211> 390

<212> DNA

<213> Homo sapiens

<400> 703

```

ttctctgctc catacacacc tcagcagaat ggcatcgccg agcgcaagaa cataactctt
60
attgagatgg cccgaacgat gcttgatgag tacaagactc cgcggaagtt ctggcctgaa
120
gccattgata ctgcttgatc caccatcaac cgcggtttatc ttcacaaggt tttggagaaa
180
acctcttatg agttcctaac tggttaagaaa cccaatgtaa gctatttcag agtatttggt
240
gctaggtgct ggatcaagga tcctcatcac acttcaaaaat ttgcaccgaa agcacatgaa
300
ggttttatgc ttggttacgg aaaggattcg cactcctaca gagtcttcaa cctctttcac
360
tataaagtgg ttcaaactgt ggatgtgcgn
390

```

<210> 704

<211> 130

<212> PRT

<213> Homo sapiens

<400> 704

```

Phe Ser Ala Pro Tyr Thr Pro Gln Gln Asn Gly Ile Ala Glu Arg Lys
 1           5           10           15
Asn Ile Thr Leu Ile Glu Met Ala Arg Thr Met Leu Asp Glu Tyr Lys

```

```

      20      25      30
Thr Pro Arg Lys Phe Trp Pro Glu Ala Ile Asp Thr Ala Cys His Thr
      35      40      45
Ile Asn Arg Val Tyr Leu His Lys Val Leu Glu Lys Thr Ser Tyr Glu
      50      55      60
Phe Leu Thr Gly Lys Lys Pro Asn Val Ser Tyr Phe Arg Val Phe Gly
65      70      75      80
Ala Arg Cys Trp Ile Lys Asp Pro His His Thr Ser Lys Phe Ala Pro
      85      90      95
Lys Ala His Glu Gly Phe Met Leu Gly Tyr Gly Lys Asp Ser His Ser
      100      105      110
Tyr Arg Val Phe Asn Leu Phe His Tyr Lys Val Val Gln Thr Val Asp
      115      120      125
Val Arg
      130

```

<210> 705  
 <211> 513  
 <212> DNA  
 <213> Homo sapiens

```

<400> 705
acgcgtat t cgtccaaatg attcaaatca aaacgcgcgc gttaaaaacg atgcaggcga
60
agacaatgcg aataaaaaag gtggtaaata agcatgagtt ttaaaatgac acaatctcaa
120
tacacaagtc tttatggacc aactgtagga gactccgtga gattaggaga tacgaacttg
180
tttgacaaag ttgagaaaga ctatgcaa attggggatg aagctacttt cgggtggcga
240
aaatcaattc gtgatgggat ggctcaaaat cctaattgta caagagatga taaaaatgta
300
gccgatttag ttttaactaa cgcattaatt attgattatg acaagattgt taaagcagat
360
atcggtatta aaaatgggta ttttttaag attggtaaag ctggaaaccc agatataatg
420
gataacgttg acatcatcat tgggtcaaca actgatatta ttgctgctga aggtaaaatt
480
gttactgccg gcggtatcga tacacacgtg cac
513

```

<210> 706  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

```

<400> 706
Met Ser Phe Lys Met Thr Gln Ser Gln Tyr Thr Ser Leu Tyr Gly Pro
1      5      10      15
Thr Val Gly Asp Ser Val Arg Leu Gly Asp Thr Asn Leu Phe Ala Gln
      20      25      30
Val Glu Lys Asp Tyr Ala Asn Tyr Gly Asp Glu Ala Thr Phe Gly Gly
      35      40      45
Gly Lys Ser Ile Arg Asp Gly Met Ala Gln Asn Pro Asn Val Thr Arg

```



```

      50              55              60
Asp Asp Lys Asn Val Ala Asp Leu Val Leu Thr Asn Ala Leu Ile Ile
65              70              75              80
Asp Tyr Asp Lys Ile Val Lys Ala Asp Ile Gly Ile Lys Asn Gly Tyr
      85              90              95
Ile Phe Lys Ile Gly Lys Ala Gly Asn Pro Asp Ile Met Asp Asn Val
      100              105              110
Asp Ile Ile Ile Gly Ala Thr Thr Asp Ile Ile Ala Ala Glu Gly Lys
      115              120              125
Ile Val Thr Ala Gly Gly Ile Asp Thr His Val His
      130              135              140

```

&lt;210&gt; 707

&lt;211&gt; 409

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 707

```

acgcgtggca tcctcagacc accaaagaca atcctgtcct gggaggcagg gagaaagccg
60
gcacactaca cagtgcacag gtgaagccct caggggggtcc tggagcaggg ccacctccct
120
gggggatccc caggtgccat ttcatggca gtgtctatgg acggtcccc ttggcatggt
180
gctgggtggc aatcctggct gtagctgcc cccctgccc tttttgcttc cctccgaggg
240
cattgtgatc atcagtgtga gtctgttggg aaggagagcc aggtccccag gtttgggaaa
300
ggagttaggt tccccagcct gtctggccat cccccccag cccagccct cctgctgggt
360
gacgtgctca gttcgcccc tgctgtactg ggagggggct aggagcata
409

```

&lt;210&gt; 708

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 708

```

Met Leu Leu Ala Pro Ser Gln Tyr Ser Arg Gly Arg Thr Glu His Val
1      5      10      15
Thr Gln Gln Glu Gly Leu Gly Trp Gly Val Met Ala Arg Gln Ala Gly
      20      25      30
Lys Pro Tyr Ser Phe Pro Lys Pro Gly Asp Leu Ala Leu Leu Pro Asn
      35      40      45
Arg Leu Thr Leu Met Ile Thr Met Pro Ser Glu Gly Ser Lys Lys Gly
      50      55      60
Arg Gly Trp Gln Leu Gln Pro Gly Leu Pro Pro Ser Thr Met Pro Arg
65      70      75      80
Gly Ala Val His Arg His Cys His Glu Asn Gly Thr Trp Gly Ser Pro
      85      90      95
Arg Glu Val Ala Leu Leu Gln Asp Pro Leu Arg Ala Ser Pro Val His
      100      105      110
Cys Val Val Cys Arg Leu Ser Pro Cys Leu Pro Gly Gln Asp Cys Leu

```

115 120 125  
 Trp Trp Ser Glu Asp Ala Thr Arg  
 130 135

<210> 709  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 709  
 acgcgtctga cggagagcct cctgagtctc cccacgcaga ggactcagaa agggaatcgg  
 60  
 tgaccacacc tgggccagcg acgtgtggtg cgccagcctc cccagcggat cacctcctcc  
 120  
 tcccctccca ggaggagagt ttctccgaag tccccatgag tgaagcaagc tcagcgaaag  
 180  
 acactccact ctttaggatg gagggagagg atgcccttgt gactcagtat cagagcaaag  
 240  
 ccagtgacca cgaaggttta ttgtctgacc ccttgagtga ccttcagttg gtctcagatt  
 300  
 ttaaattctcc aatcatggcc gatctgaact taagccttcc ttccattcct gaagtcgcat  
 360  
 cggatgatga aagaatagat cagggtgaag atgacggaga tcagggtgaa gatgatggag  
 420  
 agacagcaaa gtcgtcaact ctggacatag gagctttgtc cttgggcttg gtagtcccct  
 480  
 gtcttgagag gggaaagggg cccagtggcg aggcagatag gttggtactg ggggagggcc  
 540  
 tgtgtgattt caggctgcaa gcaccccgag catctgtgac agctccttca gagcagacca  
 600  
 cagagttcgg aattcacaaa ccacatcttg gcaagagctc aagcttggat aaacagctgc  
 660  
 caggccccag tgggtgtgag gaagaaaaac cgatgggaaa tgggagtcca agcccgctc  
 720  
 ctggcacatc cctggacaat cctgtacca gccctcccc ttctgagatc t  
 771

<210> 710  
 <211> 205  
 <212> PRT  
 <213> Homo sapiens

<400> 710  
 Met Ser Glu Ala Ser Ser Ala Lys Asp Thr Pro Leu Phe Arg Met Glu  
 1 5 10 15  
 Gly Glu Asp Ala Leu Val Thr Gln Tyr Gln Ser Lys Ala Ser Asp His  
 20 25 30  
 Glu Gly Leu Leu Ser Asp Pro Leu Ser Asp Leu Gln Leu Val Ser Asp  
 35 40 45  
 Phe Lys Ser Pro Ile Met Ala Asp Leu Asn Leu Ser Leu Pro Ser Ile  
 50 55 60  
 Pro Glu Val Ala Ser Asp Asp Glu Arg Ile Asp Gln Val Glu Asp Asp  
 65 70 75 80  
 Gly Asp Gln Val Glu Asp Asp Gly Glu Thr Ala Lys Ser Ser Thr Leu

```

      85              90              95
Asp Ile Gly Ala Leu Ser Leu Gly Leu Val Val Pro Cys Pro Glu Arg
      100              105              110
Gly Lys Gly Pro Ser Gly Glu Ala Asp Arg Leu Val Leu Gly Glu Gly
      115              120              125
Leu Cys Asp Phe Arg Leu Gln Ala Pro Gln Ala Ser Val Thr Ala Pro
      130              135              140
Ser Glu Gln Thr Thr Glu Phe Gly Ile His Lys Pro His Leu Gly Lys
      145              150              155              160
Ser Ser Ser Leu Asp Lys Gln Leu Pro Gly Pro Ser Gly Gly Glu Glu
      165              170              175
Glu Lys Pro Met Gly Asn Gly Ser Pro Ser Pro Pro Pro Gly Thr Ser
      180              185              190
Leu Asp Asn Pro Val Pro Ser Pro Ser Pro Ser Glu Ile
      195              200              205

```

<210> 711  
 <211> 432  
 <212> DNA  
 <213> Homo sapiens

```

<400> 711
nnggatccga cggcgcaaag ccttaatgaa gggtaggcag ttacctcttt ttctgtagga
60
attctcctgt tttatatcta ctcccccta ggttcacccat actccctcat cttctgagct
120
aatgtgcccg ctttatttgc acttgcatgg aatatgatta tgaacacagt tttatcatt
180
gatgaccacc ccgttatcag gttggcgatt cgtatgttgt tggaacacga gggttataag
240
gtcgttggtg aaacggacaa cggttgtgac gcgatccaaa tggttcgaga atgcctgccg
300
gacctgatca tcctggatat cagcatcccg aaactcgacg gcctcgaagt gctctgccga
360
ttcaacgcca tgaacacatc catgaaaacc ctgattctta ccgccagag tccgacgttg
420
ttcgccacgc gt
432

```

<210> 712  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

```

<400> 712
Met Ile Met Asn Thr Val Phe Ile Ile Asp Asp His Pro Val Ile Arg
1      5      10      15
Leu Ala Ile Arg Met Leu Leu Glu His Glu Gly Tyr Lys Val Val Gly
20     25     30
Glu Thr Asp Asn Gly Cys Asp Ala Ile Gln Met Val Arg Glu Cys Leu
35     40     45
Pro Asp Leu Ile Ile Leu Asp Ile Ser Ile Pro Lys Leu Asp Gly Leu
50     55     60
Glu Val Leu Cys Arg Phe Asn Ala Met Asn Thr Ser Met Lys Thr Leu

```

```

65                               70                               75                               80
Ile Leu Thr Ala Gln Ser Pro Thr Leu Phe Ala Thr Arg
      85                               90

<210> 713
<211> 465
<212> DNA
<213> Homo sapiens

<400> 713
atcctgatcg ccaacggtgg tatgcagaac ccggtgggcg cggtgttcaa ccccgacacc
60
atgcgcatgg aaatgaccga cttcgccgcg gtgatcttca acccggtggc gcaggccaag
120
ttcgtgcata cggtcagcgc gggctacgtg gccggcgcca tgttcgtcat gtcgatcagc
180
gcctggtacc tgctcaaggg ccgccacacc gacctggcca agcgctcgat ggcggtcgcc
240
gccagcttcg gcctggcgtc ggcgctgtcg gtcgctcgtc tgggtgacga aagcggttat
300
ctcaccaccg aacaccagaa gatgaagatc gcggccatgg aatccatgtg gcacaccgag
360
ccggcgcccc cgtccttcaa cctgatcgcg ctgcccaccc aggccgaacg caagaacgac
420
ttgccatcg agattcccta cgtcatgngc ctcatcgga cgcgt
465

```

```
<210> 714
<211> 155
<212> PRT
<213> Homo sapiens
```

```

<400> 714
Ile Leu Ile Ala Asn Gly Gly Met Gln Asn Pro Val Gly Ala Val Phe
  1                      5                      10                      15
Asn Pro Asp Thr Met Arg Met Glu Met Thr Asp Phe Ala Ala Val Ile
      20                      25                      30
Phe Asn Pro Val Ala Gln Ala Lys Phe Val His Thr Val Ser Ala Gly
      35                      40                      45
Tyr Val Ala Gly Ala Met Phe Val Met Ser Ile Ser Ala Trp Tyr Leu
      50                      55                      60
Leu Lys Gly Arg His Thr Asp Leu Ala Lys Arg Ser Met Ala Val Ala
65                      70                      75                      80
Ala Ser Phe Gly Leu Ala Ser Ala Leu Ser Val Val Val Leu Gly Asp
      85                      90                      95
Glu Ser Gly Tyr Leu Thr Thr Glu His Gln Lys Met Lys Ile Ala Ala
      100                      105                      110
Met Glu Ser Met Trp His Thr Glu Pro Ala Pro Ala Ser Phe Asn Leu
      115                      120                      125
Ile Ala Leu Pro Asn Gln Ala Glu Arg Lys Asn Asp Phe Ala Ile Glu
      130                      135                      140
Ile Pro Tyr Val Met Xaa Leu Ile Gly Thr Arg
145                      150                      155

```

<210> 715  
 <211> 354  
 <212> DNA  
 <213> Homo sapiens

<400> 715  
 nnaccggtgg atgccaacga atatcgtggc gagctgaaag tcggcgccat caccaccgcc  
 60  
 cagaccggcc tgctgcctca ggcaactggtg cgtttgcgcc aggcagcgcc gacggtggag  
 120  
 tgcaagtggg taccgggggt ttccctggag ttgctcagcc aggtggacgc aggcgagctg  
 180  
 gactcggcga tcatcattcg cccgcccttt gatttgccca aggagttgca cgtacaggta  
 240  
 ctgcgcaagg agccgtttgt gttgatcgtg cccagggcgg tcgggggtga tgaccggtg  
 300  
 caactgctcg aagctcatcc ccacgtgcgc tacgaccgcg cttcgtttgg cggg  
 354

<210> 716  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 716  
 Xaa Pro Val Asp Ala Asn Glu Tyr Arg Gly Glu Leu Lys Val Gly Ala  
 1 5 10 15  
 Ile Thr Thr Ala Gln Thr Gly Leu Leu Pro Gln Ala Leu Val Arg Leu  
 20 25 30  
 Arg Gln Ala Ala Pro Thr Val Glu Cys Lys Leu Val Pro Gly Val Ser  
 35 40 45  
 Leu Glu Leu Leu Ser Gln Val Asp Ala Gly Glu Leu Asp Ser Ala Ile  
 50 55 60  
 Ile Ile Arg Pro Pro Phe Asp Leu Pro Lys Glu Leu His Val Gln Val  
 65 70 75 80  
 Leu Arg Lys Glu Pro Phe Val Leu Ile Val Pro Gln Ala Val Gly Gly  
 85 90 95  
 Asp Asp Pro Leu Gln Leu Leu Glu Ala His Pro His Val Arg Tyr Asp  
 100 105 110  
 Arg Ala Ser Phe Gly Gly  
 115

<210> 717  
 <211> 401  
 <212> DNA  
 <213> Homo sapiens

<400> 717  
 acgcgtatct tttcggtaaa cctactaatt tttcattcaa cgctcgacgc ccaggtaaag  
 60  
 ccgttaagtc atctaaatag gccattctgt ggctctccat cagtaagaac caaatccata  
 120  
 ggagaagttg agcggatagt aatgcatcaa attgatgctg agaaaccgaa aaatgggaca  
 180

atataatcaa gctgacaata ctgatcaaac cactcgcacg aaagctacta ccgcttgacc  
 240  
 accaagcaga aaaaaccaat gaaatgctta aaaataaaat cgtccaaagt aaaaagctag  
 300  
 accaggtggt agccagatta aaaataggcc gctctagaaa atgaaaagaa atccaatgag  
 360  
 attcaacggc gtagcaccag cacagcaaca tagccactag t  
 401

<210> 718

<211> 130

<212> PRT

<213> Homo sapiens

<400> 718

Met	Leu	Leu	Cys	Trp	Cys	Tyr	Ala	Val	Glu	Ser	His	Trp	Ile	Ser	Phe
1			5					10						15	
His	Phe	Leu	Glu	Arg	Pro	Ile	Phe	Asn	Leu	Ala	Thr	Thr	Trp	Ser	Ser
		20					25						30		
Phe	Leu	Leu	Trp	Thr	Ile	Leu	Phe	Leu	Ser	Ile	Ser	Leu	Val	Phe	Ser
	35					40					45				
Ala	Trp	Trp	Ser	Ser	Gly	Ser	Ser	Phe	His	Ala	Ser	Gly	Leu	Ile	Ser
	50					55					60				
Ile	Val	Ser	Leu	Ile	Ile	Leu	Ser	His	Phe	Ser	Val	Ser	Gln	His	Gln
65				70				75					80		
Phe	Asp	Ala	Leu	Leu	Ser	Ala	Gln	Leu	Leu	Leu	Trp	Ile	Trp	Phe	Leu
			85					90					95		
Leu	Met	Glu	Ser	His	Arg	Met	Ala	Tyr	Leu	Asp	Asp	Leu	Thr	Ala	Leu
			100				105						110		
Pro	Gly	Arg	Arg	Ala	Leu	Asn	Glu	Lys	Leu	Val	Gly	Leu	Pro	Lys	Arg
		115				120						125			
Tyr	Ala														
	130														

<210> 719

<211> 685

<212> DNA

<213> Homo sapiens

<400> 719

tatatagggc tatctacctt attcacagca cattccatct acacaacctt gtagcggtca  
 60  
 ctcttgaagg cggattttca taggcgctgc gcctctcata ttcaagcatc aaggcaatcc  
 120  
 aatctccctg cggttggttaac tgggcaaaag aaagacctct gcagtccagc aacctcatcg  
 180  
 tgcaaatgcc gtggcggtggt caactctgac ggcttggaag ctgcagacct tgtcaaagga  
 240  
 cctcggccga aattcacctt tgatctcttt gtcttggtcca actcttggtcc ctgagaatga  
 300  
 aactgtcttc tgagagtcca tcaatgcgac gctgactcgt gagaagtgct gaatcacgtc  
 360  
 gccattttgg agacctgcca acgcagctct ggaacctgcc aggacgcctt ccacaacacc  
 420

agaacgcagc gactttgcgt taaatccaag ctcaaacacc tcttgctcca caggcctgag  
 480  
 cataaaaagg tattctgcga cgggaaatgt aaagtctgag cttaggtgca gagtaccgcc  
 540  
 atcgatcagt gtctgatact gcttgctccg gacttctttg ccgagcaatg ggtatagcgt  
 600  
 tttcaaccaa gtggaagcag tcgtttgctc accctggcga ttccggcgag ttagggacat  
 660  
 gaccacgtca tcgatgggat ttgac  
 685

<210> 720

<211> 161

<212> PRT

<213> Homo sapiens

<400> 720

Met	Ser	Leu	Thr	Arg	Arg	Asn	Arg	Gln	Gly	Glu	Gln	Thr	Thr	Ala	Ser
1				5				10						15	
Thr	Trp	Leu	Lys	Thr	Leu	Tyr	Pro	Leu	Leu	Gly	Lys	Glu	Val	Ala	Asp
		20					25					30			
Lys	Gln	Tyr	Gln	Thr	Leu	Ile	Asp	Gly	Gly	Thr	Leu	His	Leu	Ser	Ser
	35					40					45				
Asp	Phe	Thr	Phe	Pro	Val	Ala	Glu	Tyr	Leu	Phe	Met	Leu	Arg	Pro	Val
50						55				60					
Glu	Gln	Glu	Val	Phe	Glu	Leu	Gly	Phe	Asn	Ala	Lys	Ser	Leu	Arg	Ser
65					70					75				80	
Gly	Val	Val	Glu	Gly	Val	Leu	Ala	Gly	Ser	Arg	Ala	Ala	Leu	Ala	Gly
			85					90					95		
Leu	Gln	Asn	Gly	Asp	Val	Ile	Gln	His	Phe	Ser	Arg	Val	Ser	Val	Ala
		100						105					110		
Leu	Met	Asp	Ser	Gln	Lys	Thr	Val	Ser	Phe	Ser	Gly	Thr	Arg	Val	Gly
		115					120					125			
Gln	Asp	Lys	Glu	Ile	Lys	Gly	Glu	Phe	Arg	Pro	Arg	Ser	Phe	Asp	Lys
130						135					140				
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<211> 579

<212> DNA

<213> Homo sapiens

<400> 721

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 Val Tyr Pro Glu Met Arg Met Tyr Ser Asp Ile Ile Ala Tyr Gly Val  
 100 105 110  
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<211> 128

<212> PRT

<213> Homo sapiens

<400> 724

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		20					25					30			
Thr	Pro	Pro	Gln	Trp	Arg	Leu	Phe	Arg	Glu	Gly	Asp	Tyr	Gln	Met	Arg
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Ile	Asp	Thr	Arg	Ser	Gly	Thr	Pro	Thr	Leu	Met	Leu	Thr	Val	Gln	Ser
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Val	Thr	Asp	Lys	Pro	Val	Thr	Asp	Val	Thr	Arg	Gln	Cys	Pro	Lys	Trp
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Asp	Gly	Lys	Pro	Leu	Thr	Leu	Asp	Val	Thr	Asn	Thr	Phe	Pro	Glu	Gly
			85					90					95		
Ser	Val	Val	Arg	Asp	Phe	Tyr	Ser	Lys	Gln	Thr	Ala	Met	Val	Gln	Gln
			100					105				110			
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<211> 521

<212> DNA

<213> Homo sapiens

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 Ser Thr Pro Ser Pro Ser Ser Cys Ser Leu Pro Glu Arg Leu Cys Trp  
 50 55 60  
 Glu Trp Cys Ile Gly Gly Leu Gln Ala Leu Leu Gly Ser Arg Cys Ser  
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 85 90 95  
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 Ala His Val His Gly Ser Leu Asp Gly Gln Val Gly Val Phe Phe Val  
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&lt;210&gt; 730

&lt;211&gt; 797

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 730

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Ala	Ser	Ser	Leu	Ser	Ser	Gln	Lys	Glu	Val	Ala	Ala	Thr	Glu	Glu	Asp
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Val	Thr	Arg	Leu	Pro	Ser	Pro	Thr	Ser	Pro	Phe	Ser	Ser	Leu	Ser	Gln
			100					105					110		
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Trp Val Trp Asp Gln Glu Glu Glu Arg Lys Arg Gln Glu Arg Trp Gln
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Lys Glu Gln Asp Arg Leu Leu Gln Glu Lys Tyr Gln Arg Glu Gln Glu
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Gly Lys Lys Pro Gln Asp Gln Leu Val Ile Glu Arg Glu Arg Lys Trp
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Glu Gln Gln Leu Gln Glu Glu Gln Glu Gln Lys Arg Leu Gln Ala Glu
465          470          475          480
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Pro Gly Asp Arg Asn Lys Ser Arg Ser Thr Thr Glu Leu Asp Asp Tyr
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Ser	Gly	Ala	Glu	Val	Arg	Ile	Arg	Asn	His	Gln	Leu	Tyr	Cys	Asn	Asp			
770										775				780				
Cys	Tyr	Leu	Arg	Phe	Lys	Ser	Gly	Arg	Pro	Thr	Ala	Met						
785	790										795							

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<210> 731
<211> 513
<212> DNA
<213> Homo sapiens
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<400> 731
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60
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120
tcttcaaatg actgactggg gaaacagatt gttggaaaaa cactttcggg ttgcctcgat
180
ggggtcaata ccttatcagg ccacaggaaa gacaaaggaa aatgcttcct gctggagcat
240
gtgcacatat gttgttcctt taactccaaa tacgtatgca ggggtggtgg taggatcaga
300
aaatgtgtga tcagaaagtg accagttccc caccattttg tgtgggtttt attttctttc
360
tgctccgtgt tgactctttt ccccaaca cggaagctgc ttaatccaaa gacttggaac
420
atctcattct gtttcagatc cattccaaca aaatgatcag ttggtggcct atgtaaaaag
480
cagctccatg actacattta aatattgact agt
513

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<210> 732



<211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 732  
 Met Asp Leu Lys Gln Asn Glu Met Val Gln Val Phe Gly Leu Ser Ser  
 1 5 10 15  
 Phe Arg Val Val Gly Lys Arg Val Asn Thr Glu Gln Lys Glu Asn Lys  
 20 25 30  
 Thr His Thr Lys Trp Trp Gly Thr Gly His Phe Leu Ile Thr His Phe  
 35 40 45  
 Leu Ile Leu Pro Pro Pro Leu His Thr Tyr Leu Glu Leu Lys Glu Gln  
 50 55 60  
 His Met Cys Thr Cys Ser Ser Arg Lys His Phe Pro Leu Ser Phe Leu  
 65 70 75 80  
 Trp Pro Asp Lys Val Leu Thr Pro Ser Arg Gln Pro Glu Ser Val Phe  
 85 90 95  
 Pro Thr Ile Cys Phe Pro Ser Gln Ser Phe Glu Glu Ser Arg Glu Ala  
 100 105 110  
 Glu

<210> 733  
 <211> 4366  
 <212> DNA  
 <213> Homo sapiens

<400> 733  
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 120  
 ggaggectct tgaagaactc caggcctatc atgctgtctc tccgctaaag cctgaggccc  
 180  
 gaggtcagag gattcaggaa ggctctgcag tcggcccagg agggcggggt cccgtggtgg  
 240  
 aggcggggag agggaaggac cgcacggagc accaaccctt gctcggcccc gtaccaggaa  
 300  
 gcgctggggg gcagaggagc ggagttgagg cagaagccag gtgaggctgg agtcctgggg  
 360  
 taggcaggct gtcgctgccg ccgccgctgc ctgagatgga aatcggggga ggaagctcgc  
 420  
 ggaagaaaca gcggagggtt cgtggaaaaa aaagcaatgg ctgagctaag ggatggggta  
 480  
 ccaggttagg gggaggaaac ggtagagaga aatagggtgg gctcccgcgc atgctcaata  
 540  
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 600  
 ggcgcggaat ttggagaccc acttcgggaa aggtaaaatg cgggcgcaat tttagggtag  
 660  
 ctgtgggacc cgggctctta gggctttgac acaggacggg cctgggcccga aagcccaggc  
 720  
 acgcccagacc agagagtgtt tctccactcc cggactctgc cagtcaggat ggtggtgcct  
 780

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 960  
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 1140  
 tgcactttga gcacatggg ctctgctgag atgtgccgag acctggcccc agagggtggag  
 1200  
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 1260  
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 1320  
 catgagcgtc accatggcat cctgctgggc accatcacgc tgatcacgga gctctgcgaa  
 1380  
 cgaagccctg cagccctcag gcacttccga aaggtggtac cccagctggt acacatcctc  
 1440  
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 1500  
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 1620  
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 1740  
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 1920  
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 1980  
 atcctgctgg ctgcagagag gtttgtctca accaaacgct ggcacataga caccatcctg  
 2040  
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 2100  
 ctgattgggg gggcccagga gctacatgcc tactctgtgc gccgcctcta caatgccctg  
 2160  
 gcagaagaca tttcccagca accactggtg caggtggcag cctggtgcat tggggagtat  
 2220  
 ggggacctcc tgctggcagg gaactgcgag gagattgagc cccttcaggc ggacgaagag  
 2280  
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 2340  
 ggatatgccc tcacagccct catgaagctc agcactcgcc tctgtgggga caacaaccgc  
 2400

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2460  
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2940  
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3540  
agtcagatta gaatttctag agttctaaca gcgattccca accatttctt caacttttct  
3600  
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 4140  
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 4200  
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 4260  
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 4320  
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 4366

<210> 734

<211> 364

<212> PRT

<213> Homo sapiens

<400> 734

Met	Val	Val	Pro	Ser	Leu	Lys	Leu	Gln	Asp	Leu	Ile	Glu	Glu	Ile	Arg
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Gly	Ala	Lys	Thr	Gln	Ala	Gln	Glu	Arg	Glu	Val	Ile	Gln	Lys	Glu	Cys
			20					25					30		
Ala	His	Ile	Arg	Ala	Ser	Phe	Arg	Asp	Gly	Asp	Pro	Val	His	Arg	His
		35					40					45			
Arg	Gln	Leu	Ala	Lys	Leu	Leu	Tyr	Val	His	Met	Leu	Gly	Tyr	Pro	Ala
	50				55						60				
His	Phe	Gly	Gln	Met	Glu	Cys	Leu	Lys	Leu	Ile	Ala	Ser	Ser	Arg	Phe
65					70					75				80	
Thr	Asp	Lys	Arg	Val	Gly	Tyr	Leu	Gly	Ala	Met	Leu	Leu	Leu	Asp	Glu
			85					90						95	
Arg	His	Asp	Ala	His	Leu	Leu	Ile	Thr	Asn	Ser	Ile	Lys	Asn	Asp	Leu
			100					105					110		
Ser	Gln	Gly	Ile	Gln	Pro	Val	Gln	Gly	Leu	Ala	Leu	Cys	Thr	Leu	Ser
		115					120					125			
Thr	Met	Gly	Ser	Ala	Glu	Met	Cys	Arg	Asp	Leu	Ala	Pro	Glu	Val	Glu
	130					135					140				
Lys	Leu	Leu	Leu	Gln	Pro	Ser	Pro	Tyr	Val	Arg	Lys	Lys	Ala	Ile	Leu
145					150					155				160	
Thr	Ala	Val	His	Met	Ile	Arg	Lys	Val	Pro	Glu	Leu	Ser	Ser	Val	Phe
			165						170					175	
Leu	Pro	Pro	Cys	Ala	Gln	Leu	Leu	His	Glu	Arg	His	His	Gly	Ile	Leu
			180					185					190		
Leu	Gly	Thr	Ile	Thr	Leu	Ile	Thr	Glu	Leu	Cys	Glu	Arg	Ser	Pro	Ala
		195					200					205			
Ala	Leu	Arg	His	Phe	Arg	Lys	Val	Val	Pro	Gln	Leu	Val	His	Ile	Leu
	210					215						220			
Arg	Thr	Leu	Val	Thr	Met	Gly	Tyr	Ser	Thr	Glu	His	Ser	Ile	Ser	Gly
225					230					235				240	
Val	Ser	Asp	Pro	Phe	Leu	Gln	Val	Gln	Ile	Leu	Arg	Leu	Leu	Arg	Ile
			245						250					255	
Leu	Gly	Arg	Asn	His	Glu	Glu	Ser	Ser	Glu	Thr	Met	Asn	Asp	Leu	Leu
		260						265				270			
Ala	Gln	Val	Ala	Thr	Asn	Thr	Asp	Thr	Ser	Arg	Asn	Ala	Gly	Asn	Ala

275	280	285
Val Leu Phe Glu Thr	Val Leu Thr Ile Met Asp	Ile Arg Ser Ala Ala
290	295	300
Gly Leu Arg Val Leu Ala	Val Asn Ile Leu Gly Arg	Phe Leu Leu Asn
305	310	315
Ser Asp Arg Asn Ile Arg	Tyr Val Ala Leu Thr	Ser Leu Leu Arg Leu
325	330	335
Val Gln Ser Asp His Ser	Ala Val Gln Arg His Arg	Pro Thr Val Val
340	345	350
Glu Cys Leu Arg Glu Thr	Asp Ala Ser Leu Ser Arg	
355	360	

<210> 735  
 <211> 597  
 <212> DNA  
 <213> Homo sapiens

<400> 735  
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 120  
 tgcttggtgt cctcgatccc gctctgaccg ccactggac cgctcaaccc aggacatcct  
 180  
 cagtgccatc cagcagctgg ctgcaccgct ggactaccc atcttcgtgg tgggtgccac  
 240  
 agcgcgcgac attctgctga cacacgtgtt cggtatcgag accggacgtg ccacgctcga  
 300  
 cgtggatttc gccgttgccg tagaacattg gccgcagttc gaaaacatca agcagcacct  
 360  
 gctagccaac gaccatttcg actctgccgc cagcatcacc catcgactgc tctatcgcac  
 420  
 gagcgacaac acgatcgccc ggccaatcga tctcatccca ttggcgcgca tcgaacagcc  
 480  
 gccagccacc atcaaattggc cgcccgacat ggctgtcatg atgaatgttg ctgggtacgc  
 540  
 agatgcctgg cgggcccgcag tcgaagtaga gtttgtgccc gggcgagca tacgcgt  
 597

<210> 736  
 <211> 175  
 <212> PRT  
 <213> Homo sapiens

<400> 736  
 Met Asp Ser Arg Asn Leu Glu Thr Ala Asn Leu Ile Pro Glu Lys Ile  
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 Ile Ala Trp Cys Pro Arg Ser Arg Ser Asp Arg Pro Leu Asp Arg Ser  
 20 25 30  
 Thr Gln Asp Ile Leu Ser Ala Ile His Asp Val Ala Ala Pro Leu Ala  
 35 40 45  
 Leu Pro Ile Phe Val Val Gly Ala Thr Ala Arg Asp Ile Leu Leu Thr  
 50 55 60  
 His Val Phe Gly Ile Glu Thr Gly Arg Ala Thr Leu Asp Val Asp Phe

```

65              70              75              80
Ala Val Ala Val Glu His Trp Pro Gln Phe Glu Asn Ile Lys Gln His
              85              90              95
Leu Leu Ala Asn Asp His Phe Asp Ser Ala Ala Ser Ile Thr His Arg
              100             105             110
Leu Leu Tyr Arg Thr Ser Asp Asn Thr Ile Ala Arg Pro Ile Asp Leu
              115             120             125
Ile Pro Phe Gly Gly Ile Glu Gln Pro Pro Ala Thr Ile Lys Trp Pro
              130             135             140
Pro Asp Met Ala Val Met Met Asn Val Ala Gly Tyr Ala Asp Ala Trp
145              150              155              160
Arg Ala Ala Val Glu Val Glu Phe Val Pro Gly Arg Ser Ile Arg
              165              170              175

```

<210> 737  
 <211> 497  
 <212> DNA  
 <213> Homo sapiens

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<400> 737
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60
cgcgccggga tcgttgggta cggatacgat cccaaccctc acgccgaccg tgccgacctc
120
caccctgccc tgtcctggat cagccacgac accttcgtta aaactgtcag tgtgggggat
180
accatcggct acggcagaac atggacagcc agcgaaacga caaaaatcgc caccgtccca
240
gtcgggttacg ccgacggact gtcccaggga ctgtcaaata aaggacacgt tctcattaga
300
gggtccgttc atcccatcgt cggtcggatac tgcattggacc aattcatggt cgatcttggc
360
cccgattcga acgtcacggt gggagatgag gtggtgctca ttggaacca ggaggacgaa
420
actctgaccg ctgatgacat ggccgaactc ctcggaacca ttagctacga gatcacttgc
480
gccatttcca aacgcgt
497

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<210> 738  
 <211> 165  
 <212> PRT  
 <213> Homo sapiens

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<400> 738
Xaa Arg Leu Ala Asn Ser Gly Ala Ile Leu Gly His Asp Leu Gly Lys
1              5              10              15
Thr Ser Met Val Arg Ala Gly Ile Val Gly Tyr Gly Tyr Asp Pro Asn
              20              25              30
Pro His Ala Asp Arg Ala Asp Leu His Pro Ala Leu Ser Trp Ile Ser
              35              40              45
His Val Thr Phe Val Lys Thr Val Ser Val Gly Asp Thr Ile Gly Tyr
              50              55              60
Gly Arg Thr Trp Thr Ala Ser Glu Thr Thr Lys Ile Ala Thr Val Pro

```

```

65          70          75          80
Val Gly Tyr Ala Asp Gly Leu Ser Arg Gly Leu Ser Asn Lys Gly His
          85          90          95
Val Leu Ile Arg Gly Ser Val His Pro Ile Val Gly Arg Ile Cys Met
          100          105          110
Asp Gln Phe Met Val Asp Leu Gly Pro Asp Ser Asn Val Thr Val Gly
          115          120          125
Asp Glu Val Val Leu Ile Gly Thr Gln Glu Asp Glu Thr Leu Thr Ala
          130          135          140
Asp Asp Met Ala Glu Leu Leu Gly Thr Ile Ser Tyr Glu Ile Thr Cys
145          150          155          160
Ala Ile Ser Lys Arg
          165

```

<210> 739  
 <211> 438  
 <212> DNA  
 <213> Homo sapiens

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<400> 739
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acggcctcat cagcagctgt gggctcaggc cccctcccag aggcggagca ggcgtggccg
120
cagagcagcg gggaggagga gctgcagctc cagctggccc tggccatgag caaggaggag
180
gccgaccagc ccccgctctg cgcccccgag gacgacgccc agctccagct ggcccttagt
240
ttgagccgag aagagcatga taaggaggag cggatccgct gcggggatga cctgcggctg
300
cagatggcaa tcgaggagag caagagggag actgggggca aggaggagtc gtccctcatg
360
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420
ccagcaccca tggctgct
438

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<210> 740  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens

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<400> 740
Arg Leu Arg Glu Glu Arg Ala His Ala Leu Lys Thr Lys Glu Lys Leu
1      5      10      15
Ala Gln Thr Ala Thr Ala Ser Ser Ala Ala Val Gly Ser Gly Pro Pro
20     25     30
Pro Glu Ala Glu Gln Ala Trp Pro Gln Ser Ser Gly Glu Glu Glu Leu
35     40     45
Gln Leu Gln Leu Ala Leu Ala Met Ser Lys Glu Glu Ala Asp Gln Pro
50     55     60
Pro Ser Cys Gly Pro Glu Asp Asp Ala Gln Leu Gln Leu Ala Leu Ser
65     70     75     80
Leu Ser Arg Glu Glu His Asp Lys Glu Glu Arg Ile Arg Arg Gly Asp

```

				85					90					95					
Asp	Leu	Arg	Leu	Gln	Met	Ala	Ile	Glu	Glu	Ser	Lys	Arg	Glu	Thr	Gly				
			100						105					110					
Gly	Lys	Glu	Glu	Ser	Ser	Leu	Met	Asp	Leu	Ala	Asp	Val	Phe	Thr	Pro				
		115					120					125							
Pro	Ala	Pro	Ala	Pro	Thr	Thr	Asp	Pro	Trp	Gly	Gly	Pro	Ala	Pro	Met				
		130				135						140							
Ala	Ala																		
145																			

&lt;210&gt; 741

&lt;211&gt; 726

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 741

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60
aatttgccgg tcactctgct cgtcggggccc actgctagcg gaaaatcagg gctagcgggtg
120
cgagtgtgcc gccgcttgta tgtcgatgag caccgcgcg aaattattaa tactgactcg
180
atgggtgggtg atcgcgggat ggacattggc actgccaccc ctacactgcg cgagcagcgc
240
acggtagtgc atcacctggg gtcgattctt gatgtgactg tgccctcttc gctagtactg
300
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360
ttggtgggag ggtctgcgct gtacaccaag gccatcattg acgaaatgtc catcccgcca
420
actgatccgg aagtgagggc tcggtggcag gagaagctag atgccgaggg gccgcgagtt
480
ctgcatgacg agcttgcccg tcgcatccc aaggcggctg agtcaatctt gcccggaac
540
ggcagggcga tcgtttcgtg ccctcgaagt ttattgaccc tgacagggtc ctttactgcc
600
accgatcccc gacgggaccc tccactggcc aagacgggtc aaatgggctt agaactgtcg
660
cgcaaagaca tagaccagcg tattgccgat cgggttgacc agatgtgggc atacggtttc
720
gtcgac
726

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&lt;210&gt; 742

&lt;211&gt; 242

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 742

Ala	Ser	Leu	Arg	Pro	Arg	Cys	Cys	Lys	Asp	Val	Ala	Thr	Val	Arg	Lys				
1				5				10						15					
Asn	Glu	Tyr	Val	Asn	Leu	Pro	Val	Ile	Cys	Leu	Val	Gly	Pro	Thr	Ala				
		20					25					30							
Ser	Gly	Lys	Ser	Gly	Leu	Ala	Val	Arg	Val	Cys	Arg	Arg	Leu	Tyr	Val				



```

      35              40              45
Asp Glu His Pro Ala Glu Ile Ile Asn Thr Asp Ser Met Val Val Tyr
      50              55              60
Arg Gly Met Asp Ile Gly Thr Ala Thr Pro Thr Leu Arg Glu Gln Arg
      65              70              75              80
Thr Val Val His His Leu Val Ser Ile Leu Asp Val Thr Val Pro Ser
      85              90              95
Ser Leu Val Leu Met Gln Thr Leu Ala Arg Asp Ala Val Glu Asp Cys
      100             105             110
Leu Ser Arg Gly Val Ile Pro Val Leu Val Gly Gly Ser Ala Leu Tyr
      115             120             125
Thr Lys Ala Ile Ile Asp Glu Met Ser Ile Pro Pro Thr Asp Pro Glu
      130             135             140
Val Arg Ala Arg Trp Gln Glu Lys Leu Asp Ala Glu Gly Pro Arg Val
      145             150             155             160
Leu His Asp Glu Leu Ala Arg Arg Asp Pro Lys Ala Ala Glu Ser Ile
      165             170             175
Leu Pro Gly Asn Gly Arg Arg Ile Val Ser Cys Pro Arg Ser Leu Leu
      180             185             190
Thr Leu Thr Gly Ser Phe Thr Ala Thr Asp Pro Arg Arg Asp Pro Pro
      195             200             205
Leu Ala Lys Thr Val Gln Met Gly Leu Glu Leu Ser Arg Lys Asp Ile
      210             215             220
Asp Gln Arg Ile Ala Asp Arg Val Asp Gln Met Trp Ala Tyr Gly Phe
      225             230             235             240
Val Asp

```

&lt;210&gt; 743

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 743

```

naaaaaagtg atggtttcgg atctgtggcc agtcgtcttg caagaaatca ttatgacgtg
60
gatgaggggca acagcancat tcatgttaat caagacattg cgcgcagaac agggacggga
120
aagctatttg tacgagtgtg cccggcgcac gtgtactcag aggagcccga tggcactatt
180
tccgtggagt acgcagcgtg tctggagtgt ggcacttgtc tggcgggtgc tgcgccaggg
240
tcgcttgaat ggcactatcc cgcaggtgca atgggtatct cgttcagaga aggatgaagt
300
ccttggtgggc gactgtaaag cgacatggcc gtcgctcggg aggaggaatt gtggtgtccg
360
caccaaatag tgctcaggat gaagttcgtc atggaaatcc ggctccaacc gtttcggggag
420
ctggtcgcga
430

```

&lt;210&gt; 744

&lt;211&gt; 98

&lt;212&gt; PRT

<213> Homo sapiens

<400> 744

```

Xaa Lys Ser Asp Gly Phe Gly Ser Val Ala Ser Arg Leu Ala Arg Asn
 1           5           10           15
His Tyr Asp Val Asp Glu Gly Asn Ser Xaa Ile His Val Asn Gln Asp
      20           25           30
Ile Ala Arg Arg Thr Gly Thr Gly Lys Leu Leu Val Arg Val Cys Pro
      35           40           45
Ala His Val Tyr Ser Glu Glu Pro Asp Gly Thr Ile Ser Val Glu Tyr
      50           55           60
Ala Ala Cys Leu Glu Cys Gly Thr Cys Leu Ala Val Ala Ala Pro Gly
65           70           75           80
Ser Leu Glu Trp His Tyr Pro Ala Gly Ala Met Gly Ile Ser Phe Arg
      85           90           95
Glu Gly

```

<210> 745

<211> 362

<212> DNA

<213> Homo sapiens

<400> 745

```

cggccgattg aagcgctcgct gcggtttgag tcggtgatgg atgcggtgga cggtgcttcg
60
gcgtcgtggt ggcgcatggc gcggtatttc atcgccgagc ttgaacgcag cagcgagttg
120
tatgagcagg cggcgtttac ccgcgatctg gaaagctcgc tgatcaaggg cctgacctc
180
gcccagccga acaactactc cgaagaactg cgcgacgtac tcggcgtgaa gctgccgcat
240
tacttgattc gcgcgcgga gtacatccac gacaacgccc gcgaagccgt gcatctggaa
300
gacctggaaa ccgctgccgg ggtatcgcgg ttcaagttgt tcgatgcggt tcgcaaatac
360
tt
362

```

<210> 746

<211> 108

<212> PRT

<213> Homo sapiens

<400> 746

```

Met Asp Ala Val Asp Gly Ala Ser Ala Ser Trp Trp Arg Met Ala Arg
 1           5           10           15
Tyr Phe Ile Ala Glu Leu Glu Arg Ser Ser Glu Leu Tyr Glu Gln Ala
      20           25           30
Ala Phe Thr Arg Asp Leu Glu Ser Ser Leu Ile Lys Gly Leu Ile Leu
      35           40           45
Ala Gln Pro Asn Asn Tyr Ser Glu Glu Leu Arg Asp Val Leu Gly Val
      50           55           60
Lys Leu Pro His Tyr Leu Ile Arg Ala Arg Gln Tyr Ile His Asp Asn

```

65                      70                      75                      80  
 Ala Arg Glu Ala Val His Leu Glu Asp Leu Glu Thr Ala Ala Gly Val  
                          85                      90                      95  
 Ser Arg Phe Lys Leu Phe Asp Ala Phe Arg Lys Tyr  
                          100                      105

<210> 747  
 <211> 416  
 <212> DNA  
 <213> Homo sapiens

<400> 747  
 nacgcgttga tcgcccgcga ccgtttcatc ccgcaatcac ccgacatggc ggcctatttt  
 60  
 ctgaatgccg atggcacgcc taaagccacc ggcacgctgc tcaagaaccc agcgctggcc  
 120  
 gccgtgttca aacgtatcgc caaggaagga ccggacgcgc tgtaccacgg gccgattgcc  
 180  
 gacgagatcg cgcgcaaggt tcagggcaac cgcaatgcgg gcagcctgtc gcaagcggac  
 240  
 ctcaaggctt acaccgcaa ggaacgcacg ccgctgtgca ccgactacaa gcaatatcag  
 300  
 gtgtgcggca tgccaccgcc gtcgtcaggg gggattgcgg tggcgcagat cctcggcacg  
 360  
 ctgcaggccg tggaagcccg cgacccaagc ctggccatcg ccccatgaa accggt  
 416

<210> 748  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

<400> 748  
 Xaa Ala Leu Ile Ala Ala Asp Arg Phe Ile Pro Gln Ser Pro Asp Met  
 1                      5                      10                      15  
 Ala Ala Tyr Phe Leu Asn Ala Asp Gly Thr Pro Lys Ala Thr Gly Thr  
                          20                      25                      30  
 Leu Leu Lys Asn Pro Ala Leu Ala Ala Val Phe Lys Arg Ile Ala Lys  
                          35                      40                      45  
 Glu Gly Pro Asp Ala Leu Tyr His Gly Pro Ile Ala Asp Glu Ile Ala  
                          50                      55                      60  
 Arg Lys Val Gln Gly Asn Arg Asn Ala Gly Ser Leu Ser Gln Ala Asp  
 65                      70                      75                      80  
 Leu Lys Ala Tyr Thr Ala Lys Glu Arg Thr Pro Leu Cys Thr Asp Tyr  
                          85                      90                      95  
 Lys Gln Tyr Gln Val Cys Gly Met Pro Pro Pro Ser Ser Gly Gly Ile  
                          100                      105                      110  
 Ala Val Ala Gln Ile Leu Gly Thr Leu Gln Ala Val Glu Ala Arg Asp  
                          115                      120                      125  
 Pro Arg Leu Ala Ile Ala Pro Met Lys Pro  
                          130                      135

<210> 749  
 <211> 1211

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 749

nagtcctaga cgccagaccc gctcagaccc tcctgccagg tgacagccgc caagatgggg  
 60  
 tcttggggccc tgctgtggcc tcccctgctg ttcaccgggc tgctcgccg acccccgggg  
 120  
 accatggccc agggccagta ctgctctgtg aacaaggaca tctttgaagt agaggagaac  
 180  
 acaaatgtca ccgagccgct ggtggacatc cacgtcccgg agggccagga ggtgaccctc  
 240  
 ggagccttgt ccacccccctt tgcatttcgg atccaggga accagctgtt tctcaacgtg  
 300  
 actcctgatt acgaggagaa gtcactgctt gaggtcagc tgctgtgtca gagcggaggc  
 360  
 acattggtga cccagctaag ggtgttcgtg tcagtgtctg acgtcaatga caatgcccc  
 420  
 gaattccccct ttaagaccaa ggagataagg gtggaggagg acacgaaagt gaactccacc  
 480  
 gtcacccccg agacgcaact gcaggctgag gaccgcgaca aggacgacat tctgttctac  
 540  
 accctccagg aatgacagc aggtgccagt gactacttct ccctggtgag tgtaaaccgt  
 600  
 ccgcccctga ggctggaccg gcccctggac ttctacgagc ggccgaacat gaccttctgg  
 660  
 ctgctggtgc gggacactcc gggggagaat gtggaacca gccacactgc caccgccaca  
 720  
 ctagtgtgta acgtggtgcc cgccgacctg cgcccccggt ggttcctgcc ctgcaccttc  
 780  
 tcagatggct acgtctgcat tcaagctcag taccacgggg ctgtccccac ggggcacata  
 840  
 ctgccatctc ccctcgctct gcgtcccgga cccatctacg ctgaggacgg agaccgcggc  
 900  
 atcaaccagc ccatcatcta cagcatcttt aggggaaacg tgaatggtac attcatcatc  
 960  
 caccagact cgggcaacct caccgtggcc aggagtgtcc ccagccccat gaccttcctt  
 1020  
 ctgctggtga agggccaaca ggccgacctt gcccgctact cagtgaacca ggtcaccgtg  
 1080  
 gagggctgtg gctgcggccg ggagcccgcc ccgcttcccc cagagcctgt atcgtggcac  
 1140  
 cgtggcgcggt ggcgctggag cgggcgttgt ggtcaaggat gcagctgccc cttttcagcc  
 1200  
 tctgaggatc c  
 1211

&lt;210&gt; 750

&lt;211&gt; 385

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 750

Met Gly Ser Trp Ala Leu Leu Trp Pro Pro Leu Leu Phe Thr Gly Leu

```

1           5           10           15
Leu Val Arg Pro Gly Thr Met Ala Gln Ala Gln Tyr Cys Ser Val
      20      25      30
Asn Lys Asp Ile Phe Glu Val Glu Glu Asn Thr Asn Val Thr Glu Pro
      35      40      45
Leu Val Asp Ile His Val Pro Glu Gly Gln Glu Val Thr Leu Gly Ala
      50      55      60
Leu Ser Thr Pro Phe Ala Phe Arg Ile Gln Gly Asn Gln Leu Phe Leu
      65      70      75      80
Asn Val Thr Pro Asp Tyr Glu Glu Lys Ser Leu Leu Glu Ala Gln Leu
      85      90      95
Leu Cys Gln Ser Gly Gly Thr Leu Val Thr Gln Leu Arg Val Phe Val
      100     105     110
Ser Val Leu Asp Val Asn Asp Asn Ala Pro Glu Phe Pro Phe Lys Thr
      115     120     125
Lys Glu Ile Arg Val Glu Glu Asp Thr Lys Val Asn Ser Thr Val Ile
      130     135     140
Pro Glu Thr Gln Leu Gln Ala Glu Asp Arg Asp Lys Asp Asp Ile Leu
      145     150     155     160
Phe Tyr Thr Leu Gln Glu Met Thr Ala Gly Ala Ser Asp Tyr Phe Ser
      165     170     175
Leu Val Ser Val Asn Arg Pro Ala Leu Arg Leu Asp Arg Pro Leu Asp
      180     185     190
Phe Tyr Glu Arg Pro Asn Met Thr Phe Trp Leu Leu Val Arg Asp Thr
      195     200     205
Pro Gly Glu Asn Val Glu Pro Ser His Thr Ala Thr Ala Thr Leu Val
      210     215     220
Leu Asn Val Val Pro Ala Asp Leu Arg Pro Pro Trp Phe Leu Pro Cys
      225     230     235     240
Thr Phe Ser Asp Gly Tyr Val Cys Ile Gln Ala Gln Tyr His Gly Ala
      245     250     255
Val Pro Thr Gly His Ile Leu Pro Ser Pro Leu Val Leu Arg Pro Gly
      260     265     270
Pro Ile Tyr Ala Glu Asp Gly Asp Arg Gly Ile Asn Gln Pro Ile Ile
      275     280     285
Tyr Ser Ile Phe Arg Gly Asn Val Asn Gly Thr Phe Ile Ile His Pro
      290     295     300
Asp Ser Gly Asn Leu Thr Val Ala Arg Ser Val Pro Ser Pro Met Thr
      305     310     315     320
Phe Leu Leu Leu Val Lys Gly Gln Gln Ala Asp Leu Ala Arg Tyr Ser
      325     330     335
Val Thr Gln Val Thr Val Glu Gly Cys Gly Cys Gly Arg Glu Pro Ala
      340     345     350
Pro Leu Pro Pro Glu Pro Val Ser Trp His Arg Gly Ala Trp Arg Trp
      355     360     365
Ser Gly Arg Cys Gly Gln Gly Cys Ser Cys Pro Phe Ser Ala Ser Glu
      370     375     380
Asp
385

```

&lt;210&gt; 751

&lt;211&gt; 345

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 751

cgcgctcgcg tcacgtcaca cgacatgagc gaggtcaaca tcgacgcggc gctgggtggcg  
60  
gcaggcgggc ggctgtcgcg caccgaggag aagctcgtcg agatgtcgaa cggctgcatc  
120  
tgctgcacgc tgcgcgacga cctgatgcag gaagtggcga gactggcggg cgaaggccgc  
180  
ttcgatgcgc tggatcatga gagcaccggc gtgtccgagc cgatgccggt cgccgccacg  
240  
ttcgatttcc gtgaccagga cggcgtctcg ctgcccgacg tcgcgcggct ggataccatg  
300  
gtcaccgtcg tcgacgcgcg gtccttctcg cgcgactacg gctcg  
345

&lt;210&gt; 752

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 752

Arg	Val	Ala	Val	Ile	Val	Asn	Asp	Met	Ser	Glu	Val	Asn	Ile	Asp	Ala
1				5					10					15	
Ala	Leu	Val	Ala	Ala	Gly	Gly	Gly	Leu	Ser	Arg	Thr	Glu	Glu	Lys	Leu
			20					25						30	
Val	Glu	Met	Ser	Asn	Gly	Cys	Ile	Cys	Cys	Thr	Leu	Arg	Asp	Asp	Leu
			35				40							45	
Met	Gln	Glu	Val	Ala	Arg	Leu	Ala	Gly	Glu	Gly	Arg	Phe	Asp	Ala	Leu
			50				55							60	
Val	Ile	Glu	Ser	Thr	Gly	Val	Ser	Glu	Pro	Met	Pro	Val	Ala	Ala	Thr
					70					75					80
Phe	Asp	Phe	Arg	Asp	Gln	Asp	Gly	Val	Ser	Leu	Ala	Asp	Val	Ala	Arg
					85					90					95
Leu	Asp	Thr	Met	Val	Thr	Val	Val	Asp	Ala	Ala	Ser	Phe	Leu	Arg	Asp
					100					105					110
Tyr	Gly	Ser													
															115

&lt;210&gt; 753

&lt;211&gt; 352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 753

gcgcgccagt acgccaagac cgtccgcaag gaccgcaagg gcgaacggcg gcgtcggggc  
60  
gcgtcggact agtccacgat gcatccgaac cgcgccttcc gctttgccga tgatgtctcg  
120  
atgctcgatt tcgcgcccaa gcgagccttt gcgcacatct tcgtgagcac gcccgagggg  
180  
cctatggtag cgcattgccc gggtacgccc ttgcacggag ccttccgctt ccatgtcgcg  
240  
cgcggaatc ggatcgcgcg gcacctggat ggcgcgacgc tgctgctcag catcagcgcg  
300

accgacggct atatcagccc gagctgggtac gccgaccgc agggaccaca gt  
352

<210> 754

<211> 91

<212> PRT

<213> Homo sapiens

<400> 754

Met	His	Pro	Asn	Arg	Ala	Phe	Arg	Phe	Ala	Asp	Asp	Val	Ser	Met	Leu
1			5						10					15	
Asp	Phe	Ala	Ala	Lys	Arg	Ala	Phe	Ala	His	Ile	Phe	Val	Ser	Thr	Pro
		20						25				30			
Glu	Gly	Pro	Met	Val	Ala	His	Ala	Pro	Val	Thr	Pro	Phe	Asp	Gly	Ala
		35					40					45			
Phe	Arg	Phe	His	Val	Ala	Arg	Gly	Asn	Arg	Ile	Ala	Arg	His	Leu	Asp
	50					55				60					
Gly	Ala	Thr	Leu	Leu	Leu	Ser	Ile	Ser	Ala	Thr	Asp	Gly	Tyr	Ile	Ser
65				70						75				80	
Pro	Ser	Trp	Tyr	Ala	Asp	Pro	Gln	Gly	Pro	Gln					
				85						90					

<210> 755

<211> 301

<212> DNA

<213> Homo sapiens

<400> 755

tgggatgcag ggtctttctt ctccaaggat ttcattcctg gagggagaaa agggccccag  
60  
ctgtctgccca tcaaaccggg ttgccgggct ggagctcctc ccaggcccg gtgaggaaga  
120  
gcaaaggccg gcaggggctc gatgggacca gtcgctcgct caggcccagg aaaaccacac  
180  
agctgggggc tgtcaggatt ggaccagggt caggccggcc aggcgatggc gggaaaagca  
240  
ggcccactct gcagacctca atgtctcagg tgcactgcag ggcaaccccg cctaccccg  
300  
g  
301

<210> 756

<211> 99

<212> PRT

<213> Homo sapiens

<400> 756

Met	Gln	Gly	Leu	Ser	Ser	Pro	Arg	Ile	Ser	Phe	Leu	Glu	Gly	Glu	Lys
1				5					10					15	
Gly	Pro	Ser	Cys	Leu	Pro	Ser	Asn	Arg	Val	Ala	Gly	Leu	Glu	Leu	Leu
			20					25				30			
Pro	Gly	Pro	Cys	Glu	Glu	Glu	Gln	Arg	Pro	Ala	Gly	Ala	Arg	Trp	Asp
		35					40					45			
Gln	Ser	Leu	Ala	Gln	Ala	Gln	Glu	Asn	His	Thr	Ala	Gly	Gly	Cys	Gln

```

      50              55              60
Asp Trp Thr Arg Val Arg Pro Ala Arg Arg Trp Arg Glu Lys Gln Ala
65              70              75              80
His Ser Ala Asp Leu Asn Val Ser Gly Ala Leu Gln Gly Asn Pro Ala
      85              90              95
Tyr Pro Gly

```

&lt;210&gt; 757

&lt;211&gt; 311

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 757

```

actgaggcga tcgccagagg ggtgggcgtg cgagggtgc tcaacatcca gttcgccctg
60
gtctccgatg ttctctacgt catcgaggcc aaccccaggg catcgcgcac agtccccctc
120
gtctcaaagg catccggcgt gcagctcgcc aaagcggcgg ccctcatcat gacaggggag
180
acgatcgctt cgctcaggcg ctccggccac ctgcccaggg cgcacgccgc cgtcaccgat
240
cccgatgacc cgatcgccgt caaggaggcg gtctaccctt tcaaacgatt ccgcaccacc
300
gagggacgcg t
311

```

&lt;210&gt; 758

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 758

```

Thr Glu Ala Ile Ala Arg Gly Val Gly Val Arg Gly Leu Leu Asn Ile
1      5      10      15
Gln Phe Ala Leu Val Ser Asp Val Leu Tyr Val Ile Glu Ala Asn Pro
      20      25      30
Arg Ala Ser Arg Thr Val Pro Phe Val Ser Lys Ala Ser Gly Val Gln
      35      40      45
Leu Ala Lys Ala Ala Ala Leu Ile Met Thr Gly Glu Thr Ile Ala Ser
      50      55      60
Leu Arg Arg Ser Gly His Leu Pro Glu Ala Asp Ala Val Thr Asp
65      70      75      80
Pro Asp Asp Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Lys Arg
      85      90      95
Phe Arg Thr Thr Glu Gly Arg
      100

```

&lt;210&gt; 759

&lt;211&gt; 391

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 759



gtgcacaccg gcaagctggt gtggaactgg gacagcggca acccggacga cactacgccg  
60  
attgccgagg gcaagaccta caccgcaac togccgaaca tgtggtccat gttcgccgtc  
120  
gacgaaaaac tcggcatgct ctacctgccg atgggcaacc agaccccgga ccagttcggg  
180  
ggctaccgca cgcctgcgtc ggaactgcac gctgccggcc tgacagcgtt ggatatcgac  
240  
actggtaaag tgcgctggca ctaccagttc acccaccatg acctgtggga catggacgtg  
300  
ggcggccagc cgagcctgat cgacatcaag accgccgccg gcgtgaaaca agccgtgatg  
360  
gcctcgacca agcaaggcag catctacgct t  
391

<210> 760

<211> 130

<212> PRT

<213> Homo sapiens

<400> 760

Val	His	Thr	Gly	Lys	Leu	Val	Trp	Asn	Trp	Asp	Ser	Gly	Asn	Pro	Asp
1				5					10					15	
Asp	Thr	Thr	Pro	Ile	Ala	Glu	Gly	Lys	Thr	Tyr	Thr	Arg	Asn	Ser	Pro
			20					25					30		
Asn	Met	Trp	Ser	Met	Phe	Ala	Val	Asp	Glu	Lys	Leu	Gly	Met	Leu	Tyr
	35						40					45			
Leu	Pro	Met	Gly	Asn	Gln	Thr	Pro	Asp	Gln	Phe	Gly	Gly	Tyr	Arg	Thr
	50				55					60					
Pro	Ala	Ser	Glu	Leu	His	Ala	Ala	Gly	Leu	Thr	Ala	Leu	Asp	Ile	Asp
65					70					75				80	
Thr	Gly	Lys	Val	Arg	Trp	His	Tyr	Gln	Phe	Thr	His	His	Asp	Leu	Trp
			85					90					95		
Asp	Met	Asp	Val	Gly	Gly	Gln	Pro	Ser	Leu	Ile	Asp	Ile	Lys	Thr	Ala
			100					105					110		
Ala	Gly	Val	Lys	Gln	Ala	Val	Met	Ala	Ser	Thr	Lys	Gln	Gly	Ser	Ile
		115					120						125		
Tyr	Ala														
	130														

<210> 761

<211> 324

<212> DNA

<213> Homo sapiens

<400> 761

cctaggtagg cccaaagggg cctaactttc ttgctgccct ggtggagcaa gaaatatctt  
60  
ctaggagagg ccaatccttc cctgccccac agctccttct ctgcaaagct cagggggcaa  
120  
tcaggtacct cctgcccag agggcccat ggttcctcgc ctaaggaagg cagggcgggg  
180  
cattgggagc cgttgacagc tgggctcagc tggggggagg ggtcagtttg ggagcaggtg  
240

cagatttcag ggaggggggg gcctaaaggg aagtagggat cttggtaggc tgcaaaattt  
 300  
 tcctcccat ccccatcca caga  
 324

<210> 762  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 762  
 Met Gly Asp Gly Glu Glu Asn Phe Ala Ala Tyr Gln Asp Pro Tyr Phe  
 1 5 10 15  
 Pro Leu Gly Pro Pro Leu Pro Glu Ile Cys Thr Cys Ser Gln Thr Asp  
 20 25 30  
 Pro Ser Pro Gln Leu Ser Pro Ala Val Asn Gly Ser Gln Cys Pro Ala  
 35 40 45  
 Leu Pro Ser Leu Gly Glu Glu Pro Trp Gly Pro Leu Gly Gln Glu Val  
 50 55 60  
 Pro Asp Cys Pro Leu Ser Phe Ala Glu Lys Glu Leu Trp Gly Arg Glu  
 65 70 75 80  
 Gly Leu Ala Ser Pro Arg Arg Tyr Phe Leu Leu His Gln Gly Ser Lys  
 85 90 95  
 Lys Val Arg Pro Leu Trp Ala Tyr Leu  
 100 105

<210> 763  
 <211> 301  
 <212> DNA  
 <213> Homo sapiens

<400> 763  
 acgcgttatg ggcggcccgg atgggcgatg cgctatccca cacctcgatg atggcggaca  
 60  
 tcctcggcgg tgtgctggaa gtggcgcca atatcgcat tactgcgggc ggcaccgctg  
 120  
 ccgcggtggc cgccaccggc ttaccgagg ccaccggcgg cctcggctgc ttctgctgg  
 180  
 gcgctgcctt gggcaccatt gccggcctgg ccatgagcaa cattggcgcg gacacagggc  
 240  
 tgaccaagat atgcaatgcc tttaacaacg ccttatttgc gcccaccgtg catgcgaaca  
 300  
 t  
 301

<210> 764  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 764  
 Met Phe Ala Cys Thr Val Gly Ala Asn Lys Ala Leu Leu Lys Ala Leu  
 1 5 10 15  
 His Ile Leu Val Ser Pro Val Ser Ala Pro Met Leu Leu Met Ala Arg

```

      20      25      30
Pro Ala Met Val Pro Lys Ala Ala Pro Ser Arg Lys Gln Pro Arg Pro
      35      40      45
Pro Val Ala Ser Val Lys Pro Val Ala Ala Thr Ala Ala Ala Val Ala
      50      55      60
Pro Ala Val Ile Ala Ile Leu Ala Ala Thr Ser Ser Thr Pro Pro Arg
65      70      75      80
Met Ser Ala Ile Ile Glu Val Trp Asp Ser Ala Ser Pro Ile Arg Ala
      85      90      95
Ala His Asn Ala
      100

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<210> 765  
 <211> 831  
 <212> DNA  
 <213> Homo sapiens

<400> 765  
 ngcacactcc agcctctgtt ctttctctcc ttgtgccttt gcccttacca cggttcctca  
 60  
 taacattggt gttcctgtat ttaaggccct ataaacaggg agatgcgcca cctcatcagt  
 120  
 agcctccaga atcacaatca ccagctgaaa ggggaggtcc tgagatataa gcggaaattg  
 180  
 agagaagccc agtctgacct gaacaagaca cgctgcgta gtggtagtgc cctcctgcag  
 240  
 tcccagtcta gtactgagga cccgaaggat gagcctgcgg agctaaaacc agattctggg  
 300  
 gacttatcct ccagtcctc agcttcaaag gcatctcagg aggatgccaa tgaaatcaag  
 360  
 tctaaacggg atgaagaaga acgagaacga gaaaggaggg agaaggagag ggaacgagaa  
 420  
 agagaacggg agaaggagaa ggagagagaa cgagagaagc agaagctaaa agagtcagaa  
 480  
 aaagagagag attctgctaa ggataaagag aaaggcaaac atgatgatgg acggaaaaag  
 540  
 gaagcagaaa ttatcaaaca attgaagatt gaactcaaga aggcacagga gagccaaaag  
 600  
 gagatgaaac tattgctgga tatgtaccgt tctgccccaa aggaacagag agacaaagtt  
 660  
 cagctgatgg cagctgagaa gaagtctaag gcagagttgg aagatctaag gcaaagactc  
 720  
 aaggatctgg aagataaaga gaagaaagag aacaagaaaa tggctgatga ggatgccttg  
 780  
 aggaagatcc gggcagtgga ggagcagata gaatacctac agaagaagct a  
 831

<210> 766  
 <211> 243  
 <212> PRT  
 <213> Homo sapiens

<400> 766  
 Met Arg His Leu Ile Ser Ser Leu Gln Asn His Asn His Gln Leu Lys

1	5	10	15
Gly Glu Val Leu Arg Tyr Lys Arg Lys Leu Arg Glu Ala Gln Ser Asp			
20	25	30	
Leu Asn Lys Thr Arg Leu Arg Ser Gly Ser Ala Leu Leu Gln Ser Gln			
35	40	45	
Ser Ser Thr Glu Asp Pro Lys Asp Glu Pro Ala Glu Leu Lys Pro Asp			
50	55	60	
Ser Gly Asp Leu Ser Ser Gln Ser Ser Ala Ser Lys Ala Ser Gln Glu			
65	70	75	80
Asp Ala Asn Glu Ile Lys Ser Lys Arg Asp Glu Glu Glu Arg Glu Arg			
85	90	95	
Glu Arg Arg Glu Lys Glu Arg Glu Arg Glu Arg Glu Arg Glu Lys Glu			
100	105	110	
Lys Glu Arg Glu Arg Glu Lys Gln Lys Leu Lys Glu Ser Glu Lys Glu			
115	120	125	
Arg Asp Ser Ala Lys Asp Lys Glu Lys Gly Lys His Asp Asp Gly Arg			
130	135	140	
Lys Lys Glu Ala Glu Ile Ile Lys Gln Leu Lys Ile Glu Leu Lys Lys			
145	150	155	160
Ala Gln Glu Ser Gln Lys Glu Met Lys Leu Leu Leu Asp Met Tyr Arg			
165	170	175	
Ser Ala Pro Lys Glu Gln Arg Asp Lys Val Gln Leu Met Ala Ala Glu			
180	185	190	
Lys Lys Ser Lys Ala Glu Leu Glu Asp Leu Arg Gln Arg Leu Lys Asp			
195	200	205	
Leu Glu Asp Lys Glu Lys Lys Glu Asn Lys Lys Met Ala Asp Glu Asp			
210	215	220	
Ala Leu Arg Lys Ile Arg Ala Val Glu Glu Gln Ile Glu Tyr Leu Gln			
225	230	235	240
Lys Lys Leu			

&lt;210&gt; 767

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 767

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ccccggcacc agaagttcct ctgcgcgtcc gacggcgaca tgggcgtccc cacggccccg  
120  
gaggccggca gctggcgctg gggatccctg ctcttcgctc tcttctggc tgcgtcccta  
180  
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240  
cagaacgtca cctcacctg caggctcttg ggccctgtgg acaaagggca cgatgtgacc  
300  
ttctacaaga cgtggtaccg cagctcgagg ggcgaggtgc agacctgctc agagcgccg  
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420  
aacaccagcc a  
431

<210> 768  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 768  
 Met Gly Val Pro Thr Ala Pro Glu Ala Gly Ser Trp Arg Trp Gly Ser  
 1 5 10 15  
 Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val Ala Ala  
 20 25 30  
 Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln  
 35 40 45  
 Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His  
 50 55 60  
 Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val  
 65 70 75 80  
 Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp  
 85 90 95  
 Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser  
 100 105 110

<210> 769  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

<400> 769  
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 60  
 cgacttcgaa ctccatcaag tgatttttgc ggtcgacgaa tctggtttcc gtatgaaaga  
 120  
 acggtatggt ttgtatgtcg cggccctgcc actcaaact caccgtgtca cccacctcaa  
 180  
 aaaaatcccc ggtcggccca caaataaatc aattgcgccg ctctccgag ttcttccatg  
 240  
 tcaacgatct cccctggctg ctcaagccaa ggccctcgcg gccgtgggac tccaagggtg  
 300  
 acgttgaccc gactgatttc ggaccagttg gcgtcggtat tgggggcagg gtagttaccg  
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 cccatgtcga tgatctacat cgccaccggc agcgtgtctt cgtagtcgtc atgcctgac  
 420  
 an  
 422

<210> 770  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 770  
 Met Phe Cys Met Ser Arg Pro Cys His Ser Asn Leu Thr Val Ser Pro  
 1 5 10 15  
 Thr Ser Lys Lys Ser Arg Val Gly Pro Gln Ile Asn Gln Leu Arg Arg

```

                20                25                30
Ser Ser Glu Phe Phe His Val Asn Asp Leu Pro Trp Leu Leu Lys Pro
                35                40                45
Arg Pro Ser Arg Pro Trp Asp Ser Lys Val Asp Val Asp Pro Thr Asp
                50                55                60
Phe Gly Pro Val Gly Val Gly Ile Gly Gly Arg Val Val Thr Ala His
65                70                75                80
Val Asp Asp Leu His Arg His Arg Gln Arg Val Phe Val Val Val Met
                85                90                95
Pro Asp Xaa

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<210> 771  
 <211> 369  
 <212> DNA  
 <213> Homo sapiens

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<400> 771
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gcaatggcgc atcagctggg cggtttttac gatctgccgc acggcgtgtg caatgcgata
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ctgttgccac acgtgcagac gtttaactgc aaagtggcgg cctcgcgcct gcgtgattgc
180
gcccaggcca tgggtgtcga tgtcagtcaa atgacagcag aacagggcgc acaggcgtgt
240
atcgagcaga ttcgctctct ggcacgtcag gtgaatatcc cggtgggatt gcgtgacctc
300
aacgtgaagg aagcggactt cccgattctg gcgaccaacg cgctaaaaga ccctgtgggt
360
ttgattaat
369

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<210> 772  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

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<400> 772
Ala Tyr Ala Gln Phe Leu Ala Gly Met Ala Phe Asn Asn Ala Ser Leu
1                5                10                15
Gly Tyr Val His Ala Met Ala His Gln Leu Gly Gly Phe Tyr Asp Leu
                20                25                30
Pro His Gly Val Cys Asn Ala Ile Leu Leu Pro His Val Gln Thr Phe
                35                40                45
Asn Cys Lys Val Ala Ala Ser Arg Leu Arg Asp Cys Ala Gln Ala Met
50                55                60
Gly Val Asp Val Ser Gln Met Thr Ala Glu Gln Gly Ala Gln Ala Cys
65                70                75                80
Ile Ala Glu Ile Arg Ser Leu Ala Arg Gln Val Asn Ile Pro Val Gly
                85                90                95
Leu Arg Asp Leu Asn Val Lys Glu Ala Asp Phe Pro Ile Leu Ala Thr
                100                105                110
Asn Ala Leu Lys Asp Pro Val Gly Leu Ile Asn

```

115

120

<210> 773  
 <211> 309  
 <212> DNA  
 <213> Homo sapiens

<400> 773  
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 120  
 tccggttccct gccgggattc ggcggtggtg ctggtgcaac tgctgcgcaa cctgggcctg  
 180  
 gcggcgcgat ttgtgtctgg ctatctgata caactgaccg ccgacgtcaa agccctcgac  
 240  
 ggccccgtccg gcaccgaggt ggatttcacc gacctgcatg cctggtgcga agtgattttg  
 300  
 cccggcgcc  
 309

<210> 774  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 774  
 Pro Pro Leu Pro Ala Val Asp Phe Leu Val Gly Leu Asn Gln Arg Leu  
 1 5 10 15  
 Ala Ala Asp Ile Gly Tyr Leu Ile Arg Val Glu Pro Gly Val Gln Thr  
 20 25 30  
 Pro Glu Phe Thr Leu Glu Asn Ala Ser Gly Ser Cys Arg Asp Ser Ala  
 35 40 45  
 Trp Leu Leu Val Gln Leu Leu Arg Asn Leu Gly Leu Ala Ala Arg Phe  
 50 55 60  
 Val Ser Gly Tyr Leu Ile Gln Leu Thr Ala Asp Val Lys Ala Leu Asp  
 65 70 75 80  
 Gly Pro Ser Gly Thr Glu Val Asp Phe Thr Asp Leu His Ala Trp Cys  
 85 90 95  
 Glu Val Tyr Leu Pro Gly Ala  
 100

<210> 775  
 <211> 4125  
 <212> DNA  
 <213> Homo sapiens

<400> 775  
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 120  
 gctaccagcg aagactccga cctgagcatg cgcacactga gcacgcccag cccagccctg  
 180

atatgtccac cgaatctccc aggatttcag aatggaaggg gctcgtccac ctccctcgccc  
240  
tccatcacccg gggagacggg ggccatgggtg cactccccgc ccccgaccgc cctcacacac  
300  
ccgctcatcc ggctcgccctc cagaccccag aaggatcagg ccagcataga ccggctccccg  
360  
gaccactcca tgggtgcagat cttctccttc ctgcccacca accagctgtg ccgctgcgcg  
420  
cgagtgtgcc gccgctggta caacctggcc tgggaccgc ggctctggag gactatccgc  
480  
ctgacgggcg agaccatcaa cgtggaccgc gccctcaagg tgctgaccgc cagactctgc  
540  
caggacaccc ccaacgtgtg tctcatgctg gaaaccgtaa ctgtcagtgg ctgcaggcgg  
600  
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660  
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720  
aatctggagc acctggatgt gtcaggatgc tccaaagtga cctgcatcag cttgaccgcg  
780  
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840  
atgacggact gcttcgtgct ggaggacgaa ggctgcaca ccatcgcggc gactgcacg  
900  
cagctcacc accctctacct gcgcgctgc gtccgcctga ccgacgaagg cctgcgctac  
960  
ctggtgatct actgcgcctc catcaaggag ctgagcgtca gcgactgccg cttcgtcagc  
1020  
gacttcggcc tgcgggagat cgccaagctg gagtcccgcc tgcggtacct gagcatcgcc  
1080  
cactgcggcc gggtcaccga cgtgggcac cgtacgtgg ccaagtactg cagcaagctg  
1140  
cgctacctca acgcgagggg ctgcgagggc atcacggacc acggtgtgga gtacctcgcc  
1200  
aagaactgca ccaaactcaa atccctggat atcggcaa at gccctttggg atccgacacg  
1260  
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1380  
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gcgttgatt cacacaaacc tgaacaaagc aaattttttt aaaagcagcg tatgtaagca  
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1620  
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1680  
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1800



gccctttccc tcgcacacag gccccacccc cacagttcca cgccccccc ccaaggccac  
1860  
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1920  
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1980  
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2040  
aaaaattcat tacagcaaac agctggggaa ggacatgcag tcctccccc gctctgtcaa  
2100  
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2160  
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2220  
accatacac agaagcacct tggcatagag caccaggca tcgacctctt ccaggagaac  
2280  
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2340  
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2400  
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2580  
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2640  
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2700  
gacagatgcc tcggttcttt gtcattcaga ttgcatttga cctcttctca tctatttatt  
2760  
tctttataca tccagacttc atcacatgaa gcctattggg gtttaagtttg taagtgttta  
2820  
attgtgcaaa ttgccaccct gtgtacctcc tccatgtctg tctgcgtgtt ttccaccaa  
2880  
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2940  
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3180  
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3240  
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3300  
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3360  
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3420

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 3480  
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 3540  
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 3600  
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 3720  
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 3780  
 agcacatacc gtcttgccag tttcttcttt tctcccagtc tctgttcat ccattctgtt  
 3840  
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 3900  
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 3960  
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 4020  
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 4125

<210> 776

<211> 483

<212> PRT

<213> Homo sapiens

<400> 776

Tyr	Gly	Ser	Glu	Gly	Lys	Gly	Ser	Ser	Ser	Ile	Ser	Ser	Asp	Val	Ser
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Ser	Ser	Thr	Asp	His	Thr	Pro	Thr	Lys	Ala	Gln	Lys	Asn	Val	Ala	Thr
			20					25					30		
Ser	Glu	Asp	Ser	Asp	Leu	Ser	Met	Arg	Thr	Leu	Ser	Thr	Pro	Ser	Pro
		35					40					45			
Ala	Leu	Ile	Cys	Pro	Pro	Asn	Leu	Pro	Gly	Phe	Gln	Asn	Gly	Arg	Gly
	50					55					60				
Ser	Ser	Thr	Ser	Ser	Ser	Ser	Ile	Thr	Gly	Glu	Thr	Val	Ala	Met	Val
65					70					75				80	
His	Ser	Pro	Pro	Pro	Thr	Arg	Leu	Thr	His	Pro	Leu	Ile	Arg	Leu	Ala
			85						90					95	
Ser	Arg	Pro	Gln	Lys	Asp	Gln	Ala	Ser	Ile	Asp	Arg	Leu	Pro	Asp	His
		100						105					110		
Ser	Met	Val	Gln	Ile	Phe	Ser	Phe	Leu	Pro	Thr	Asn	Gln	Leu	Cys	Arg
		115					120					125			
Cys	Ala	Arg	Val	Cys	Arg	Arg	Trp	Tyr	Asn	Leu	Ala	Trp	Asp	Pro	Arg
	130						135					140			
Leu	Trp	Arg	Thr	Ile	Arg	Leu	Thr	Gly	Glu	Thr	Ile	Asn	Val	Asp	Arg
145					150					155				160	
Ala	Leu	Lys	Val	Leu	Thr	Arg	Arg	Leu	Cys	Gln	Asp	Thr	Pro	Asn	Val
			165						170					175	
Cys	Leu	Met	Leu	Glu	Thr	Val	Thr	Val	Ser	Gly	Cys	Arg	Arg	Leu	Thr

```
<210> 777
<211> 705
<212> DNA
<213> Homo sapiens
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843

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 360  
 tcaccaggag ggaaccgccc caatgaccgc cggacgtcca gcaacacttg ttggtagtcc  
 420  
 ttgtcatct gccgtagggt cttccctgat ataggagggtg ggtcattggc attgacattg  
 480  
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 gccatgcgtc taagggcagc cacatcagtg ggatcactgt tcagagcctg gtgtatctct  
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 aacactttct ttttcctttt ggcgttaaag tctgccttct ccgcgccgcc gtcccagtgg  
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 ccggagggtgg gccgtcccct gcgcactccg gaggccatcc ccggg  
 705

<210> 778  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 778  
 Met Ala Ser Gly Val Arg Arg Gly Arg Pro Thr Ser Gly His Trp Asp  
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 Gly Gly Ala Glu Lys Ala Asp Phe Asn Ala Lys Arg Lys Lys Lys Val  
 20 25 30  
 Leu Glu Ile His Gln Ala Leu Asn Ser Asp Pro Thr Asp Val Ala Ala  
 35 40 45  
 Leu Arg Arg Met Ala Ile Ser Glu Gly Gly Leu Leu Thr Asp Glu Ile  
 50 55 60  
 Arg Arg Lys Val Trp Pro Lys Leu Leu Asn Val Asn Ala Asn Asp Pro  
 65 70 75 80  
 Pro Pro Ile Ser Gly Lys Asn Leu Arg Gln Met Ser Lys Asp Tyr Gln  
 85 90 95  
 Gln Val Leu Leu Asp Val Arg Arg Ser Leu Arg Arg Phe Pro Pro Gly  
 100 105 110  
 Glu Lys Leu Ser Arg Ser Cys His Ile Trp Glu Glu Arg Ile Cys Phe  
 115 120 125  
 Arg Ser Tyr His Val Thr  
 130

<210> 779  
 <211> 322  
 <212> DNA  
 <213> Homo sapiens

<400> 779  
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 gactgtgagt gattctgagg ataccgttgc gccgtcccag ctggttcgat cccctcgtaa  
 120  
 cgccttgccct ttgaaggaac ccagtgggaa ggctagacca agtaaatatg aatcaccaaa  
 180

cgccagcaac ttcacgtca ggcacgtggc aactggcaaa gagggcactg atgatgagta  
 240  
 tgctaactca aactactact actcgaatgc tgccaatcga ctaggagacg aggaaacgga  
 300  
 ggaaatgata ggtttggcta cc  
 322

<210> 780  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 780  
 Met Cys Lys Gln Phe Asn Asp Val Val Arg Arg His Gly Val His His  
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 Ser Val Thr Val Ser Asp Ser Glu Asp Thr Val Ala Pro Ser Gln Leu  
 20 25 30  
 Val Arg Ser Pro Arg Asn Ala Leu Pro Leu Lys Glu Pro Ser Gly Lys  
 35 40 45  
 Ala Arg Pro Ser Lys Tyr Glu Ser Pro Asn Ala Ser Asn Phe Ile Val  
 50 55 60  
 Arg His Val Ala Thr Gly Lys Glu Gly Thr Asp Asp Glu Tyr Ala Asn  
 65 70 75 80  
 Ser Asn Tyr Tyr Tyr Ser Met Ser Ala Asn Arg Leu Gly Asp Glu Glu  
 85 90 95  
 Thr Glu Glu Met Ile Gly Leu Ala Thr  
 100 105

<210> 781  
 <211> 297  
 <212> DNA  
 <213> Homo sapiens

<400> 781  
 nntcgcgtgc ctggaatgtg tgtctgtgta tgtgtgtgta tgtatgtgtg tatggaatgt  
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 120  
 gaatgtgtgt ctgtgtatgg aatatgtgtg agtatngaa tgtgtgtgtg tgtttggaat  
 180  
 gtatcgaatg tgtgtctgtg tgtaaggaat gtgtgtgtat ggaatgtgtt tacgtgcatg  
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 tgtctggaat gtgtgtgtat ggaatgtgtg tgtatgtgta tgngaattgtg tgtgtgt  
 297

<210> 782  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 782  
 Xaa Arg Val Pro Gly Met Cys Val Cys Val Cys Val Cys Met Tyr Val  
 1 5 10 15  
 Cys Met Glu Cys Val Cys Met Xaa Ile Cys Val Cys Met Xaa Met Cys

```

      20      25      30
Val Cys Val Trp Asn Val Cys Met Glu Cys Val Ser Val Tyr Gly Ile
      35      40      45
Cys Val Ser Met Xaa Met Cys Val Cys Val Trp Asn Val Ser Asn Val
      50      55      60
Cys Leu Cys Val Arg Asn Val Cys Val Trp Asn Val Phe Thr Cys Met
65      70      75      80
Cys Leu Glu Cys Val Cys Met Glu Cys Val Cys Met Cys Met Xaa Met
      85      90      95
Cys Val Cys

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<210> 783  
 <211> 612  
 <212> DNA  
 <213> Homo sapiens

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<400> 783
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120
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240
gttcgatgac acgtgtcttc accgtgatat tcagcagccc cagtacgtcc accggcaact
300
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360
gttcgaggtt gacgtccagg gcgctcttgt ccgtgccgtt ttgtatattg atcaggtcgc
420
ccaggtgcag gatctgcgtg cctggggcaa tcagcttgat tgcttcgagg ttattgatca
480
ccacctggac cgcattaccg ccagcttga gcacatcgat ggcggcctgg atcaactggc
540
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600
tggccgacgc gt
612

```

<210> 784  
 <211> 190  
 <212> PRT  
 <213> Homo sapiens

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<400> 784
Met Ser Ile Cys Val Pro Gly Thr Gly Ser Ser Glu Leu Pro Ser Ser
1      5      10      15
Lys Pro Thr Thr Ser Val Thr Arg Pro Ile Thr Leu Leu Ser Thr Ser
      20      25      30
Met Thr Gly Asn Phe Lys Glu Ile Gln Val Arg Thr Cys Ala Val Arg
      35      40      45
Thr Lys Ile Gly Trp Val Ser Ile Asn Cys Gly Leu Pro Ile Ala Glu

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      50              55              60
Phe Ala Arg Phe Asp Asp Thr Cys Leu His Arg Asp Ile Gln Gln Pro
65              70              75              80
Gln Tyr Val His Arg Gln Leu Asp Gly His Arg Ala Gly Phe Val Gly
      85              90              95
Gln Leu His Lys Ala Leu Asn Gln Val Glu Gln Leu Gln Val Asp Val
      100              105              110
Gln Gly Ala Leu Val Arg Ala Val Leu Tyr Ile Asp Gln Val Ala Gln
      115              120              125
Val Gln Asp Leu Arg Ala Trp Gly Asn Gln Leu Asp Cys Phe Glu Val
      130              135              140
Ile Asp His His Leu Asp Arg Ile Thr Ala Gln Leu Glu His Ile Asp
145              150              155              160
Gly Gly Leu Asp Gln Leu Ala Asp Gly Arg Val Gly Leu Glu Gln Leu
      165              170              175
Val Val Val Ala Gly Ala Asp Val Glu Ala Asp Gly Arg Arg
      180              185              190

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<210> 785  
 <211> 408  
 <212> DNA  
 <213> Homo sapiens

```

<400> 785
accttggaact acttcactat cgaccctcgg ctaggcgacg acgatgactt cgatcacctg
60
cttcaggccg cccacgctcg tggctctgtca gtactgctcg acgggggtggt caaccacgtc
120
tcgcgtcgca accgcatcgt gcaggatgcg cagagtgtcg ggccagattc agacgccggc
180
cgtatgggttc gctgggtgtga ggggcgcctc gacgttttcg agggtcatag tgacctggtc
240
gcactcaacc acgacaaccc cgcagtgcgg gaacatgtca cccggatcat gaactattgg
300
tgccggtcgcg gtgttgacgg ctggcggctg gacgccgcta ttccgtcaat cctgagttct
360
gggctgcggt gctgcctccg gtgcgagaga agcgccctga cgtgagga
408

```

<210> 786  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

```

<400> 786
Thr Leu Asp Tyr Phe Thr Ile Asp Pro Arg Leu Gly Asp Asp Asp Asp
1              5              10              15
Phe Asp His Leu Leu Gln Ala Ala His Ala Arg Gly Leu Ser Val Leu
      20              25              30
Leu Asp Gly Val Val Asn His Val Ser Arg Arg Asn Arg Ile Val Gln
      35              40              45
Asp Ala Gln Ser Ala Gly Pro Asp Ser Asp Ala Gly Arg Met Val Arg
      50              55              60
Trp Cys Glu Gly Arg Leu Asp Val Phe Glu Gly His Ser Asp Leu Val

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65              70              75              80
Ala Leu Asn His Asp Asn Pro Ala Val Arg Glu His Val Thr Arg Ile
              85              90              95
Met Asn Tyr Trp Cys Gly Arg Gly Val Asp Gly Trp Arg Leu Asp Ala
              100              105              110
Ala Ile Pro Ser Ile Leu Ser Ser Gly Leu Arg Cys Cys Leu Arg Cys
              115              120              125
Glu Arg Ser Ala Leu Thr
              130

```

```

<210> 787
<211> 310
<212> DNA
<213> Homo sapiens

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```

<400> 787
acgcgtgaag gggaatgaaa gggtttttcc tggatcaaaa tgatgcttgt ggcagacaca
60
gttggaacca cagacgatgc cacgcttggtg tcagcagtgc gacactggcc cacgtggcgt
120
ccttggtctc tcctcattgc tgcgcact gtgtgctggg catgccctgc agttacccca
180
aagctttatg tcacaacatt gaggtggcg gagaaagacc ggcccccttca cccacctta
240
gacttcctgg aagggccgcc cgggtccaca acctggcccg ttaactccct gggcagctgc
300
tgggggagaa
310

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```

<210> 788
<211> 90
<212> PRT
<213> Homo sapiens

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```

<400> 788
Met Met Leu Val Ala Asp Thr Val Gly Thr Thr Asp Asp Ala Thr Leu
1      5      10      15
Val Ser Ala Val Arg His Trp Pro Thr Trp Arg Pro Trp Ser Leu Leu
20     25     30
Ile Ala Ala Val Thr Val Cys Trp Ala Cys Pro Ala Val Thr Pro Lys
35     40     45
Leu Tyr Val Thr Thr Leu Arg Leu Ala Glu Lys Asp Arg Pro Leu His
50     55     60
Pro Thr Leu Asp Phe Leu Glu Gly Pro Pro Gly Ser Thr Thr Trp Pro
65     70     75     80
Val Asn Ser Leu Gly Ser Cys Trp Gly Arg
85     90

```

```

<210> 789
<211> 369
<212> DNA
<213> Homo sapiens

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<400> 789

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acgcgtgaag ttgcagcagc aagcaatctg cctcgcttct ggtgccacc gaaaccaagg  
 60  
 tctgccagac agcagcgctg ggacctctcc cctccccagc aggatgggcc ggctctggaa  
 120  
 gcacgaggtg ttccaaagtg caaacaagct gctgttaaata aattattccc aaacgccaaa  
 180  
 gcccttgctg gtttgcttgc ttgctttttt ctttttttgc ctgcacaga tatcgctagg  
 240  
 gcagagtatt gacatttcgt tttctttttg ttatgggtga taaagcacgg tgtttcttgt  
 300  
 gagtgtatgc ctgtatttcc ctgcagagct gattgccagt ccattttctt ctatcccatc  
 360  
 cccattttc  
 369

&lt;210&gt; 790

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 790

Met	Asp	Trp	Gln	Ser	Ala	Leu	Gln	Gly	Asn	Thr	Gly	Ile	His	Ser	Gln
1			5					10					15		
Glu	Thr	Pro	Cys	Phe	Ile	Thr	His	Asn	Lys	Lys	Lys	Thr	Lys	Cys	Gln
		20						25				30			
Tyr	Ser	Ala	Leu	Ala	Ile	Ser	Val	Arg	Gly	Lys	Lys	Arg	Lys	Lys	Gln
		35					40					45			
Ala	Ser	Lys	Pro	Ala	Arg	Ala	Leu	Ala	Phe	Gly	Asn	Asn	Tyr	Leu	Thr
		50				55				60					
Ala	Ala	Cys	Leu	His	Phe	Gly	Thr	Pro	Arg	Ala	Ser	Arg	Ala	Gly	Pro
65					70				75					80	
Ser	Cys	Trp	Gly	Gly	Glu	Arg	Ser	Gln	Arg	Cys	Cys	Leu	Ala	Asp	Leu
			85					90						95	
Gly	Phe	Gly	Gly	His	Gln	Lys	Arg	Gly	Arg	Leu	Leu	Ala	Ala	Ala	Thr
			100					105						110	
Ser	Arg														

&lt;210&gt; 791

&lt;211&gt; 420

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 791

nctctgacca aaaggaaggt atatgaaaac acaacactag gcttcattgt tgaagttgaa  
 60  
 ggtcttcag ttcttggtgt gaaatggtat cgaaataaat ctttactaga gccagatgaa  
 120  
 agaatcaaaa tggaaagagt gggtaatgtg tggtcactgg aaatttctaa cattcaaaaa  
 180  
 ggagaagggg gagagtacat gtgtcatgct gtaaacatca taggggaagc aaagagcttt  
 240  
 gcaaagttag acataatgcc ccaggaagaa agagtgggtgg cactaccacc tccagtaaca  
 300

catcagcatg tcatggagtt tgatttggaa cacaccacat catcaagaac accttctcct  
 360  
 caagaaattg tcttggaggt tgaattaagt gaaaaagacg ttaaagaatt tgagaagcag  
 420

<210> 792  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

<400> 792  
 Thr Lys Arg Lys Val Tyr Glu Asn Thr Thr Leu Gly Phe Ile Val Glu  
 1 5 10 15  
 Val Glu Gly Leu Pro Val Pro Gly Val Lys Trp Tyr Arg Asn Lys Ser  
 20 25 30  
 Leu Leu Glu Pro Asp Glu Arg Ile Lys Met Glu Arg Val Gly Asn Val  
 35 40 45  
 Cys Ser Leu Glu Ile Ser Asn Ile Gln Lys Gly Glu Gly Gly Glu Tyr  
 50 55 60  
 Met Cys His Ala Val Asn Ile Ile Gly Glu Ala Lys Ser Phe Ala Asn  
 65 70 75 80  
 Val Asp Ile Met Pro Gln Glu Glu Arg Val Val Ala Leu Pro Pro Pro  
 85 90 95  
 Val Thr His Gln His Val Met Glu Phe Asp Leu Glu His Thr Thr Ser  
 100 105 110  
 Ser Arg Thr Pro Ser Pro Gln Glu Ile Val Leu Glu Val Glu Leu Ser  
 115 120 125  
 Glu Lys Asp Val Lys Glu Phe Glu Lys Gln  
 130 135

<210> 793  
 <211> 479  
 <212> DNA  
 <213> Homo sapiens

<400> 793  
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 60  
 ccgcgaacag tactgcggga acccaaacga tcatttttaa cccagacgt ccctgaacca  
 120  
 aagccaaagt ctacaggtca ctggggcaga ggccgcccga aaccagcttc ccctcccggc  
 180  
 ctaggcgcgc caggtccccg ccagccggg gcgatccttt ggtcggacag tgaggttggg  
 240  
 agcccaccgc acccaagtcc gccgcatcca ccggcgagc gcgacccccg acgggcagcc  
 300  
 gctcaccttc tcttggcccc ggcttcagga aaactgcctg gaggtggccg gggttccta  
 360  
 gcggaggctg ggccggcggc ttcgcgcctg cctcagtcct cccatccgtg gcccggggga  
 420  
 tggagcccgc tgcgcgcaga ggctgcggca ggtcccagcc aggtgccctg gaacgtgga  
 479

<210> 794

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 794

```

Xaa Ala Cys Arg Phe Ser Glu Ile His Tyr Gly Asn Val Arg Val Val
 1           5           10           15
Glu Met Leu Arg Pro Arg Thr Val Leu Arg Glu Pro Lys Arg Ser Phe
      20           25           30
Leu Thr Pro Asp Val Pro Glu Pro Lys Pro Lys Ser Thr Gly His Trp
      35           40           45
Gly Arg Gly Arg Pro Lys Pro Ala Ser Pro Pro Gly Leu Gly Ala Pro
      50           55           60
Gly Pro Arg Pro Ala Gly Ala Ile Leu Trp Ser Asp Ser Glu Val Gly
65           70           75           80
Ser Pro Pro His Pro Ser Pro Pro His Pro Pro Gly Ala Gly Asp Pro
      85           90           95
Arg Arg Ala Ala Ala His Leu Leu Leu Ala Pro Ala Ser Gly Lys Leu
      100          105          110
Pro Gly Gly Gly Arg Gly Ser Leu Ala Glu Ala Gly Arg Arg Ala Ser
      115          120          125
Arg Leu Pro Gln Ser Pro His Pro Trp Pro Gly Gly Trp Ser Pro Leu
      130          135          140
Arg Ala Glu Ala Ala Ala Gly Pro Ser Gln Val Pro Trp Asn Val
145          150          155

```

&lt;210&gt; 795

&lt;211&gt; 1418

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 795

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gccggcgccg gggaggccgg ggccctgcagg cccccgtac gacaagatcc ggactccggc
60
ccggactacg aggcgctgcc ggctggagcc actgtcacca cgcacatggt ggcaggcgcc
120
gtggcaggga tcctggagca ctgcgtgatg taccocatcg actgcgtcaa gaccgggatg
180
cagagtctac agcctgaccc agctgcccgc tatcgcaatg tggtggaggc cctctggagg
240
attataagaa cggagggcct atggaggccc atgagggggc tgaacgtcac agcaacaggc
300
gcagggcctg ccacagccct ttattttgcc tgctacgaaa agttaaaaaa gacattgagt
360
gatgtaatcc accctggggg caatagccat attgccaatg gtgcggccgg gtgtgtggca
420
acattacttc atgatgcagc catgaaccct gcggaaggct gatctgctga cttggggctc
480
tgaatctgga tactctccat caccggttgg ctgctgtcac catttccttc ctggttgatg
540
gcactactag tggtaagca gaggatgcag atgtacaact caccatacca ccgggtgaca
600
gactgtgtac gggcagtgtg gcaaaatgaa ggggcccggg ccttttaccg cagctacacc
660

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acccagctga ccatgaacgt tcctttccaa gccattcact tcatgaccta tgaattcctg  
 720  
 caggagcact ttaaccccca gagacggtac aacccaagct cccacgtcct ctctggagct  
 780  
 tgcgcaggag ctgtagctgc cgcagccaca accccactgg acgtttgcaa aacactgctc  
 840  
 aacacccagg agtccttggc tttgaactca cacattacag gacatatcac aggcattggct  
 900  
 agtgccttca ggacggtata tcaagtaggt ggggtgaccg cctatttccg aggggtgcag  
 960  
 gccagagtaa ttaccagat cccctccaca gccatcgcat ggtctgtgta tgagttcttc  
 1020  
 aaatacctaa tcaactaaaag gcaagaagag tggagggctg gcaagtgaag tagcactgaa  
 1080  
 cgaagccagg ggttcagatg acactgctgc atcctggtca cattctctgt ctcttggaat  
 1140  
 gctccacct caagtggagt tagaaggaag gtagaggggc tctccccag gattttggtg  
 1200  
 ttttgactaa caccagttec tgccaacctc tgttgccacc acctttcctt ccaggcccta  
 1260  
 agcacgtgca gcaaagcaca ccacagcacc tttgataacc tctctccatc ctgggcctga  
 1320  
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 1380  
 agcctttaa ttaaaaaaaaa aaaaaaaaaa aaaaaaaaa  
 1418

<210> 796

<211> 176

<212> PRT

<213> Homo sapiens

<400> 796

Met	Ala	Leu	Leu	Val	Val	Lys	Gln	Arg	Met	Gln	Met	Tyr	Asn	Ser	Pro
1				5					10					15	
Tyr	His	Arg	Val	Thr	Asp	Cys	Val	Arg	Ala	Val	Trp	Gln	Asn	Glu	Gly
			20					25					30		
Ala	Gly	Ala	Phe	Tyr	Arg	Ser	Tyr	Thr	Thr	Gln	Leu	Thr	Met	Asn	Val
			35				40					45			
Pro	Phe	Gln	Ala	Ile	His	Phe	Met	Thr	Tyr	Glu	Phe	Leu	Gln	Glu	His
			50			55					60				
Phe	Asn	Pro	Gln	Arg	Arg	Tyr	Asn	Pro	Ser	Ser	His	Val	Leu	Ser	Gly
65				70					75					80	
Ala	Cys	Ala	Gly	Ala	Val	Ala	Ala	Ala	Ala	Thr	Thr	Pro	Leu	Asp	Val
			85					90					95		
Cys	Lys	Thr	Leu	Leu	Asn	Thr	Gln	Glu	Ser	Leu	Ala	Leu	Asn	Ser	His
			100				105					110			
Ile	Thr	Gly	His	Ile	Thr	Gly	Met	Ala	Ser	Ala	Phe	Arg	Thr	Val	Tyr
		115				120					125				
Gln	Val	Gly	Gly	Val	Thr	Ala	Tyr	Phe	Arg	Gly	Val	Gln	Ala	Arg	Val
		130				135				140					
Ile	Tyr	Gln	Ile	Pro	Ser	Thr	Ala	Ile	Ala	Trp	Ser	Val	Tyr	Glu	Phe
145				150					155					160	
Phe	Lys	Tyr	Leu	Ile	Thr	Lys	Arg	Gln	Glu	Glu	Trp	Arg	Ala	Gly	Lys

165

170

175

&lt;210&gt; 797

&lt;211&gt; 585

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 797

aaatttaccg gcggcaaaac ccacgtcacc gactacacca acgcctcgcg caccatgctc  
 60  
 ttcaacatcc acacgctgga gtgggatgcg aagatgctgg agattctcga cgtgccgcgc  
 120  
 gagatgctgc cggaagttaa gtcgtcttca gaaatctacg gccgcaccaa aagcggatc  
 180  
 gctatcggcg gcacgcggcg cgaccaacag gctgctctgt tcggccagat gtgcgtggaa  
 240  
 gccgggcagg ccaagaacac ttatggcacc ggctgcttcc tgctgatgaa caccggcgac  
 300  
 aaagccgtca aatccaaaca cggcatgctc accaccatcg cctgcgggtcc acgcggcgaa  
 360  
 gtggcttatg cgctggaagg cgcggtgttc aacggtgggt cccccgtgca gtggctgcgt  
 420  
 gatgagctga agatcatcgc ggacgccacc gacaccgaat acttcgccgg caaggtcaag  
 480  
 gacagcaacg gcgtctacct ggtgccggcc ttaccggcc tgggcgctcc gtactgggac  
 540  
 ccgtatgccc gtggcgcttt gtttggcctg actcgtggcg tacgc  
 585

&lt;210&gt; 798

&lt;211&gt; 195

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 798

Lys	Phe	Thr	Gly	Gly	Lys	Thr	His	Val	Thr	Asp	Tyr	Thr	Asn	Ala	Ser
1				5					10					15	
Arg	Thr	Met	Leu	Phe	Asn	Ile	His	Thr	Leu	Glu	Trp	Asp	Ala	Lys	Met
			20					25					30		
Leu	Glu	Ile	Leu	Asp	Val	Pro	Arg	Glu	Met	Leu	Pro	Glu	Val	Lys	Ser
			35				40				45				
Ser	Ser	Glu	Ile	Tyr	Gly	Arg	Thr	Lys	Ser	Gly	Ile	Ala	Ile	Gly	Gly
	50					55				60					
Ile	Ala	Gly	Asp	Gln	Gln	Ala	Ala	Leu	Phe	Gly	Gln	Met	Cys	Val	Glu
65				70					75					80	
Ala	Gly	Gln	Ala	Lys	Asn	Thr	Tyr	Gly	Thr	Gly	Cys	Phe	Leu	Leu	Met
				85				90						95	
Asn	Thr	Gly	Asp	Lys	Ala	Val	Lys	Ser	Lys	His	Gly	Met	Leu	Thr	Thr
			100					105					110		
Ile	Ala	Cys	Gly	Pro	Arg	Gly	Glu	Val	Ala	Tyr	Ala	Leu	Glu	Gly	Ala
		115				120					125				
Val	Phe	Asn	Gly	Gly	Ser	Pro	Val	Gln	Trp	Leu	Arg	Asp	Glu	Leu	Lys
	130					135				140					
Ile	Ile	Ala	Asp	Ala	Thr	Asp	Thr	Glu	Tyr	Phe	Ala	Gly	Lys	Val	Lys

145		150		155		160
Asp Ser Asn Gly Val Tyr Leu Val Pro Ala Phe Thr Gly Leu Gly Ala						
		165		170		175
Pro Tyr Trp Asp Pro Tyr Ala Arg Gly Ala Leu Phe Gly Leu Thr Arg						
		180		185		190
Gly Val Arg						
		195				

<210> 799  
 <211> 2152  
 <212> DNA  
 <213> Homo sapiens

<400> 799  
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 caagtgtccc agcagcatga ctgaacatca ctcaactccc ctacttgatc tacaaggcca  
 120  
 acgccgagag cccagaccag gattccaaac aactgcacg agaattattgt ggatccgctg  
 180  
 tcaggtaagt gtccgtcact gacccagacg ctgttacgtg gcacatgact gtacagtgcc  
 240  
 acgtaacagc actgtacttt tctcccataa acagttacct gccatgtatc tacatgattc  
 300  
 agaacatttt gaacagttaa ttctgacact tgaataatcc catcaaaaac cgtaaaatca  
 360  
 ctttgatggt gtaacgacaa catagcatca ctttacgaca gaatcatctg gaaaaacaga  
 420  
 acaacgaata catacatctt aaaaaatgct ggggtgggcc aggcacagct cagcctgta  
 480  
 atcccagcac tttgggaggc tgaggcgggt ggatcacgta atcccagcac tttgaggggc  
 540  
 agaggtggac agatcatgag gtcaagagat caagaccatc ctgggtcaaaa tgggtgaaacc  
 600  
 ccgtctctac taaaaatata aaaattagct gagcttagtg gcacacacct gtagtcccag  
 660  
 ctacttggga ggctgaggca ggagaatcgc ttgaaccag gagacacagg ctgcagtgc  
 720  
 tcgagatcac gccactgcac tccagcctgg cgacagagcg agactccatc tcaaaaaaaaa  
 780  
 aaaccaacaa aaaaactggg gtgaaaatct aacggataat tcagcattgc cgcatagaaa  
 840  
 cctccgcaaa accggccaaa caaacgcgga caggcggccc tggcgtcagc gcacgacagt  
 900  
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 960  
 ttccagatcc accaccggga cctgctccac caccagaagg gagggcccgt ctttccagc  
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 actgggattc gttgtgggat ctggaagttg tccagagact gcacggcctt cagtatctga  
 1080  
 gagtgatcct tctcttttat tttctaaagt gtactttttc atttctgcca ttttcagaat  
 1140  
 gagggcatcc atgacatcct tgcaaatctg cagactgggtg gcacttggtta cttccaaaaa  
 1200

caaatcagaa gtcgttttct taacctttgt cttctcactg ttggttattg gtgggaagga  
 1260  
 aatcacatca ccgtctgcat ccacaagaca cgggtaattt tcatttccat ccagcaagtg  
 1320  
 aaggatatctg tgcaggccccg acacactctg ccgcttcttc tgcttcctct gctcctcggc  
 1380  
 ctccagctgc agctgccgca ccagctcctt ggccttggtt tctttccgcc ccaaggggac  
 1440  
 aatcttgagg tcctgtgggg gccgggcgca gtacagcagg ggccctttga cggcacggag  
 1500  
 ctcggtgggtg gcaaggggtg cagccgtcct cttctcacag agatcttcgt ggagcttggt  
 1560  
 ctgagagggtg aggaagcgct tgagtgcatt ccctggctgc aggtccatgc ctgcaccac  
 1620  
 ggccccaca atgtagggcc gcacatcccg gacctgggg ctcactctga ctgtcagagg  
 1680  
 tacgggggtt tcagagacgt gcaggacct gagcagcagc cggccggcat ctcccacgtc  
 1740  
 ctgctcctcc ccataccac cttccgcct ctgcttctc tccctcctct tctccggct  
 1800  
 ctcttcttc tccgagcct cggcacggcc cttgcccttc ccgccaccac ggctccgac  
 1860  
 gcgcaggtac tccaggatgg atctggtctg gcagccgctg accatcttct ccaggcgctt  
 1920  
 gtccctcagc ttgttccac ggaaattgat ctccttgagc ttggggcagt ccgcaagctc  
 1980  
 tgcagggatc tcgctcagct ggtgttcga gaggtccaac gtcttgagcg aggccagggtg  
 2040  
 ggcgatgtcg gggctgagtt ctcgaggga gttgtcagca gccgccagtt cactgagcag  
 2100  
 gggcagcgcg ccggggcgaa agagctcggc gggaaaggag tctaggcaat tg  
 2152

&lt;210&gt; 800

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 800

Cys	Cys	Asn	Asp	Asn	Ile	Ala	Ser	Leu	Tyr	Asp	Arg	Ile	Ile	Trp	Lys
1				5					10					15	
Asn	Arg	Thr	Thr	Asn	Thr	Tyr	Ile	Leu	Lys	Asn	Ala	Gly	Val	Gly	Gln
		20						25					30		
Ala	Gln	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Glu	Ala	Glu	Ala	Gly
		35					40				45				
Gly	Ser	Arg	Asn	Pro	Ser	Thr	Leu	Arg	Gly	Arg	Gly	Gly	Gln	Ile	Met
	50					55				60					
Arg	Ser	Arg	Asp	Gln	Asp	His	Pro	Gly	Gln	Asn	Gly	Glu	Thr	Pro	Ser
65				70				75						80	
Leu	Leu	Lys	Ile	Gln	Lys	Leu	Ala	Glu	Leu	Ser	Gly	Thr	His	Leu	
			85					90						95	

&lt;210&gt; 801

&lt;211&gt; 424

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 801

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nntcatgaat cggtataaac acaatgggta gtgtatatca tatctatagg agatactatg
60
tatcaaatta atcagctgtc tttttcttat gaaacaaaag aagtgttaaa gaatatttct
120
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&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 802

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50           55           60
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Gln Ser Arg Asp Ala Met Ile Asp Asp Phe Leu Val Lys Asp Ile Val
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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 803

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<211> 1400

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<400> 804

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 Gly Val Lys Ile Lys Gly Cys Pro Ser Glu Pro Tyr Phe Gly Ser Leu  
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 Ser Ala Leu Val Ser Gln His Ser Ile Ser Pro Ile Ser Leu Pro Cys  
 1220 1225 1230  
 Cys Leu Arg Ile Pro Ser Lys Asp Pro Leu Glu Glu Thr Pro Glu Ala  
 1235 1240 1245  
 Pro Val Pro Thr Asn Met Ser Thr Ala Ala Asp Leu Leu Arg Gln Gly  
 1250 1255 1260  
 Ala Ala Cys Ser Val Leu Tyr Leu Thr Ser Val Glu Thr Glu Ser Leu  
 1265 1270 1275 1280  
 Thr Gly Pro Gln Ala Val Ala Arg Ala Ser Ser Ala Ala Leu Ser Cys  
 1285 1290 1295  
 Ser Pro Arg Pro Thr Pro Ala Val Val His Phe Lys Val Ser Ala Gln  
 1300 1305 1310  
 Gly Ile Thr Leu Thr Asp Asn Gln Arg Lys Leu Phe Phe Arg Arg His  
 1315 1320 1325  
 Tyr Pro Val Asn Ser Ile Thr Phe Ser Ser Thr Asp Pro Gln Asp Arg  
 1330 1335 1340  
 Arg Trp Thr Asn Pro Asp Gly Thr Thr Ser Lys Ile Phe Gly Phe Val  
 1345 1350 1355 1360  
 Ala Lys Lys Pro Gly Ser Pro Trp Glu Asn Val Cys His Leu Phe Ala  
 1365 1370 1375  
 Glu Leu Asp Pro Asp Gln Pro Ala Gly Ala Ile Val Thr Phe Ile Thr  
 1380 1385 1390  
 Lys Val Leu Leu Gly Gln Arg Lys  
 1395 1400

&lt;210&gt; 805

&lt;211&gt; 550

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 805

cccgagagag gcttcaatcc aatgagctgc cagctgaact tactcaacaa gcaaggaccc  
 60  
 atgggcagac ccaggaaatc tcgccaagta cccattcat gggaggccag cagcacaatt  
 120  
 agtcatccat ttacttatca agctgttact gtgtgtgcaa gaagcgccag agagatgata  
 180  
 tcaaggagct cttaccatgg ctggcataga gcggctgatg agtaagttcc gtctgcacaa  
 240  
 agagtcccta agcattcatt cttggctgac attcttggct caggggggtct ccatggcctt  
 300  
 gttcccctcc tcgggtcacc agttcaggte gagggggcct atgcttggaa gggccacacc  
 360  
 aatggacctt gccaggacac tcagtcacag gtttcacacc caaagagaag acagcccaac  
 420  
 ccagaccctc aaaagagagc acctggggga agggagcgtg gaaaccagga ctcagaaaga  
 480



cacaagagaa aaagaagctg tacactgggg aggcttccgg ggtacctgtg cctgccatgt  
 540  
 ctctgaaggc  
 550

<210> 806  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 806  
 Met Ala Gly Ile Glu Arg Leu Met Ser Lys Phe Arg Leu His Lys Glu  
 1 5 10 15  
 Ser Leu Ser Ile His Ser Trp Leu Thr Phe Leu Ala Gln Gly Val Ser  
 20 25 30  
 Met Ala Leu Phe Pro Ser Ser Gly His Gln Phe Arg Ser Arg Gly Pro  
 35 40 45  
 Met Leu Gly Arg Ala Thr Pro Met Asp Leu Ala Arg Thr Leu Ser His  
 50 55 60  
 Arg Phe His Thr Gln Arg Glu Asp Ser Pro Thr Gln Thr Leu Lys Arg  
 65 70 75 80  
 Glu His Leu Gly Glu Gly Ser Val Glu Thr Arg Thr Gln Lys Asp Thr  
 85 90 95  
 Arg Glu Lys Glu Ala Val His Trp Gly Gly Phe Arg Gly Thr Cys Ala  
 100 105 110  
 Cys His Val Ser Glu Gly  
 115

<210> 807  
 <211> 287  
 <212> DNA  
 <213> Homo sapiens

<400> 807  
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 cccgaggtgg gagagcgcgc ggcattggcga ccgtaaactg atcgttgtcc gatgcgatga  
 120  
 ccgagtgggt cgaagctcag accgggacag gccgctatac cagcgcgagc gattatatct  
 180  
 gcgccctgat tcgccaggac caggagcgaa gcgacggcct caggcagctt caaacgttga  
 240  
 tcaccgaggg gttcgacagc ggcattcagcg cctcgctcgt tgatgac  
 287

<210> 808  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 808  
 Met Ala Val Ala Leu Pro His Trp Gln Asp Ala Lys Phe Leu Ala Met  
 1 5 10 15  
 Ile Ser Arg Gly Gly Arg Ala Arg Gly Met Ala Thr Val Asn Val Ser

```

      20      25      30
Leu Ser Asp Ala Met Thr Glu Trp Val Glu Ala Gln Thr Gly Thr Gly
      35      40      45
Arg Tyr Thr Ser Ala Ser Asp Tyr Ile Cys Ala Leu Ile Arg Gln Asp
      50      55      60
Gln Glu Arg Ser Asp Gly Leu Arg Gln Leu Gln Thr Leu Ile Thr Glu
      65      70      75      80
Gly Phe Asp Ser Gly Ile Ser Ala Ser Ser Leu Asp Asp
      85      90

```

&lt;210&gt; 809

&lt;211&gt; 405

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 809

```

nngggggggg gggggggggg gggttttttc ccccaaaga aaaaaaagg gggggggggg
60
gggccccccc ccccccccc ccttttttc cccggggggg tttattcca gggccaacag
120
gacgcgtggt cgcgtcaaat ggagagacga tcggtgccgc ccttgcccca cgatcctgat
180
ggccccgaga ttcctgacga tgtcaccacc ctgcccaac aggtaatggg tctgccacgt
240
cacctgggta tccactcagc tggaatggtg ctgacgcgag aaccagtagg acgcatctgc
300
cccattgagc cggctcgaat gtttggtcgc acggggctgc agtgggacaa anaaaactgt
360
gcctggatgg gggtggggaa gtttgatctg cttgggttg ggatg
405

```

&lt;210&gt; 810

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 810

```

Xaa Gly Gly Gly Gly Gly Gly Val Phe Phe Pro Pro Lys Lys Lys Lys
1      5      10      15
Gly Gly Gly Gly Gly Pro Pro Pro Pro Pro Pro Leu Phe Phe Pro Arg
      20      25      30
Gly Val Tyr Ser Gln Gly Gln Gln Asp Ala Trp Ser Arg Gln Met Glu
      35      40      45
Arg Arg Ser Val Pro Pro Leu Pro His Asp Pro Asp Gly Pro Glu Ile
      50      55      60
Pro Asp Asp Val Thr Thr Leu Ala Gln Gln Val Met Gly Leu Pro Arg
      65      70      75      80
His Leu Gly Ile His Ser Ala Gly Met Val Leu Thr Arg Glu Pro Val
      85      90      95
Gly Arg Ile Cys Pro Ile Glu Pro Ala Arg Met Phe Gly Arg Thr Gly
      100      105      110
Leu Gln Trp Asp Lys Xaa Asn Cys Ala Trp Met Gly Leu Gly Lys Phe
      115      120      125
Asp Leu Leu Gly Leu Gly Met

```

130

135

<210> 811  
 <211> 642  
 <212> DNA  
 <213> Homo sapiens

<400> 811  
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 60  
 cagtgccaat gactgccaat ggcaaagaag agctccaacc aaacaccagg tgcttcatgg  
 120  
 tggtagacaca ttaacaacac ccgggaagca gtactgccaac cacctagata tgagaaaaag  
 180  
 aaaacaggca cttaaagcga ggctaaccac ctttcaggaa tgataaaggg cagaggaccc  
 240  
 tgtcacctct acccctgcta ctaaaggcgt ggcccacaga gcagcagcac cagcagcaca  
 300  
 taaaatgggg ttaaatatga caggaaaaac aaggtgacag ggaaatgggg tgaagatcaa  
 360  
 gttcgtggta ngtctttctt tcttagagggc tttgggcctg agctcttggg gaaagctctc  
 420  
 caacacctca ggggtgtgctt gttccctcgc cctgtgggga tgctctttgt acgggtgggt  
 480  
 gactggctcc cactttcttc cgtattgttg tcttgtctct tccctcaca ccatcaaggc  
 540  
 tctttccctt aattctataa gacagtacct ctggcttaga aattatatgc cctcctttaa  
 600  
 aaaaacgaaa tgctagagga catagaactt gaggaaaaat tt  
 642

<210> 812  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 812  
 Met Val Val Arg Glu Glu Thr Arg Gln Gln Tyr Gly Gly Lys Trp Glu  
 1 5 10 15  
 Pro Val Ser His Pro Tyr Lys Glu His Pro His Arg Ala Gly Glu Gln  
 20 25 30  
 Ala His Pro Glu Val Leu Glu Ser Phe Leu Gln Glu Leu Arg Pro Lys  
 35 40 45  
 Ala Ser Arg Lys Glu Arg Xaa Thr Thr Asn Leu Ile Phe Thr Pro Phe  
 50 55 60  
 Pro Cys His Leu Val Phe Pro Val Ile Phe Asn Pro Ile Leu Cys Ala  
 65 70 75 80  
 Ala Gly Ala Ala Ala Leu Trp Ala Thr Pro Leu Val Ala Gly Val Glu  
 85 90 95  
 Val Thr Gly Ser Ser Ala Leu Tyr His Ser  
 100 105

<210> 813  
 <211> 558

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 813

```

ccccggcgat agtcgctggt ggtcatggcg gatgaggggt taagagcgcg tttactgcgg
60
cgccccgactc cgatcagccg ttcggaaagg cgacgccgaa gatcatgaca ttctcggccc
120
gttcgctgac cagcaccggg ccgcccggct gggccgggaa accgtggaac aagggaaagcg
180
ggggcgggcg gcggggtgac gccttcggcc ccctcgctt cggtcagcgt gcggcgcaat
240
tcgggggtcga ggatgatccg cggcccttcg atcttgacca cgatctccag ttgcccgcc
300
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gcgagggttca gcatcacctt cagcgcggac ttgggcagcg tctccgtttc caccaccag
420
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480
gcgtcgacct gttcgccgaa cccgcccggc gcgcagaagg cgaggcgga gaatttgagc
540
ttgttggcgg atacgcgt
558

```

&lt;210&gt; 814

&lt;211&gt; 151

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 814

```

Met Thr Phe Ser Ala Gly Ser Leu Thr Ser Thr Gly Pro Pro Gly Trp
 1           5           10           15
Ala Gly Lys Pro Trp Asn Lys Gly Ser Gly Gly Gly Ala Arg Gly Asp
 20           25           30
Ala Phe Gly Pro Leu Ala Phe Gly Gln Arg Ala Ala Gln Phe Gly Val
 35           40           45
Glu Asp Asp Pro Arg Pro Phe Asp Leu Asp His Asp Leu Gln Leu Pro
 50           55           60
Ala Ile Val Phe Ala Ala Asp Ile Gln Arg Ala Ala Ala His Gln Arg
 65           70           75           80
Leu Ala Gly Asp Gln Gly Glu Val Gln His His Leu Gln Arg Gly Leu
 85           90           95
Gly Gln Arg Leu Arg Phe His Pro Pro Val Glu Leu Arg Ala Leu Ile
100           105           110
Val Gly Asn Gln Pro Leu Val Arg Gly Phe Arg Phe Ala Arg Val Asp
115           120           125
Leu Phe Ala Glu Pro Ala Gly Gly Ala Glu Gly Glu Ala Glu Glu Phe
130           135           140
Glu Leu Val Gly Gly Tyr Ala
145           150

```

&lt;210&gt; 815

&lt;211&gt; 315

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 815

acgcgttgag actgtcacia ggctaggcta acttcatata gctatgccat cagatctgcc  
 60  
 caaagtggac gatgagaaag ctcacgacgc gcctcacacg gatgggtcgg agcctggaca  
 120  
 agctagcgca ggagaaagcc gagacctcac gtccgaagcg gattcagcaa gtgcacaacc  
 180  
 ttctaccacac gctgagggtt ccagtgaagt tactgctacg tccagtatag atgagcaggt  
 240  
 agacctcatt gctgcaccgt taagcgaaga gtccaatgtc agcaagctcg ggccgtcccc  
 300  
 tgaggccgat acatc  
 315

&lt;210&gt; 816

&lt;211&gt; 90

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 816

Met	Pro	Ser	Asp	Leu	Pro	Lys	Val	Asp	Asp	Glu	Lys	Ala	His	Asp	Ala
1				5				10					15		
Pro	His	Thr	Asp	Gly	Ser	Glu	Pro	Gly	Gln	Ala	Ser	Ala	Gly	Glu	Ser
			20					25					30		
Arg	Asp	Leu	Thr	Ser	Glu	Ala	Asp	Ser	Ala	Ser	Ala	Gln	Pro	Ser	Thr
		35					40					45			
His	Ala	Glu	Val	Ser	Ser	Glu	Val	Thr	Ala	Thr	Ser	Ser	Ile	Asp	Glu
		50				55					60				
Gln	Val	Asp	Leu	Ile	Ala	Ala	Pro	Leu	Ser	Glu	Glu	Ser	Asn	Val	Ser
65				70						75					80
Lys	Leu	Gly	Pro	Ser	Pro	Glu	Ala	Asp	Thr						
				85					90						

&lt;210&gt; 817

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 817

gaattcaaag agaaatatct gcctagacct tatgtgatta atctaattga cgaactgacc  
 60  
 ctgaaaggaa tcacacaata ttatgctttt gttgaagagg ggcagaaggt tcattgcctg  
 120  
 aatacacttt totcaaagct tcaaattaat caatccatta tattctgcaa ctctgttaat  
 180  
 agtggtgagc tgctggctaa aaaaataact gaactcgggt attcatgctt ctacattcat  
 240  
 gctaagatgt tgcaagacca cagaaatcga gtattccatg attgtcgtaa tgggtgcttg  
 300  
 agaaaccttg tgtgcacaga t  
 321

<210> 818  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 818  
 Glu Phe Lys Glu Lys Tyr Leu Pro Arg Pro Tyr Val Ile Asn Leu Met  
 1 5 10 15  
 Asp Glu Leu Thr Leu Lys Gly Ile Thr Gln Tyr Tyr Ala Phe Val Glu  
 20 25 30  
 Glu Gly Gln Lys Val His Cys Leu Asn Thr Leu Phe Ser Lys Leu Gln  
 35 40 45  
 Ile Asn Gln Ser Ile Ile Phe Cys Asn Ser Val Asn Ser Val Glu Leu  
 50 55 60  
 Leu Ala Lys Lys Ile Thr Glu Leu Gly Tyr Ser Cys Phe Tyr Ile His  
 65 70 75 80  
 Ala Lys Met Leu Gln Asp His Arg Asn Arg Val Phe His Asp Cys Arg  
 85 90 95  
 Asn Gly Ala Cys Arg Asn Leu Val Cys Thr Asp  
 100 105

<210> 819  
 <211> 3422  
 <212> DNA  
 <213> Homo sapiens

<400> 819  
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 120  
 gcagggggccc atggactctc caaaggcccc ctggagaagc ggccctatct tggccccggc  
 180  
 ctgcccctga ctccccgaga cagggccagt ggcacacaag gggccagtga ggacaactct  
 240  
 ggtggaggag gcaagaagcc aaagatggag gagctgggccc tggcctccca cccccggag  
 300  
 ggcaggccct gccagcccca gacaaggcca cagaaacagc caggccacac caactacagc  
 360  
 agctattcca agcgggaagcg cctcactcgg ggccgggcca agaacaccac ctcttcaccc  
 420  
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 480  
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 540  
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1800  
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1860  
cgacgtggca cacattccac gtgggtgctg ccgccacccc agtcgggtcgt ggcgtgcagc  
1920  
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1980  
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2100  
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2160  
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2280  
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ctgtgtaccc ctctatatat atgttacata gaatgtatat atgttgggaa catgctcgct  
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 3180  
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 3240  
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 3300  
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 3360  
 atccatcagc tgaagacaca aaaccagat tataaataat ttcattttta attctctgta  
 3420  
 ca  
 3422

&lt;210&gt; 820

&lt;211&gt; 494

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 820

Met	Asn	Ser	Lys	Lys	Leu	Ser	Ser	Thr	Asp	Cys	Phe	Lys	Thr	Glu	Ala
1			5					10					15		
Phe	Thr	Ser	Pro	Glu	Ala	Leu	Gln	Pro	Gly	Gly	Thr	Ala	Leu	Ala	Pro
			20					25				30			
Lys	Lys	Arg	Ser	Arg	Lys	Gly	Arg	Ala	Gly	Ala	His	Gly	Leu	Ser	Lys
		35				40					45				
Gly	Pro	Leu	Glu	Lys	Arg	Pro	Tyr	Leu	Gly	Pro	Ala	Leu	Pro	Leu	Thr
	50				55					60					
Pro	Arg	Asp	Arg	Ala	Ser	Gly	Thr	Gln	Gly	Ala	Ser	Glu	Asp	Asn	Ser
65					70				75					80	
Gly	Gly	Gly	Gly	Lys	Lys	Pro	Lys	Met	Glu	Glu	Leu	Gly	Leu	Ala	Ser



										85			90			95		
His	Pro	Pro	Glu	Gly	Arg	Pro	Cys	Gln	Pro	Gln	Thr	Arg	Ala	Gln	Lys			
			100				105						110					
Gln	Pro	Gly	His	Thr	Asn	Tyr	Ser	Ser	Tyr	Ser	Lys	Arg	Lys	Arg	Leu			
			115				120						125					
Thr	Arg	Gly	Arg	Ala	Lys	Asn	Thr	Thr	Ser	Ser	Pro	Cys	Lys	Gly	Arg			
			130				135						140					
Ala	Lys	Arg	Arg	Arg	Gln	Gln	Val	Leu	Pro	Leu	Asp	Pro	Ala	Glu				
145				150			155						160					
Pro	Glu	Ile	Arg	Leu	Lys	Tyr	Ile	Ser	Ser	Cys	Lys	Arg	Leu	Arg	Ser			
			165			170						175						
Asp	Ser	Arg	Thr	Pro	Ala	Phe	Ser	Pro	Phe	Val	Arg	Val	Glu	Lys	Arg			
			180			185						190						
Asp	Ala	Phe	Thr	Thr	Ile	Cys	Thr	Val	Val	Asn	Ser	Pro	Gly	Asp	Ala			
			195			200						205						
Pro	Lys	Pro	His	Arg	Lys	Pro	Ser	Ser	Ser	Ala	Ser	Ser	Ser	Ser	Ser			
			210			215						220						
Ser	Ser	Ser	Phe	Ser	Leu	Asp	Ala	Ala	Gly	Ala	Ser	Leu	Ala	Thr	Leu			
225				230			235						240					
Pro	Gly	Gly	Ser	Ile	Leu	Gln	Pro	Arg	Pro	Ser	Leu	Pro	Leu	Ser	Ser			
			245			250						255						
Thr	Met	His	Leu	Gly	Pro	Val	Val	Ser	Lys	Ala	Leu	Ser	Thr	Ser	Cys			
			260			265						270						
Leu	Val	Cys	Cys	Leu	Cys	Gln	Asn	Pro	Ala	Asn	Phe	Lys	Asp	Leu	Gly			
			275			280						285						
Asp	Leu	Cys	Gly	Pro	Tyr	Tyr	Pro	Glu	His	Cys	Leu	Pro	Lys	Lys	Lys			
			290			295						300						
Pro	Lys	Leu	Lys	Glu	Lys	Val	Arg	Pro	Glu	Gly	Thr	Cys	Glu	Glu	Ala			
305				310			315						320					
Ser	Leu	Pro	Leu	Glu	Arg	Thr	Leu	Lys	Gly	Pro	Glu	Cys	Ala	Ala	Ala			
			325			330						335						
Ala	Thr	Ala	Gly	Lys	Pro	Pro	Arg	Pro	Asp	Gly	Pro	Ala	Asp	Pro	Ala			
			340			345						350						
Lys	Gln	Gly	Pro	Leu	Arg	Thr	Ser	Ala	Arg	Gly	Leu	Ser	Arg	Arg	Leu			
			355			360						365						
Gln	Ser	Cys	Tyr	Cys	Cys	Asp	Gly	Arg	Glu	Asp	Gly	Gly	Glu	Glu	Ala			
			370			375						380						
Ala	Pro	Ala	Asp	Lys	Gly	Arg	Lys	His	Glu	Cys	Ser	Lys	Glu	Ala	Pro			
385				390			395						400					
Ala	Glu	Pro	Gly	Gly	Glu	Ala	Gln	Glu	His	Trp	Val	His	Glu	Ala	Cys			
			405			410						415						
Ala	Val	Trp	Thr	Gly	Gly	Val	Tyr	Leu	Val	Ala	Gly	Lys	Leu	Phe	Gly			
			420			425						430						
Leu	Gln	Glu	Ala	Met	Lys	Val	Ala	Val	Asp	Met	Met	Cys	Ser	Ser	Cys			
			435			440												

<210> 821

<211> 420

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 821

acgcgtccccg tcacctgcgg tatggaccaa gtgagttgtg tgctcgacaa tgggttcgcc  
60  
gccatcatgg atgtgccggg tttcaactat cgcgcccatc gttacaccga agcctatcgg  
120  
cgtttgccgc aaaatgtggt gctaggttcg gaaacgacct cgacggtgag cagccgtggt  
180  
gtctacaagt ttcctgttgt gctgaagtcc gatgccatct atcccgacca tcagtcgtca  
240  
ggctacgaca cagagtattg ttcgtggtcg aacacccccg atgtcgattt cgcctcggc  
300  
gaagactatc cctggacgat ggggcagttt gtctggacgg gcttcgacta cctcggtgaa  
360  
ccttcgcctt acgacaccga tgctggccc tctcagcct ccctcttcgg cattgtcgac  
420

&lt;210&gt; 822

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 822

Met	Asp	Gln	Val	Ser	Cys	Val	Leu	Asp	Asn	Gly	Phe	Ala	Ala	Ile	Met
1				5				10						15	
Asp	Val	Pro	Gly	Phe	Asn	Tyr	Arg	Ala	His	Arg	Tyr	Thr	Glu	Ala	Tyr
		20					25						30		
Arg	Arg	Leu	Pro	Gln	Asn	Val	Val	Leu	Gly	Ser	Glu	Thr	Thr	Ser	Thr
		35				40						45			
Val	Ser	Ser	Arg	Gly	Val	Tyr	Lys	Phe	Pro	Val	Val	Leu	Lys	Ser	Asp
	50					55					60				
Ala	Ile	Tyr	Pro	Asp	His	Gln	Ser	Ser	Gly	Tyr	Asp	Thr	Glu	Tyr	Cys
65					70				75					80	
Ser	Trp	Ser	Asn	Thr	Pro	Asp	Val	Asp	Phe	Ala	Leu	Ala	Glu	Asp	Tyr
			85				90							95	
Pro	Trp	Thr	Met	Gly	Gln	Phe	Val	Trp	Thr	Gly	Phe	Asp	Tyr	Leu	Gly
		100					105						110		
Glu	Pro	Ser	Pro	Tyr	Asp	Thr	Asp	Ala	Trp	Pro	Ser	His	Ala	Ser	Leu
		115				120						125			
Phe	Gly	Ile	Val	Asp											
		130													

&lt;210&gt; 823

&lt;211&gt; 550

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 823

tctagattct tgggcagccg agcccctctt gaattcctca gcctaccatc atgatcaaca  
60  
cctcccatgt tccgtccatg aatgaccgca ctgacagcac tggagagatt taatgggtca  
120

ccaattgagg cagtgaaggc actcatggca ctcagagctg gaatggggct gatctgagtt  
 180  
 gtactgttga ctgcagtggg gatgacaacc tgcattcctt tgctggctgc atcgacaact  
 240  
 gctttgtaaa tggcatctac ggaagcatca cctggggccac ccacaacgag gccatccttc  
 300  
 acctgttgac caagagatgg gtcaatcctc ggttgcaact cacaagggtg atcttgaaaa  
 360  
 ggtggaagtg tagtgtttgg attctcagga agtgctgtga gcccaggctg agtgcttatt  
 420  
 cttttgttta ggagagctgc atcttcctgc attctcacct gaaagttctg aaacagacaa  
 480  
 gccatggggg tattgttagc tgggcaagga attgtggact gtccttgga cgcctggaga  
 540  
 ttctggtacc  
 550

<210> 824  
 <211> 161  
 <212> PRT  
 <213> Homo sapiens

<400> 824  
 Met Ala Cys Leu Phe Gln Asn Phe Gln Val Arg Met Gln Glu Asp Ala  
 1 5 10 15  
 Ala Leu Leu Asn Lys Arg Ile Ser Thr Gln Pro Gly Leu Thr Ala Leu  
 20 25 30  
 Pro Glu Asn Pro Asn Thr Thr Leu Pro Pro Phe Gln Asp Thr Pro Cys  
 35 40 45  
 Glu Leu Gln Pro Arg Ile Asp Pro Ser Leu Gly Gln Gln Val Lys Asp  
 50 55 60  
 Gly Leu Val Val Gly Gly Pro Gly Asp Ala Ser Val Asp Ala Ile Tyr  
 65 70 75 80  
 Lys Ala Val Val Asp Ala Ala Ser Lys Gly Met Gln Val Val Ile Thr  
 85 90 95  
 Thr Ala Val Asn Ser Thr Thr Gln Ile Ser Pro Ile Pro Ala Leu Ser  
 100 105 110  
 Ala Met Ser Ala Phe Thr Ala Ser Ile Gly Asp Pro Leu Asn Leu Ser  
 115 120 125  
 Ser Ala Val Ser Ala Val Ile His Gly Arg Asn Met Gly Gly Val Asp  
 130 135 140  
 His Asp Gly Arg Leu Arg Asn Ser Arg Gly Ala Arg Leu Pro Lys Asn  
 145 150 155 160  
 Leu

<210> 825  
 <211> 327  
 <212> DNA  
 <213> Homo sapiens

<400> 825  
 gcggttgcga ccggccgtaa cccgcagaat gcggcgggtg gttgcactga gggatatttg  
 60

cagttgctgg atgagcgcga gatgcgcggc gtgctcggcc acgagctgat gcacgtgtac  
 120  
 aaccgcgata tcctcacctc ttcggtggcg gcggtatcg cctccatcat cggtacgatt  
 180  
 gcgcagattc tttcgtttgg cgcgatgttc ggtggatcca accgcgatgg tgaacgttcc  
 240  
 aacccccctcg ccattgttcgt ggttgctatg ctggctccca ttgctactca ggtcatccag  
 300  
 atggctatta gccgcacccg tgaattc  
 327

<210> 826

<211> 109

<212> PRT

<213> Homo sapiens

<400> 826

Ala	Phe	Ala	Thr	Gly	Arg	Asn	Pro	Gln	Asn	Ala	Ala	Val	Cys	Cys	Thr
1				5					10					15	
Glu	Gly	Ile	Leu	Gln	Leu	Leu	Asp	Glu	Arg	Glu	Met	Arg	Gly	Val	Leu
			20					25					30		
Gly	His	Glu	Leu	Met	His	Val	Tyr	Asn	Arg	Asp	Ile	Leu	Thr	Ser	Ser
	35						40					45			
Val	Ala	Ala	Gly	Ile	Ala	Ser	Ile	Ile	Gly	Thr	Ile	Ala	Gln	Ile	Leu
	50					55					60				
Ser	Phe	Gly	Ala	Met	Phe	Gly	Gly	Ser	Asn	Arg	Asp	Gly	Glu	Arg	Ser
65					70					75				80	
Asn	Pro	Leu	Ala	Met	Phe	Val	Val	Ala	Met	Leu	Ala	Pro	Ile	Ala	Thr
				85					90					95	
Gln	Val	Ile	Gln	Met	Ala	Ile	Ser	Arg	Thr	Arg	Glu	Phe			
			100					105							

<210> 827

<211> 534

<212> DNA

<213> Homo sapiens

<400> 827

nacgcgtacg tcaatatgca tcgtccagtc gttatcgcaa cgccgaaatc gatgctgcgc  
 60  
 aacaagatgg cgacctcgga tcccgaagag ttcaccaccg gtaggtggcg tcctgttcta  
 120  
 cccgacccat cgatcaccga cccgacggcc gttacgagga ttatcttggt ctctggcaag  
 180  
 gcgcggtggg agctggtcaa gcaacgtaag gccgccagtc ttgacggaca gctcgccatc  
 240  
 atccccgatgg agcgtctcta cccgctacca gtcgacgagt tggctgaggt ttttgcgcct  
 300  
 tacaccaacg tcacggatgt ccgctgggtc caagaagagc cagagaacca gggcgccctgg  
 360  
 tactacatgc tgaccacact gccccaggcc atgtcggaga agctgccagg attctttgat  
 420  
 gggttagtcg gcatcaccgg cccaccgtcc tcagctccgt cgggtgggaca gcacagcgtc  
 480

cacatccgtg aagagcagga gttactcgag aaggctatag cctgagcgac ctga  
534

<210> 828  
<211> 174  
<212> PRT  
<213> Homo sapiens

<400> 828  
Xaa Ala Tyr Val Asn Met His Arg Pro Val Val Ile Ala Thr Pro Lys  
1 5 10 15  
Ser Met Leu Arg Asn Lys Met Ala Thr Ser Asp Pro Glu Glu Phe Thr  
20 25 30  
Thr Gly Arg Trp Arg Pro Val Leu Pro Asp Pro Ser Ile Thr Asp Pro  
35 40 45  
Thr Ala Val Thr Arg Ile Ile Leu Cys Ser Gly Lys Ala Arg Trp Glu  
50 55 60  
Leu Val Lys Gln Arg Lys Ala Ala Ser Leu Asp Gly Gln Leu Ala Ile  
65 70 75 80  
Ile Pro Met Glu Arg Leu Tyr Pro Leu Pro Val Asp Glu Leu Ala Glu  
85 90 95  
Val Phe Ala Pro Tyr Thr Asn Val Thr Asp Val Arg Trp Val Gln Glu  
100 105 110  
Glu Pro Glu Asn Gln Gly Ala Trp Tyr Tyr Met Leu Thr His Leu Pro  
115 120 125  
Gln Ala Met Ser Glu Lys Leu Pro Gly Phe Phe Asp Gly Leu Val Gly  
130 135 140  
Ile Thr Arg Pro Pro Ser Ser Ala Pro Ser Val Gly Gln His Ser Val  
145 150 155 160  
His Ile Arg Glu Glu Gln Glu Leu Leu Glu Lys Ala Ile Ala  
165 170

<210> 829  
<211> 492  
<212> DNA  
<213> Homo sapiens

<400> 829  
nagtggccgg gtggccggcg ggtgccagcc gccatggagg cegtgcctcg catgccccatg  
60  
atctggctgg acctgaagga ggccggtgac tttcacttcc agccagctgt gaagaagttt  
120  
gtcctgaaga attatggaga gaaccagaa gcctacaatg aagaactgaa gaagctggag  
180  
ttgctcagac agaatgctgt cegtgtccca cgagactttg agggctgtag tgtcctccgc  
240  
aagtacctcg gccagcttca ttacctgcag agtcgggtcc ccatgggctc gggccaggag  
300  
gccgtgtcc ctgtcacatg gacagagatc ttctcaggca agtctgtggc ccatgaggag  
360  
atcaagtacg agcaggcctg tattttctcc aacnttgag cgctgcactc catgctgggg  
420  
gccatggaca agcgggtgtc tgaggagggc atgaaggtct cctgtacca tttccagtgc  
480

gcagccggcg cc  
492

<210> 830  
<211> 164  
<212> PRT  
<213> Homo sapiens

<400> 830  
Xaa Trp Pro Gly Gly Arg Arg Val Pro Ala Ala Met Glu Ala Val Pro  
1 5 10 15  
Arg Met Pro Met Ile Trp Leu Asp Leu Lys Glu Ala Gly Asp Phe His  
20 25 30  
Phe Gln Pro Ala Val Lys Lys Phe Val Leu Lys Asn Tyr Gly Glu Asn  
35 40 45  
Pro Glu Ala Tyr Asn Glu Glu Leu Lys Lys Leu Glu Leu Leu Arg Gln  
50 55 60  
Asn Ala Val Arg Val Pro Arg Asp Phe Glu Gly Cys Ser Val Leu Arg  
65 70 75 80  
Lys Tyr Leu Gly Gln Leu His Tyr Leu Gln Ser Arg Val Pro Met Gly  
85 90 95  
Ser Gly Gln Glu Ala Ala Val Pro Val Thr Trp Thr Glu Ile Phe Ser  
100 105 110  
Gly Lys Ser Val Ala His Glu Asp Ile Lys Tyr Glu Gln Ala Cys Ile  
115 120 125  
Phe Ser Asn Xaa Gly Ala Leu His Ser Met Leu Gly Ala Met Asp Lys  
130 135 140  
Arg Val Ser Glu Glu Gly Met Lys Val Ser Cys Thr His Phe Gln Cys  
145 150 155 160  
Ala Ala Gly Ala

<210> 831  
<211> 303  
<212> DNA  
<213> Homo sapiens

<400> 831  
gcgttgctgc ggcgtggcga gaccatgacg gcggagaatc agcgtgccaa tgtgcgcac  
60  
gccgcaaacc acatcaagga ggttgcggtc gatcacgagg tcgttgtagc ccattggaat  
120  
ggccccagg taggtctgtt ggctctgcaa tcgacagcct acgaggaagt cggatatctat  
180  
ccgctggatg tcctgggcgc agagtcacag gccatgatcg gctacatgat cgagcaggaa  
240  
ctcggcaatg tgatgcctca ggatcagcag atcgtcacca tgatcacgat gacagtcgctc  
300  
gac  
303

<210> 832  
<211> 101  
<212> PRT

<213> Homo sapiens

<400> 832

```

Ala Leu Leu Arg Arg Gly Glu Thr Met Thr Ala Glu Asn Gln Arg Ala
 1           5           10           15
Asn Val Arg Ile Ala Ala Asn His Ile Lys Glu Val Ala Val Asp His
      20           25           30
Glu Val Val Val Ala His Gly Asn Gly Pro Gln Val Gly Leu Leu Ala
      35           40           45
Leu Gln Ser Thr Ala Tyr Glu Glu Val Gly Ile Tyr Pro Leu Asp Val
      50           55           60
Leu Gly Ala Glu Ser Gln Ala Met Ile Gly Tyr Met Ile Glu Gln Glu
      65           70           75           80
Leu Gly Asn Val Met Pro Gln Asp Gln Gln Ile Val Thr Met Ile Thr
      85           90           95
Met Thr Val Val Asp
      100

```

<210> 833

<211> 466

<212> DNA

<213> Homo sapiens

<400> 833

```

nngatccgcg cgatcgacga ggcgggtgcg tgatgttgac agcgaaaatg cgcagccggc
60
catttgacga gggctgaaaa cgtcttctac cggctctgctg tgccgcctgg tgtcagcaaa
120
cgacgccatg atcgtccagt gggatatgat ttgttctgcg gcgctggggg attcagttgc
180
ggattccacc aggccgggtg gcatgttgcg gcggcggttg agcacgacgt gtcggcgctc
240
ctgacctatg tcatgaatct cgctcggccc ggcgtcaaga ttcacatcga ccccgagcac
300
ccggagctgg gcccaagacc accgcgaacc aagaagaaga gcggcggcgc agtgccgttc
360
gatgcgcgat tcggaactgg gtggatcgcc agcgagcccg ccgacgatcc cggctgcgaa
420
cacttctacg tgtacgacgt caagaacctc agcggcgagc ggatcc
466

```

<210> 834

<211> 142

<212> PRT

<213> Homo sapiens

<400> 834

```

Gln Arg Lys Cys Ala Ala Gly His Leu Thr Arg Ala Glu Asn Val Phe
 1           5           10           15
Tyr Arg Ser Ala Val Pro Pro Gly Val Ser Lys Arg Arg His Asp Arg
      20           25           30
Pro Val Gly Ile Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser Cys Gly
      35           40           45
Phe His Gln Ala Gly Trp His Val Ala Ala Ala Val Glu His Asp Val

```

```

      50              55              60
Ser Ala Ser Leu Thr Tyr Val Met Asn Leu Ala Arg Pro Gly Val Lys
65              70              75              80
Ile His Ile Asp Pro Glu His Pro Glu Leu Gly Pro Arg Pro Pro Arg
      85              90              95
Thr Lys Lys Lys Ser Gly Gly Ala Val Pro Phe Asp Ala His Val Gly
      100              105              110
Thr Gly Trp Ile Ala Ser Glu Pro Ala Asp Asp Pro Gly Cys Glu His
      115              120              125
Phe Tyr Val Tyr Asp Val Lys Asn Leu Ser Gly Glu Arg Ile
      130              135              140

```

&lt;210&gt; 835

&lt;211&gt; 482

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 835

```

acgcgtgaag ggattttgat caccagaac aaccacctgt ctttttagat caagaagcag
60
aagctcagag caaagaacat cacaccacgt ccctcagtga ttgaagcagt gattgagtca
120
cagaataaat ctggaactca ggtcttctga tctttgctcc agatgtaga gacaaaacta
180
aaagtaaaat accaagtga atcaaagcat cagcattgag ccagaacat gaaaaagaac
240
ttcctggccc acttgagaaa ctgttaaacc ggacatacct ttggggactt cttcccttct
300
ctggaataag attgatgttt ccagtctgtg aaagacgatg atgttccttc tcccagattc
360
ctgctgtctt caaaaggcct agcaaaaacc actgctgctg ggtgcagttg agaaagggaa
420
tgaagaacaa tcccatggcc atgcaggcac tcctcccttc cacctctctg cccttcacgc
480
gt
482

```

&lt;210&gt; 836

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 836

```

Met Ala Met Gly Leu Phe Phe Ile Pro Phe Leu Asn Cys Thr Gln Gln
1              5              10              15
Gln Trp Phe Leu Leu Gly Leu Leu Lys Thr Ala Gly Ile Trp Glu Lys
      20              25              30
Glu His His Arg Leu Ser Gln His Gly Asn Ile Asn Leu Ile Pro Glu
      35              40              45
Lys Gly Arg Ser Pro Gln Arg Tyr Val Arg Phe Asn Ser Phe Ser Ser
      50              55              60
Gly Pro Gly Ser Ser Phe Ser Cys Ser Gly Leu Asn Arg Asp Ala Leu
65              70              75              80
Ile Ser Leu Gly Ile Leu Leu Leu Val Leu Ser Leu Thr Ser Gly Ala

```



85 90 95  
 Lys Ile Arg Arg Pro Glu Phe Gln Ile Tyr Ser Val Thr Gln Ser Leu  
 100 105 110  
 Leu Gln Ser Leu Arg Asp Val Val  
 115 120

<210> 837  
 <211> 509  
 <212> DNA  
 <213> Homo sapiens

<400> 837  
 acgcgtggac ccccggttctg cccgcctttg cagtcacgcg cctccctgaa gtcaccgctg  
 60  
 cagaaatacg caggcactga cctgggggta cagccaggca agggagagac gaggggctca  
 120  
 ctctgcacca gccaaaggcct gtgtcctggc atggctcccc caggaagcga ggatggcggg  
 180  
 gcctggcggg cgagccccctc ttatcctggg gaatgctggg gggcggttct gagcagacct  
 240  
 gcctgctgcc cctgctggct ggcactgccc ctcccccggg gaaagggttg gtggtcccc  
 300  
 caggggaact caaagcaggg gagccccctg aggccccaaag tccctggaat atcttggcgc  
 360  
 tcagatggcc cccctcgaac accctcacac gggggggccg cgcggtggga ggtgaccag  
 420  
 cagccactct tacttggcga agacttttct cccaatgcga gcgcgggttg tatcagcctg  
 480  
 agccttcagg ttggtgaggc tgggggtacc  
 509

<210> 838  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 838  
 Met Ala Pro Pro Gly Ser Glu Asp Gly Gly Ala Trp Arg Ser Ser Pro  
 1 5 10 15  
 Ser Tyr Pro Gly Glu Cys Trp Gly Ala Phe Leu Ser Arg Pro Ala Cys  
 20 25 30  
 Cys Pro Cys Trp Leu Ala Leu Pro Leu Pro Arg Gly Lys Val Gly Trp  
 35 40 45  
 Ser Pro Gln Gly Asn Ser Lys Gln Gly Ser Pro Trp Arg Pro Gln Val  
 50 55 60  
 Pro Gly Ile Ser Trp Arg Ser Asp Gly Pro Pro Arg Thr Pro Ser His  
 65 70 75 80  
 Gly Gly Ala Ala Arg Trp Glu Val Thr Gln Gln Pro Leu Leu Leu Gly  
 85 90 95  
 Glu Asp Phe Ser Pro Asn Ala Ser Ala Gly Gly Ile Ser Leu Ser Leu  
 100 105 110  
 Gln Val Gly Glu Ala Gly Val  
 115

<210> 839  
 <211> 347  
 <212> DNA  
 <213> Homo sapiens

<400> 839  
 acgcgtctcg tgttcgtgcg gcacggcagg acggcggtca atgtggaggg tcggctccag  
 60  
 ggccgtctcg acatgccggtt ggatgaggtg gggcgccgtc aggcactcac agtgggtcaa  
 120  
 gtcacgccc agatggaacc tgacgcgac atggcctctc cgctacaacg tgcgcgcgac  
 180  
 acagctcagg caatcggtgc ttgtgctgga ttgggcgtac agctggatga tcgactcatc  
 240  
 gagatcgatg tcggacgttg gtcgggacaa cgggctgcgg acctgcgtcg caacgatcct  
 300  
 gagtacgcag caagtgtggt cagccctatc gattaccggg tcggagn  
 347

<210> 840  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 840  
 Thr Arg Leu Val Phe Val Arg His Gly Arg Thr Ala Phe Asn Val Glu  
 1 5 10 15  
 Gly Arg Leu Gln Gly Arg Leu Asp Met Pro Leu Asp Glu Val Gly Arg  
 20 25 30  
 Arg Gln Ala Leu Thr Val Ala Gln Val Ile Ala Glu Met Glu Pro Asp  
 35 40 45  
 Ala Ile Met Ala Ser Pro Leu Gln Arg Ala Arg Asp Thr Ala Gln Ala  
 50 55 60  
 Ile Gly Ala Cys Ala Gly Leu Gly Val Gln Leu Asp Asp Arg Leu Ile  
 65 70 75 80  
 Glu Ile Asp Val Gly Arg Trp Ser Gly Gln Arg Ala Ala Asp Leu Arg  
 85 90 95  
 Arg Asn Asp Pro Glu Tyr Ala Ala Ser Val Val Ser Pro Ile Asp Tyr  
 100 105 110  
 Arg Val Gly  
 115

<210> 841  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 841  
 tccggaactc accccgacgc cgtcattatg gacgtcatga tgccgcgtct agatggcttg  
 60  
 gaagccaccc ggatgctgcg cagcaatggc aacgacgtcc cgatcctcgt cctcaccgcc  
 120  
 cgcgatgctg tcgacgatcg cggtgacggc ctcgacgctg gcgccgatga ctacatggtc  
 180

aagcccttcg cctcgcagca actcctcget cgcctacgcg cctcactcg tcgttcccgt  
 240  
 cccgagccag agcaaaacga ggcccctgaa caactctcct tcgctgacct cacccttgat  
 300  
 ccaggcaccc gcgagatcac ccgcgggaac cgtcgcatca gtttgacgcg t  
 351

<210> 842  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 842  
 Ser Gly Thr His Pro Asp Ala Val Ile Met Asp Val Met Met Pro Arg  
 1 5 10 15  
 Leu Asp Gly Leu Glu Ala Thr Arg Met Leu Arg Ser Asn Gly Asn Asp  
 20 25 30  
 Val Pro Ile Leu Val Leu Thr Ala Arg Asp Ala Val Asp Asp Arg Val  
 35 40 45  
 Asp Gly Leu Asp Ala Gly Ala Asp Asp Tyr Met Val Lys Pro Phe Ala  
 50 55 60  
 Leu Asp Glu Leu Leu Ala Arg Leu Arg Ala Leu Thr Arg Arg Ser Arg  
 65 70 75 80  
 Pro Glu Pro Glu Gln Asn Glu Ala Pro Glu Gln Leu Ser Phe Ala Asp  
 85 90 95  
 Leu Thr Leu Asp Pro Gly Thr Arg Glu Ile Thr Arg Gly Asn Arg Arg  
 100 105 110  
 Ile Ser Leu Thr Arg  
 115

<210> 843  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<400> 843  
 ctagcccagg ctctcgtcca cgaggggctg cgcgctgtgg cctctggggc aaaccgggtc  
 60  
 ggcctcaagc gcggtatcga gaaggctgtc gacgccgttg tggaggagct ccgctctatc  
 120  
 tcgcgcgcca tcgacaccac ctcggaacatg gccagcgttg ccaccatctc cagccgtgac  
 180  
 gagaccatcg gcgccctcat cgctgaggcc ttgcacaagg ttggttaagga cggggttatc  
 240  
 accgtcgacg agtcgcagac cttcggcact gagcttgact tcaccgaggg catgcagttc  
 300  
 gacaaggggtt acctgtcgcc ctacatggtc accgaccagg ttgcgatgga ggctgtgac  
 360  
 gaggatcctt acatcctcat tcaactccgc aag  
 393

<210> 844  
 <211> 131  
 <212> PRT

<213> Homo sapiens

<400> 844

```

Leu Ala Gln Ala Leu Val His Glu Gly Leu Arg Ala Val Ala Ser Gly
 1           5           10           15
Ala Asn Pro Val Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Asp Ala
      20           25           30
Val Val Glu Glu Leu Arg Ser Ile Ser Arg Ala Ile Asp Thr Thr Ser
      35           40           45
Asp Met Ala Ser Val Ala Thr Ile Ser Ser Arg Asp Glu Thr Ile Gly
      50           55           60
Ala Leu Ile Ala Glu Ala Phe Asp Lys Val Gly Lys Asp Gly Val Ile
65           70           75           80
Thr Val Asp Glu Ser Gln Thr Phe Gly Thr Glu Leu Asp Phe Thr Glu
      85           90           95
Gly Met Gln Phe Asp Lys Gly Tyr Leu Ser Pro Tyr Met Val Thr Asp
      100          105          110
Gln Val Arg Met Glu Ala Val Ile Glu Asp Pro Tyr Ile Leu Ile His
      115          120          125
Ser Arg Lys
      130

```

<210> 845

<211> 505

<212> DNA

<213> Homo sapiens

<400> 845

```

gccacctgcc caaggctgga tgacgggcct agggcacatc taaggaacaa ggacaggaca
60
gaagcaaagc cacagctgct ggggcagggt gggggccggt atgtctggcc agcagcatca
120
cccctgcccc cggcggggct ccaggaccgg gagactcatc agccggaagc tcttgagga
180
ggcggctgcc gtgaagacag gcacccttgc tcctgagagg ggcacccaga gaaccaagac
240
tcagcagagg gaacacaggg ctacgcccag gcccaggcc tgatatccag agtctaaatc
300
ccacctcagc ccagggggga gccttgagag gagctatgtc cctcatggac cccagtttcc
360
tctgcatacg ggctccgagc cctgcactgc ctccagggtg gttcccaagg tcttttccca
420
ttacctccta cgtgagcact cagtaaacca atacacatac acaagggtga cattaattcc
480
agccacagaa tcccaggcca cgcgt
505

```

<210> 846

<211> 130

<212> PRT

<213> Homo sapiens

<400> 846

```

Met Gly Lys Asp Leu Gly Asn Tyr Pro Gly Gly Ser Ala Gly Leu Gly

```

```

      1           5           10           15
Ala Arg Met Gln Arg Lys Leu Gly Ser Met Arg Asp Ile Ala Pro Leu
      20           25           30
Lys Ala Pro Trp Ala Glu Val Gly Phe Arg Leu Trp Ile Ser Gly
      35           40           45
Leu Gly Pro Gly Arg Ser Pro Val Phe Pro Leu Leu Ser Leu Gly Ser
      50           55           60
Leu Gly Ala Pro Leu Arg Ser Lys Gly Ala Cys Leu His Gly Ser Arg
      65           70           75           80
Leu Leu Gln Glu Leu Pro Ala Asp Glu Ser Pro Gly Pro Gly Ala Pro
      85           90           95
Pro Gly Ala Gly Val Met Leu Leu Ala Arg His Thr Gly Pro His Pro
      100          105          110
Ala Pro Ala Ala Val Ala Leu Leu Ser Cys Pro Cys Ser Leu Asp
      115          120          125
Val Pro
      130

```

<210> 847  
 <211> 448  
 <212> DNA  
 <213> Homo sapiens

```

<400> 847
aagcttttaa aggagcaaga aaacatgaaa gagctagtag tcaaccttct ccgcatgact
60
caaatcaaaa ttgatgaaaa ggaacaaaag tccaaggatt tcctgaaagc tcagcaaaaa
120
tacaccaaca ttgttaaaga aatgaaagca aaggatcttg aaatcaggat acacaagaag
180
aaaaaatgtg aaatttatcg gagactgaga gagcttgcta aactgtatga caccattcga
240
aatgaaagaa acaaatttgt taacttactc cacaaagctc atcagaaagt aaatgaaata
300
aaagaaaggc ataaaatgtc attaaatgaa cttgaaattc tgagaaatag tgccgtagt
360
caagaaagaa agctacaaaa ttccatgctg aaacacgcca acaatgttac catcagagag
420
agcatgcaaa acgatgtgcg caaaattt
448

```

<210> 848  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

```

<400> 848
Lys Leu Leu Lys Glu Gln Glu Asn Met Lys Glu Leu Val Val Asn Leu
1           5           10           15
Leu Arg Met Thr Gln Ile Lys Ile Asp Glu Lys Glu Gln Lys Ser Lys
      20           25           30
Asp Phe Leu Lys Ala Gln Gln Lys Tyr Thr Asn Ile Val Lys Glu Met
      35           40           45
Lys Ala Lys Asp Leu Glu Ile Arg Ile His Lys Lys Lys Lys Cys Glu

```

```

      50              55              60
Ile Tyr Arg Arg Leu Arg Glu Leu Ala Lys Leu Tyr Asp Thr Ile Arg
65              70              75              80
Asn Glu Arg Asn Lys Phe Val Asn Leu Leu His Lys Ala His Gln Lys
      85              90              95
Val Asn Glu Ile Lys Glu Arg His Lys Met Ser Leu Asn Glu Leu Glu
      100             105             110
Ile Leu Arg Asn Ser Ala Val Ser Gln Glu Arg Lys Leu Gln Asn Ser
      115             120             125
Met Leu Lys His Ala Asn Asn Val Thr Ile Arg Glu Ser Met Gln Asn
      130             135             140
Asp Val Arg Lys Ile
145

```

<210> 849  
 <211> 463  
 <212> DNA  
 <213> Homo sapiens

```

<400> 849
nnacgcgtga ttgttggggc caaggaatgc catgtggaga gtgcaggtga agtgataagt
60
cttttggaga tggggaatgc agccagacat acaggtacca ctcaaataaa tgagcactcc
120
agcagatcac atgcaatttt tacaatcagc atttgtcaag ttcataaaaa tatggaggca
180
gctgaagatg gatcatggta ttccccctgg catattgtct caaagttcca ctttgtggat
240
ttggcaggat cagaaagagt aacaaaaacg gggaataactg gtgaacggtt caaagaatcc
300
attcaaataca atagtggatt gctggcttta ggaaatgtaa taagcgctct tggggaccca
360
cgcaggaaga gttcacatat tccatatagg gatgctaaaa ttacccggct tctgaaagat
420
tctctgggag gcagtgctaa gactgtcatg atcacatgtg tca
463

```

<210> 850  
 <211> 154  
 <212> PRT  
 <213> Homo sapiens

```

<400> 850
Xaa Arg Val Ile Val Gly Ala Lys Glu Cys His Val Glu Ser Ala Gly
1              5              10              15
Glu Val Ile Ser Leu Leu Glu Met Gly Asn Ala Ala Arg His Thr Gly
      20              25              30
Thr Thr Gln Met Asn Glu His Ser Ser Arg Ser His Ala Ile Phe Thr
      35              40              45
Ile Ser Ile Cys Gln Val His Lys Asn Met Glu Ala Ala Glu Asp Gly
      50              55              60
Ser Trp Tyr Ser Pro Arg His Ile Val Ser Lys Phe His Phe Val Asp
65              70              75              80
Leu Ala Gly Ser Glu Arg Val Thr Lys Thr Gly Asn Thr Gly Glu Arg

```

```

      85              90              95
Phe Lys Glu Ser Ile Gln Ile Asn Ser Gly Leu Leu Ala Leu Gly Asn
      100              105              110
Val Ile Ser Ala Leu Gly Asp Pro Arg Arg Lys Ser Ser His Ile Pro
      115              120              125
Tyr Arg Asp Ala Lys Ile Thr Arg Leu Leu Lys Asp Ser Leu Gly Gly
      130              135              140
Ser Ala Lys Thr Val Met Ile Thr Cys Val
145              150

```

<210> 851  
 <211> 372  
 <212> DNA  
 <213> Homo sapiens

```

<400> 851
aaatttcctg tttctgatcg acgaaataaa gtttagcgtg atgagtgagc tgcttatgca
60
gttctctccat tcgcttataa acagttttat ttctcatttc gaaaactctc gatgcagaat
120
aaaggctaga gtctggggac caagtcccca gctccgttta cgcgacttcc ttgaccttgt
180
ttgttatgct gataaggtta ttcagcttga cgatttggtc gtggtcttcc aaccgttttg
240
cagctggtcg acgatattcc tggtaggaac tacgatagaa gaccagcatc ggaagaactt
300
tgtagatgct gaacaaacac ccaccgatca cttcagcctc gaagtaaggg ttatactgtc
360
taaccacgc gt
372

```

<210> 852  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

```

<400> 852
Met Ser Glu Leu Leu Met Gln Phe Leu His Ser Leu Ile Asn Ser Phe
1      5      10      15
Ile Ser His Phe Glu Asn Ser Arg Cys Arg Ile Lys Ala Arg Val Trp
      20      25      30
Gly Pro Ser Pro Gln Leu Arg Leu Arg Asp Phe Leu Asp Leu Val Cys
      35      40      45
Tyr Ala Asp Lys Val Ile Gln Leu Asp Asp Leu Phe Val Val Phe Gln
      50      55      60
Pro Phe Cys Ser Trp Ser Thr Ile Phe Leu Val Gly Thr Thr Ile Glu
65      70      75      80
Asp Gln His Arg Lys Asn Phe Val Asp Ala Glu Gln Thr Pro Thr Asp
      85      90      95
His Phe Ser Leu Glu Val Arg Val Ile Leu Ser Asn Pro Arg
      100      105      110

```

<210> 853  
 <211> 423

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 853

acgcgttcag aaacttatgg tgaaatggcc gaactagaaa acctagtcga cgaatattac  
60  
caagctatgg gcatggatgt gcgtcgagaa acctggctgc gcgagcagat actcaagaaa  
120  
gtccaagaaa cgcatttgtt agaagagctt gcaggcatag aatcaggtga tgatggcgca  
180  
gtggtggaag agagcgtatt agaaggcctc gatacctatt tatgtgagat aaaagaagca  
240  
cagattcgtc atggattgca tcgtcttgga gaattaccag aagacgataa attggccgat  
300  
accttggtcg ccttattgcg tttaccccggt ggcagtgaca ttaccagcaa ggggaattttg  
360  
catgccttaa tggcagattt agagttagaa caagacgatt ttgaccaat gcaaagcagc  
420  
cgt  
423

&lt;210&gt; 854

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 854

Thr	Arg	Ser	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Glu	Leu	Glu	Asn	Leu	Val
1				5					10					15	
Asp	Glu	Tyr	Tyr	Gln	Ala	Met	Gly	Met	Asp	Val	Arg	Arg	Glu	Thr	Trp
		20					25					30			
Leu	Arg	Glu	Gln	Ile	Leu	Lys	Lys	Val	Gln	Glu	Thr	His	Leu	Leu	Glu
	35					40					45				
Glu	Leu	Ala	Gly	Ile	Glu	Ser	Gly	Asp	Asp	Gly	Ala	Val	Val	Glu	Glu
	50					55				60					
Ser	Val	Leu	Glu	Gly	Leu	Asp	Thr	Tyr	Leu	Cys	Glu	Ile	Lys	Glu	Ala
65					70					75				80	
Gln	Ile	Arg	His	Gly	Leu	His	Arg	Leu	Gly	Glu	Leu	Pro	Glu	Asp	Asp
			85					90					95		
Lys	Leu	Ala	Asp	Thr	Leu	Val	Ala	Leu	Leu	Arg	Leu	Pro	Arg	Gly	Ser
		100					105					110			
Asp	Ile	Thr	Ser	Lys	Gly	Ile	Leu	His	Ala	Leu	Met	Ala	Asp	Leu	Glu
		115					120					125			
Leu	Glu	Gln	Asp	Asp	Phe	Asp	Pro	Met	Gln	Ser	Thr	Arg			
	130					135					140				

&lt;210&gt; 855

&lt;211&gt; 338

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 855

acgcgtgaag ggggagctca aagtagatgg acctctgact agatggagct ctgagtaaga  
60



tgaatgtctg tgcggatggt gctcacagca agatagtgtt tggagcgatt ggcacttcga  
 120  
 acaagatgga gcatggagca gatggagctc tgagcaagat ggagcgtgga gtagatagag  
 180  
 cttggagcaa gaaggagctc caagcaagat ggagcttgca gcaggtgctt ctcagtgtaa  
 240  
 gatggagctc agagaagatg atgctcagag taagattgag ctcggtgatt ggcactccaa  
 300  
 acattgctct gagccattg gagnctctga gcagaaag  
 338

<210> 856

<211> 93

<212> PRT

<213> Homo sapiens

<400> 856

Met	Asn	Val	Cys	Ala	Asp	Val	Ala	His	Ser	Lys	Ile	Val	Leu	Gly	Ala
1				5					10					15	
Ile	Gly	Thr	Ser	Asn	Lys	Met	Glu	His	Gly	Ala	Asp	Gly	Ala	Leu	Ser
			20					25					30		
Lys	Met	Glu	Arg	Gly	Val	Asp	Arg	Ala	Trp	Ser	Lys	Lys	Glu	Leu	Gln
		35				40					45				
Ala	Arg	Trp	Ser	Leu	Gln	Gln	Val	Leu	Leu	Ser	Val	Arg	Trp	Ser	Ser
	50				55					60					
Glu	Lys	Met	Met	Leu	Arg	Val	Arg	Leu	Ser	Ser	Val	Ile	Gly	Thr	Pro
65				70				75						80	
Asn	Ile	Ala	Leu	Ser	Pro	Leu	Glu	Xaa	Leu	Ser	Arg	Lys			
			85					90							

<210> 857

<211> 435

<212> DNA

<213> Homo sapiens

<400> 857

ccggacagtg ggccaccagt gtttgccccc agcaatcatg tcagtgaagc ccaacctcgg  
 60  
 gagacacccc ggccccctcat gcctcctacc aagcctttcc tagcacctga gaccaccagc  
 120  
 cctggtgaca ggggtggagac ccctgtgggg gagagagccc caaccctgt ctcagcaagc  
 180  
 tctgaggtct cccctgagag ccaagaggac tcagagaccc cagcagagga ggacagtggc  
 240  
 tctgagcagc ctccaacag cgtcctgcct gacaaactga aggtgagctg ggagaacccc  
 300  
 agcccccagg agggccctgc tgacagagagt gcagaaccgt cccaggcacc ctgttctgag  
 360  
 acttctgagg ctgccccag ggaggggtggg aagcccccta caccaccacc caagatctta  
 420  
 tcagagaaac tgaaa  
 435

<210> 858

<211> 145  
 <212> PRT  
 <213> Homo sapiens

<400> 858  
 Pro Asp Ser Gly Pro Pro Val Phe Ala Pro Ser Asn His Val Ser Glu  
 1 5 10 15  
 Ala Gln Pro Arg Glu Thr Pro Arg Pro Leu Met Pro Pro Thr Lys Pro  
 20 25 30  
 Phe Leu Ala Pro Glu Thr Thr Ser Pro Gly Asp Arg Val Glu Thr Pro  
 35 40 45  
 Val Gly Glu Arg Ala Pro Thr Pro Val Ser Ala Ser Ser Glu Val Ser  
 50 55 60  
 Pro Glu Ser Gln Glu Asp Ser Glu Thr Pro Ala Glu Glu Asp Ser Gly  
 65 70 75 80  
 Ser Glu Gln Pro Pro Asn Ser Val Leu Pro Asp Lys Leu Lys Val Ser  
 85 90 95  
 Trp Glu Asn Pro Ser Pro Gln Glu Ala Pro Ala Ala Glu Ser Ala Glu  
 100 105 110  
 Pro Ser Gln Ala Pro Cys Ser Glu Thr Ser Glu Ala Ala Pro Arg Glu  
 115 120 125  
 Gly Gly Lys Pro Pro Thr Pro Pro Pro Lys Ile Leu Ser Glu Lys Leu  
 130 135 140  
 Lys  
 145

<210> 859  
 <211> 561  
 <212> DNA  
 <213> Homo sapiens

<400> 859  
 nacgcgtggt gtggtaatcc ggtttctggt ggcgacggct gccacccctc gtggcaagac  
 60  
 atgccgttgc gtgccgatat gccatacgaa gcttggccta gtgcgaaaag ctgctggaa  
 120  
 cctcgaaga ggcagggtcg gcaggttacc gtggtcgggtg tacgcatcgt ttcgacgatg  
 180  
 aaccccatte tgggagcaga tatgacgacg taccagtacc tcattgtcgg tggcgggatg  
 240  
 gccgctgatt ctgccgcccg cggatatccgc gacatcgaca agaaagggtc gatcgccatc  
 300  
 ctacgcgctg acgtcgacgc cccgtatcct cggccagcgc tgagcaagaa gctgtggact  
 360  
 gacctgagt tcacctggga ccaggctcgac cttgctactg tcgctgacac cggcgcggaa  
 420  
 ttgcggctcg gcaactgagg gctcagcatt gaccgtgacg gcaagaccgt cctgaccgct  
 480  
 tccggccagg tattcggcta ccagaagttg ctgctcgta cccgccttac cccgtcgcgc  
 540  
 attgacgacg acggcgatgc c  
 561

<210> 860

<211> 187  
 <212> PRT  
 <213> Homo sapiens

<400> 860  
 Xaa Ala Trp Cys Gly Asn Pro Val Ser Gly Gly Asp Gly Cys His Pro  
 1 5 10 15  
 Ser Trp Gln Asp Met Pro Leu Arg Ala Asp Met Pro Tyr Glu Ala Trp  
 20 25 30  
 Pro Ser Ala Lys Ser Ser Leu Glu Pro Ser Lys Arg Gln Gly Arg Gln  
 35 40 45  
 Val Thr Val Val Gly Val Arg Ile Val Ser Thr Met Asn Pro Ile Leu  
 50 55 60  
 Gly Ala Asp Met Thr Thr Tyr Gln Tyr Leu Ile Val Gly Gly Gly Met  
 65 70 75 80  
 Ala Ala Asp Ser Ala Ala Arg Gly Ile Arg Asp Ile Asp Lys Lys Gly  
 85 90 95  
 Ser Ile Ala Ile Leu Ser Ala Asp Val Asp Ala Pro Tyr Pro Arg Pro  
 100 105 110  
 Ala Leu Ser Lys Lys Leu Trp Thr Asp Pro Glu Phe Thr Trp Asp Gln  
 115 120 125  
 Val Asp Leu Ala Thr Val Ala Asp Thr Gly Ala Glu Leu Arg Leu Gly  
 130 135 140  
 Thr Glu Val Leu Ser Ile Asp Arg Asp Gly Lys Thr Val Leu Thr Ala  
 145 150 155 160  
 Ser Gly Gln Val Phe Gly Tyr Gln Lys Leu Leu Leu Val Thr Gly Leu  
 165 170 175  
 Thr Pro Ser Arg Ile Asp Asp Asp Gly Asp Ala  
 180 185

<210> 861  
 <211> 352  
 <212> DNA  
 <213> Homo sapiens

<400> 861  
 ccattgggttt ctatgctctg aggtttcatc tgtggggaac agtattgact tacttacaaa  
 60  
 gagataatgg tcatacccta tggtcactca ccatagtctg gcggtacatg gacttctcag  
 120  
 cccagtaag atctgtatcc acaggacact taaagtcacc ttacagaggg ctatcccagt  
 180  
 gcctgaggcc tattagaggc gtctcttttc agccatcagt gttagaggcc atctgcatgg  
 240  
 gatcccagag cctgcctcgg gaatggcaga agctggctgg tgcttgccgt gggctttgcc  
 300  
 tgtttactg ctttcagga ggcctgccac aggggagaaa ctgggggggg ga  
 352

<210> 862  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 862

```

Met Gly Phe Tyr Ala Leu Arg Phe His Leu Trp Gly Thr Val Leu Thr
 1           5           10           15
Tyr Leu Gln Arg Asp Asn Gly His Thr Leu Trp Ser Leu Thr Ile Val
          20           25           30
Trp Arg Tyr Met Asp Phe Ser Ala Pro Val Arg Ser Val Ser Thr Gly
      35           40           45
His Leu Lys Ser Pro Tyr Arg Gly Leu Ser Gln Cys Leu Arg Pro Ile
      50           55           60
Arg Gly Val Ser Phe Gln Pro Ser Val Leu Glu Ala Ile Cys Met Gly
65           70           75           80
Ser Gln Ser Leu Pro Arg Glu Trp Gln Lys Leu Ala Gly Ala Trp Arg
          85           90           95
Gly Leu Cys Leu Phe His Cys Phe Gln Gly Gly Leu Pro Gln Gly Arg
          100          105          110
Asn Trp Gly Gly
          115

```

&lt;210&gt; 863

&lt;211&gt; 327

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 863

```

tccggatcga cccggacgaa ttccacgggc cagccattga cttccaaatg ctctttgaca
60
tacgccgtga catgttcaat gtccaactta cgcattgtcca cccgctcacc ggtctcattg
120
agtttgagct gcgagtagac gttgcggtag ttctcgttga ccgactgctc atacgagatg
180
tgcagaagca tcggttttgcg gccatcctcg gacggcattg gcttggttgta catggccgct
240
tggcggaaca tggttcagggt aaagcccgac ttgaagttgt gcgacagggc agaaacacac
300
agcatttctg accggcgatg acccatn
327

```

&lt;210&gt; 864

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 864

```

Met Gly His Arg Arg Ser Glu Met Leu Cys Val Ser Ala Leu Ser His
 1           5           10           15
Asn Phe Lys Ser Gly Phe Thr Leu Asn Met Phe Arg Gln Ala Ala Met
          20           25           30
Tyr Asn Lys Pro Met Pro Ser Glu Asp Gly Arg Lys Pro Met Leu Leu
          35           40           45
His Ile Ser Tyr Glu Gln Ser Val Asn Glu Asn Tyr Arg Asn Val Tyr
          50           55           60
Ser Gln Leu Lys Leu Asn Glu Thr Gly Glu Arg Val Asp Met Arg Lys
65           70           75           80
Leu Asp Ile Glu His Val Thr Ala Tyr Val Lys Glu His Leu Glu Val

```

85 90 95  
 Asn Gly Trp Thr Val Glu Phe Val Arg Val Asp Pro  
 100 105

<210> 865  
 <211> 729  
 <212> DNA  
 <213> Homo sapiens

<400> 865  
 acgcgtcatc ctcattcaag aggcccagga ggagcaccac cctccgcata ttgcgcgtgc  
 60  
 agctctcgtt ctggtctctg agcatgccca cggcgctctg cacacagctt ctcagcagcc  
 120  
 tgggtggtgc caggatcgac acatcactgc ctccgagttc agaggtttcc tttccacct  
 180  
 ttcagaact ttctgtttcc atggcctcct ctgccacctc tgccacctcc cctgatgtgc  
 240  
 tggcctccgt ctccatcgcc tcctcatggc cgtcttccgc cgggtgttcc aagcccagct  
 300  
 caggcaagtc tccgggcgcg aacagctggc tgatggtgac atgctgcagc ctggtcacat  
 360  
 cagaaaccat gaggggtgat ctccggaggt catcgatgtg gacagactgc cacagccctc  
 420  
 cgtggaagcc cacataggct gttcctcttc ccacccggga cagttttgtg atgaaataga  
 480  
 cgaagatacg gtcctcattt tctcgtattt tgttgatttc atttataaca gaatacttag  
 540  
 ctgaggcaat gagctgggcg ctacggattc catcttcaaa atctgtctga aaaatgagga  
 600  
 ttttacattt ggctgtattc gttaaacagt ttcggacttc tttgaggaat gagtactcgg  
 660  
 tgtcaaaactg ctgcagccac aggagtgtgg gtttcggagc cctgcctgtg acctctgatt  
 720  
 ctaaaattt  
 729

<210> 866  
 <211> 83  
 <212> PRT  
 <213> Homo sapiens

<400> 866  
 Ala Cys Pro Arg Arg Ser Ala His Ser Phe Ser Ala Ala Trp Trp Cys  
 1 5 10 15  
 Pro Gly Ser Thr His His Cys Leu Arg Val Gln Arg Phe Pro Phe Pro  
 20 25 30  
 Pro Ser Gln Asn Phe Leu Phe Pro Trp Pro Pro Leu Pro Pro Leu Pro  
 35 40 45  
 Pro Pro Leu Met Cys Trp Pro Pro Ser Pro Ser Pro Pro His Gly Arg  
 50 55 60  
 Leu Pro Pro Gly Val Pro Ser Pro Ala Gln Ala Ser Leu Arg Ala Arg  
 65 70 75 80  
 Thr Ala Gly

<210> 867  
 <211> 640  
 <212> DNA  
 <213> Homo sapiens

<400> 867  
 nntccggaac atcaagatcc aggcgcagaa gaccgtcaga agctgcactg gccacctcct  
 60  
 tcaggtggac tctcgttggg ggccggcgctc gctggccccc tcgcaccggtg tcccgtgtca  
 120  
 catgctccag ggccgagctc ttgtccacct ttacctcatc gaaagccttg tttttgcctc  
 180  
 ggttaatccc ttcattgagg gctttgatcc aggattcctt ctctctcccg gtgggtgcct  
 240  
 ggaatttgat gtcgctgacc ttgttccttg gggatcgag caggataaag cggtgttttc  
 300  
 gcttgaggag ggacgaagg tcctggcact tctcatagct gccagctcc acagtctcca  
 360  
 cacactttctg atcatcctca ttctcataga ccagcagctg ggctggcag aggagcagat  
 420  
 atcgggtcttt ccagaaaccc aggaggcccc cactgctctt cttgatccag ccagccttgt  
 480  
 ccaccatctg tgctccccga ggcttctcac cggttcctt cacaccctcc tcctccatgg  
 540  
 cgagtcggcc gaggtcccg cgtcccgcca ctgcttcca gcgcgcgcg ggctctgcc  
 600  
 ccgcgtctac gcccgccag gcggcgactc tccgcgttct  
 640

<210> 868  
 <211> 52  
 <212> PRT  
 <213> Homo sapiens

<400> 868  
 Gly Gly His Glu Gly Pro Gly Thr Ser His Ser Cys Pro Ala Pro Gln  
 1 5 10 15  
 Ser Pro His Thr Ser Asp His Pro His Ser His Arg Pro Ala Ala Gly  
 20 25 30  
 Pro Gly Arg Gly Ala Asp Ile Gly Leu Ser Arg Asn Pro Gly Gly Pro  
 35 40 45  
 His Cys Ser Ser  
 50

<210> 869  
 <211> 321  
 <212> DNA  
 <213> Homo sapiens

<400> 869  
 ngggtgatgc tgctcgcggc attgagcatc tttgtgctca gcgcgctgtt tatcgacaac  
 60

ttcctgtcgc cgtgaatat gcgcgggctg ggcctggcga tttcgacggt gggcatcgct  
 120  
 gcgtgcacca tgetgttctg cctggcgctg gggcatttcg acttgctcgtt gggctcgggtg  
 180  
 atcgccctgtg ccggtgtggt cgcggggatt gtgattcgtg acaccgatag cgtggcactc  
 240  
 ggcgtgtccg ctgcgttggc catgggcctg gtagtggggc tgatcaacgg catcgtgatc  
 300  
 gccaaagctgc gcatcaacgc g  
 321

<210> 870

<211> 107

<212> PRT

<213> Homo sapiens

<400> 870

Xaa	Val	Met	Leu	Leu	Ala	Ala	Leu	Ser	Ile	Phe	Val	Leu	Ser	Ala	Leu
1			5					10				15			
Phe	Ile	Asp	Asn	Phe	Leu	Ser	Pro	Leu	Asn	Met	Arg	Gly	Leu	Gly	Leu
		20						25				30			
Ala	Ile	Ser	Thr	Val	Gly	Ile	Ala	Ala	Cys	Thr	Met	Leu	Phe	Cys	Leu
		35				40					45				
Ala	Ser	Gly	His	Phe	Asp	Leu	Ser	Val	Gly	Ser	Val	Ile	Ala	Cys	Ala
	50				55				60						
Gly	Val	Val	Ala	Gly	Ile	Val	Ile	Arg	Asp	Thr	Asp	Ser	Val	Ala	Leu
65				70				75					80		
Gly	Val	Ser	Ala	Ala	Leu	Ala	Met	Gly	Leu	Val	Val	Gly	Leu	Ile	Asn
			85					90					95		
Gly	Ile	Val	Ile	Ala	Lys	Leu	Arg	Ile	Asn	Ala					
		100					105								

<210> 871

<211> 320

<212> DNA

<213> Homo sapiens

<400> 871

agatcttcag agtcctcgtc ttttaaattgg gggtaacagc agcaagtcct cagaggtgtc  
 60  
 ctgagcctca aaacacatcc tggtttgtaa cgtccgcagc ctcagcaggg gctaggcaca  
 120  
 gaacaagcat tcaggacctg gaaggtacca gcgacacctg gtcctccctt cccaggcaca  
 180  
 aggcagcccc tctccattca agctctgccc cagcccagca aagagagggg tctcagcca  
 240  
 ctgccccac cactaccaca atcatactca cctctcctgg tccatacgtg acaaaggacc  
 300  
 tgccacggcc agggagacaa  
 320

<210> 872

<211> 98

<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 872

```

Met Gly Val Thr Ala Ala Ser Pro Gln Arg Cys Pro Glu Pro Gln Asn
 1           5           10           15
Thr Ser Trp Phe Val Thr Ser Ala Ala Ser Ala Gly Ala Arg His Arg
 20           25           30
Thr Ser Ile Gln Asp Leu Glu Gly Thr Ser Asp Thr Trp Ser Ser Leu
 35           40           45
Pro Arg His Lys Ala Ala Pro Leu His Ser Ser Ser Ala Pro Ala Gln
 50           55           60
Gln Arg Glu Gly Ser Ser Ala Thr Ala Pro Thr Thr Thr Thr Ile Ile
 65           70           75           80
Leu Thr Ser Pro Gly Pro Tyr Val Thr Lys Asp Leu Pro Arg Pro Gly
 85           90           95
Arg Gln

```

&lt;210&gt; 873

&lt;211&gt; 363

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 873

```

nttgtttagc atcgtttttt acgggtgtat cagcgcgttt agcagcgttt ttagcgggatg
60
catcagcatg ttttgcgta cgtttttacaa ctgtgctacc gtgttttagca tcatttttga
120
cggaggtatc aatacgttta gcatcgtttt taacagatgt atcaacacgg ggttcacccg
180
ctttagcaga atccccagct ctagtagcca ctttagatac ttcagatttt atatgagtcg
240
cagttgtttc agcgtgagcc atgctgaatg tagaaccaag ggccaatgta attgctaaag
300
acaaagataa tttatttagt ttcattgttcg gagagaagtg tgccaattcg gcgatacagt
360
cag
363

```

&lt;210&gt; 874

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 874

```

Met Lys Leu Asn Lys Leu Ser Leu Ser Leu Ala Ile Thr Leu Ala Leu
 1           5           10           15
Gly Ser Thr Phe Ser Met Ala His Ala Glu Thr Thr Ala Thr His Ile
 20           25           30
Lys Ser Glu Val Ser Lys Val Ala Thr Arg Ala Gly Asp Ser Ala Lys
 35           40           45
Ala Asp Glu Pro Arg Val Asp Thr Ser Val Lys Asn Asp Ala Lys Arg
 50           55           60
Ile Asp Thr Ser Val Lys Asn Asp Ala Lys His Gly Ser Thr Val Val

```



65                      70                      75                      80  
 Lys Arg Asp Ala Lys His Ala Asp Ala Ser Ala Lys Asn Ala Ala Lys  
                          85                      90                      95  
 Arg Ala Asp Thr Pro Val Lys Asn Asp Ala Lys Gln  
                          100                      105

<210> 875  
 <211> 355  
 <212> DNA  
 <213> Homo sapiens

<400> 875  
 acgcgtgaag gggaccctaa ctcgtctggg ctgtaggatg cgggcgaggc ttccacaaac  
 60  
 tcaactgtctg ggggagaaga aaagcagaaa acaactcgaa tcgctaccat tcaggacgaa  
 120  
 cccgccaaagc accagctcaa gcgcaggtcc ccgggaaaaa gcgcgggctt ctctctccca  
 180  
 gcgctcagaa tccctgagcc ggaggccccg cgggattcag accgccagat ccccagggag  
 240  
 tgacaaatcg ccgcagaaac ttgggggaca actcggccct ggcaccgcgc ggcttccagg  
 300  
 cgcgggcagg cgcgcgccaa ctttccccgc gtgccacccc gcggtcctccc cggn  
 355

<210> 876  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 876  
 Met Arg Ala Arg Leu Pro Gln Thr His Cys Leu Gly Glu Lys Lys Ser  
 1                      5                      10                      15  
 Arg Lys Gln Leu Glu Ser Leu Pro Phe Arg Thr Asn Pro Pro Ser Thr  
                          20                      25                      30  
 Ser Ser Ser Ala Gly Pro Arg Glu Lys Ala Arg Ala Ser Leu Ser Gln  
                          35                      40                      45  
 Arg Ser Glu Ser Leu Ser Arg Arg Pro Arg Gly Ile Gln Thr Ala Arg  
                          50                      55                      60  
 Ser Pro Gly Ser Asp Lys Ser Pro Gln Lys Leu Gly Gly Gln Leu Gly  
 65                      70                      75                      80  
 Pro Gly Thr Ala Arg Leu Pro Gly Ala Gly Arg Arg Ala Pro Thr Phe  
                          85                      90                      95  
 Pro Ala Cys His Pro Ala Ala Pro Pro Ala  
                          100                      105

<210> 877  
 <211> 487  
 <212> DNA  
 <213> Homo sapiens

<400> 877  
 acgcgtactt tgggtaatga actgacgacc gctgagatcg actgccttta tctgtgttac  
 60

caatccacct atgctaaacg tggtcagcaa gggtatctca cacgagaatt ctttggtttg  
 120  
 ttggccaata ccatgggaga tcaaatacctt ttagtacagg cgtacagaga aggcgaagcg  
 180  
 atcgccgcgt cgtgggtgtt ctttgatgat cattcactat atgggcgtta ttggggctgt  
 240  
 atggaagaag tggattgcct gcattttgaa gcttggttatt accaaggaat cgagttttgt  
 300  
 ctcgaaaaag ggttacagca tttcgatccg ggtacacaag gggaacacaa gattgcgcgc  
 360  
 ggctttgaac ctgttttttag ccacagcgtg cattacattg ctcatcaagg ttttcgtgaa  
 420  
 gcgattggga atttctgtga ggaagaagcg caagctgtgc gcgagtatca tcaagatacc  
 480  
 cacgcgt  
 487

&lt;210&gt; 878

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 878

Thr	Arg	Thr	Leu	Gly	Asn	Glu	Leu	Thr	Thr	Ala	Glu	Ile	Asp	Cys	Leu
1				5					10					15	
Tyr	Leu	Cys	Tyr	Gln	Ser	Thr	Tyr	Ala	Lys	Arg	Gly	Gln	Gln	Gly	Tyr
		20						25				30			
Leu	Thr	Arg	Glu	Phe	Phe	Gly	Leu	Leu	Ala	Asn	Thr	Met	Gly	Asp	Gln
	35					40					45				
Ile	Leu	Leu	Val	Gln	Ala	Tyr	Arg	Glu	Gly	Glu	Ala	Ile	Ala	Ala	Ser
	50					55				60					
Trp	Cys	Phe	Phe	Asp	Asp	His	Ser	Leu	Tyr	Gly	Arg	Tyr	Trp	Gly	Cys
65				70					75					80	
Met	Glu	Glu	Val	Asp	Cys	Leu	His	Phe	Glu	Ala	Cys	Tyr	Tyr	Gln	Gly
			85					90						95	
Ile	Glu	Phe	Cys	Leu	Glu	Lys	Gly	Leu	Gln	His	Phe	Asp	Pro	Gly	Thr
		100					105					110			
Gln	Gly	Glu	His	Lys	Ile	Ala	Arg	Gly	Phe	Glu	Pro	Val	Phe	Ser	His
	115					120					125				
Ser	Val	His	Tyr	Ile	Ala	His	Gln	Gly	Phe	Arg	Glu	Ala	Ile	Gly	Asn
	130					135				140					
Phe	Cys	Glu	Glu	Glu	Ala	Gln	Ala	Val	Arg	Glu	Tyr	His	Gln	Asp	Thr
145				150					155					160	
His	Ala														

&lt;210&gt; 879

&lt;211&gt; 993

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 879

nncttagcat ttaagccaac gaggcagcta atgtcctctg aacagcaaag gaaattcagc  
 60

agccagtcca gtagggctct gacccctcct tectacagta ctgctaaaaa ttcattggga  
 120  
 tcaagatcca gtgaatcctt tgggaagtac acatcgccag taatgagtga gcatggggac  
 180  
 gagcacaggc agctcctctc tcaccaaatg caaggccctg gactccgtgc agctacctca  
 240  
 tccaaccact ctgtggacga gcaactgaag aatactgaca cgcacctcat cgacctggta  
 300  
 accaatgaga ttatcaccca aggacctcca gtggactgga atgacattgc tggctctcgac  
 360  
 ctgggtgaagg ctgtcattaa agaggaggtt ttatggccag tgttgaggtc agacgcgttc  
 420  
 agtggactga cggccttacc tcggagcatc cttttatttg gacctcgggg gacaggcaaa  
 480  
 acattattgg gcagatgcat cgctagtcag ctggggggcca catttttcaa aattgccggt  
 540  
 tctggactag tcgccaaggg gttaggagaa gcagagaaaa ttatccatgc ctcttttctt  
 600  
 gtggccaggt gtcgccagcc ctcggtgatt tttgttagtg acattgacat gcttctctcc  
 660  
 tctcaagtga atgaggaaca tagtccagtc agtcggatga gaaccgaatt tctgatgcaa  
 720  
 ctggacactg tactaacttc ggctgaggac caaatcgtag taatttgtgc caccagtaaa  
 780  
 ccagaagaaa tagatgaatc ccttcggagg tacttcatga aacgactttt aatcccactt  
 840  
 cctgacagca cagcgaggca ccagataata gtacaactgc tctcacagca caattactgt  
 900  
 ctcaatgaca aggagtttgc actgctcgtc cagcgcacag aaggcttttc tggactagat  
 960  
 gtggctcatt tgtgtcagga agcagtgggtg ggc  
 993

<210> 880

<211> 331

<212> PRT

<213> Homo sapiens

<400> 880

Xaa	Leu	Ala	Phe	Lys	Pro	Thr	Arg	Gln	Leu	Met	Ser	Ser	Glu	Gln	Gln
1				5				10					15		
Arg	Lys	Phe	Ser	Ser	Gln	Ser	Ser	Arg	Ala	Leu	Thr	Pro	Pro	Ser	Tyr
			20					25					30		
Ser	Thr	Ala	Lys	Asn	Ser	Leu	Gly	Ser	Arg	Ser	Ser	Glu	Ser	Phe	Gly
			35				40					45			
Lys	Tyr	Thr	Ser	Pro	Val	Met	Ser	Glu	His	Gly	Asp	Glu	His	Arg	Gln
			50			55				60					
Leu	Leu	Ser	His	Pro	Met	Gln	Gly	Pro	Gly	Leu	Arg	Ala	Ala	Thr	Ser
65					70					75				80	
Ser	Asn	His	Ser	Val	Asp	Glu	Gln	Leu	Lys	Asn	Thr	Asp	Thr	His	Leu
				85				90						95	
Ile	Asp	Leu	Val	Thr	Asn	Glu	Ile	Ile	Thr	Gln	Gly	Pro	Pro	Val	Asp
			100					105					110		
Trp	Asn	Asp	Ile	Ala	Gly	Leu	Asp	Leu	Val	Lys	Ala	Val	Ile	Lys	Glu

115	120	125
Glu Val Leu Trp Pro Val Leu Arg Ser Asp Ala Phe Ser Gly Leu Thr		
130	135	140
Ala Leu Pro Arg Ser Ile Leu Leu Phe Gly Pro Arg Gly Thr Gly Lys		
145	150	155
Thr Leu Leu Gly Arg Cys Ile Ala Ser Gln Leu Gly Ala Thr Phe Phe		
165	170	175
Lys Ile Ala Gly Ser Gly Leu Val Ala Lys Gly Leu Gly Glu Ala Glu		
180	185	190
Lys Ile Ile His Ala Ser Phe Leu Val Ala Arg Cys Arg Gln Pro Ser		
195	200	205
Val Ile Phe Val Ser Asp Ile Asp Met Leu Leu Ser Ser Gln Val Asn		
210	215	220
Glu Glu His Ser Pro Val Ser Arg Met Arg Thr Glu Phe Leu Met Gln		
225	230	235
Leu Asp Thr Val Leu Thr Ser Ala Glu Asp Gln Ile Val Val Ile Cys		
245	250	255
Ala Thr Ser Lys Pro Glu Glu Ile Asp Glu Ser Leu Arg Arg Tyr Phe		
260	265	270
Met Lys Arg Leu Leu Ile Pro Leu Pro Asp Ser Thr Ala Arg His Gln		
275	280	285
Ile Ile Val Gln Leu Leu Ser Gln His Asn Tyr Cys Leu Asn Asp Lys		
290	295	300
Glu Phe Ala Leu Leu Val Gln Arg Thr Glu Gly Phe Ser Gly Leu Asp		
305	310	315
Val Ala His Leu Cys Gln Glu Ala Val Val Gly		
325	330	

&lt;210&gt; 881

&lt;211&gt; 313

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 881

cgcgtgagcg tcgacaatgc tccaggaacc ggtgtgtatg aggccgggga ttctaccggt  
60

cgtgggtttgc agggcatgcg tgagcgcgcc cgtatccatg gcggcaccgc gcgctggggc  
120

gactcgcagt attatgaagg cggtttcaac gtcacggtgg agattccaac atgagcggcc  
180

aaaggatgaa catggacacg acgcgccccca atcacggtcg gggcttgccg acgatcagcc  
240

ggctgggtgc gcaccggttt tgccatggtg ctggattcgc aggacgacat cacggtggcc  
300

tggcaagccg acn

313

&lt;210&gt; 882

&lt;211&gt; 57

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 882

Arg Val Ser Val Asp Asn Ala Pro Gly Thr Gly Val Tyr Glu Ala Gly

```

      1           5           10           15
Asp Ser Thr Gly Arg Gly Leu Gln Gly Met Arg Glu Arg Ala Arg Ile
      20           25           30
His Gly Gly Thr Ala Arg Trp Gly Asp Ser Gln Tyr Tyr Glu Gly Gly
      35           40           45
Phe Asn Val Thr Val Glu Ile Pro Thr
      50           55

```

&lt;210&gt; 883

&lt;211&gt; 576

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 883

```

naattaagat ctggggtccc agtgtcattg gtgaaggcct tgggattcga ggcagctgag
60
tcctcactga ccaaggcaag ccattgcttct gagtgcttga ggccaccgaa atgaacaaat
120
ggaaaacact cccatctttt tcaagcctac ctttttagcag aagaggcaga tacacaagcc
180
ctaaagatgt aacatcaggc tgagtggagg aaggctgaga agaaaaataa agcagggtca
240
ggaggagaga gtgatgtcag gatgcccttg tgcttactcc agcctccttg tgaaaaccca
300
gctctcctgt ctcccagtga agacttggat ggcagccatc agggaaggct ggggtcccagc
360
tgggagtatg ggtgtgagct ctatagacca tccctctctg caatcaataa acacttgcct
420
gtgaaagagg cccaagccac catccgcatg gacaccagtg caagtggccc caccgcctg
480
gtcctcagtg actgtgccac cagccatggg agcctgcgca tccaactgct gcataagctc
540
tccttcctgg tgaacgcctt agctaagcag gtcattg
576

```

&lt;210&gt; 884

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 884

```

Met Pro Leu Cys Leu Leu Gln Pro Pro Cys Glu Asn Pro Ala Leu Leu
1           5           10           15
Ser Pro Ser Glu Asp Leu Asp Gly Ser His Gln Gly Arg Leu Gly Pro
      20           25           30
Ser Trp Glu Tyr Gly Cys Glu Leu Tyr Arg Pro Ser Leu Ser Ala Ile
      35           40           45
Asn Lys His Leu Pro Val Lys Glu Ala Gln Ala Thr Ile Arg Met Asp
      50           55           60
Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys Ala Thr
65           70           75           80
Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser Phe Leu
      85           90           95
Val Asn Ala Leu Ala Lys Gln Val Met

```

100

105

<210> 885  
 <211> 370  
 <212> DNA  
 <213> Homo sapiens

<400> 885  
 actagtggcg cccatcatccg ggccgctgtc ccgctctcgg agtcgggtgc gttggagtc  
 60  
 ggtgaggcga tgctgacgaa cgacacaccg gtgacttggg atggcgggaa agtacggggc  
 120  
 aggcggtgt cgcgctcgg tgctgacgag ttgtcgtcga ccccggtccg cccagatccg  
 180  
 gtacgggctc gccacgtggc gctggaagca gtgaggtctg ggggacttga cgtagcgagc  
 240  
 ctgacgaaga acggtgaatc tttgcgacgc cgtcttgccc tggcccatcg ggtgtttggt  
 300  
 gatccctggc ccgatgtcag cgatgaggct ctgctagcct gcgccgagga gtggcttgac  
 360  
 ctcgacgcgt  
 370

<210> 886  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 886  
 Thr Ser Gly Ala Leu Ile Arg Ala Ala Val Pro Leu Ser Glu Ser Ala  
 1 5 10 15  
 Ala Leu Glu Ser Gly Glu Ala Met Leu Thr Asn Asp Thr Pro Val Thr  
 20 25 30  
 Trp Asp Gly Gly Lys Val Arg Gly Arg Arg Val Ser Arg Leu Gly Ala  
 35 40 45  
 Ile Glu Leu Ser Ser Thr Pro Val Arg Pro Asp Pro Val Arg Ala Arg  
 50 55 60  
 His Val Ala Leu Glu Ala Val Arg Ser Gly Gly Leu Asp Val Ala Ser  
 65 70 75 80  
 Leu Thr Lys Asn Gly Glu Ser Leu Arg Arg Leu Ala Leu Ala His  
 85 90 95  
 Arg Val Phe Gly Asp Pro Trp Pro Asp Val Ser Asp Glu Ala Leu Leu  
 100 105 110  
 Ala Cys Ala Glu Glu Trp Leu Asp Leu Asp Ala  
 115 120

<210> 887  
 <211> 447  
 <212> DNA  
 <213> Homo sapiens

<400> 887  
 cagggcggtg cgctcggtcg cgtgctgccg atggatcatgc tcggaggctt aaccgccatc  
 60

attatctccg gctgcctgaa ccagcttggt aaacgctatc cgcattctgac cggcgaaggc  
 120  
 caactgatgc caaacctgac taatgctgat accacggctt cccaaccggc gttctccggt  
 180  
 aaagcggacg tgaccaccat tgctccggc gcgttgctgg ccgtgctgct ttacatggtg  
 240  
 ggtaggttgg ttcacaagtt gattggcctg cctgctccgg ttggcatggt gtttgtggcg  
 300  
 gtgctggtca aactgtgcaa cggcgcttct ccccgctgc tcgaaggctc gcaggtggtt  
 360  
 tacaaattct tccagacctc cgtaacctat ccgattctgt tcgccgttgg cgtggcgatt  
 420  
 acgccgtggc aggaactggt caacgcg  
 447

<210> 888  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

<400> 888  
 Gln Gly Val Ala Leu Gly Arg Val Leu Pro Met Val Met Leu Gly Gly  
 1 5 10 15  
 Leu Thr Ala Ile Ile Ile Ser Gly Cys Leu Asn Gln Leu Gly Lys Arg  
 20 25 30  
 Tyr Pro His Leu Thr Gly Glu Gly Gln Leu Met Pro Asn Arg Ala Asn  
 35 40 45  
 Ala Asp Thr Thr Ala Ser Gln Pro Ala Phe Ser Gly Lys Ala Asp Val  
 50 55 60  
 Thr Thr Ile Ala Ser Gly Ala Leu Leu Ala Val Leu Leu Tyr Met Val  
 65 70 75 80  
 Gly Arg Leu Val His Lys Leu Ile Gly Leu Pro Ala Pro Val Gly Met  
 85 90 95  
 Leu Phe Val Ala Val Leu Val Lys Leu Cys Asn Gly Ala Ser Pro Arg  
 100 105 110  
 Leu Leu Glu Gly Ser Gln Val Val Tyr Lys Phe Phe Gln Thr Ser Val  
 115 120 125  
 Thr Tyr Pro Ile Leu Phe Ala Val Gly Val Ala Ile Thr Pro Trp Gln  
 130 135 140  
 Glu Leu Val Asn Ala  
 145

<210> 889  
 <211> 450  
 <212> DNA  
 <213> Homo sapiens

<400> 889  
 ggtaccaccc cacacctgac aagaggtggc cagggaggaa gggagggttc ttacctcccc  
 60  
 atctccccctc agtaaaattc aggatgccca gtgaagtttg aatgtcagat aaacaatttg  
 120  
 ttagtataag gatgtacctc gcattgaaat gatgccttgt aatttactaa atctgcaact  
 180

atgcagcctt atttcatggc gggcagtggc ggtgatccca ggtttcaggg gcggggaagg  
 240  
 gtgctgggga gatcctgagg tcaggaaccc gtacacctct gcttctgccc tctcttccct  
 300  
 gtgccggcca caaggcaatg actcctgtgt gggcgcagag gcagaaatgg gtctggaagg  
 360  
 ggattcccag tgtctggcaa gttctggtaa attctgcatt ggaggttctc tctgtagtaa  
 420  
 ggggagttgg cctggccgcc cttcacgcgt  
 450

<210> 890

<211> 100

<212> PRT

<213> Homo sapiens

<400> 890

Met	Met	Pro	Cys	Asn	Leu	Leu	Asn	Leu	Gln	Leu	Cys	Ser	Leu	Ile	Ser
1				5					10					15	
Trp	Arg	Ala	Val	Ala	Val	Ile	Pro	Gly	Phe	Arg	Gly	Gly	Glu	Gly	Cys
			20					25					30		
Trp	Gly	Asp	Pro	Glu	Val	Arg	Asn	Pro	Tyr	Thr	Ser	Ala	Ser	Ala	Leu
		35					40					45			
Ser	Ser	Leu	Cys	Arg	Pro	Gln	Gly	Asn	Asp	Ser	Cys	Val	Gly	Ala	Glu
		50				55					60				
Ala	Glu	Met	Gly	Leu	Glu	Gly	Asp	Ser	Gln	Cys	Leu	Ala	Ser	Ser	Gly
65					70					75				80	
Lys	Phe	Cys	Ile	Gly	Gly	Ser	Leu	Cys	Ser	Lys	Gly	Ser	Trp	Pro	Gly
			85						90					95	
Arg	Pro	Ser	Arg												
			100												

<210> 891

<211> 318

<212> DNA

<213> Homo sapiens

<400> 891

nncaccgtcc cgtactgga tccgcgcgag gatttcgccg actgcatgca cattgacgta  
 60  
 ctggatccct tccacactga caacaccagt gagcacagtg acctggccac agatggccag  
 120  
 actaacggcc cggctgatag cgggactggc acccactctg agcagggaaa ctccgacata  
 180  
 tctagccccg tcagctctag tgacgtgct aacaccaccg acagcactgc tggcaatacc  
 240  
 ggtgaaggta ctgccgcgaa tatgcctggt gacatggctc attcttcgac ggctaccac  
 300  
 ccctatgcaa gcaccggt  
 318

<210> 892

<211> 106

<212> PRT



<213> Homo sapiens

<400> 892

```

Xaa Thr Val Pro Val Leu Asp Pro Arg Glu Asp Phe Ala Asp Cys Met
 1             5             10             15
His Ile Asp Val Leu Asp Pro Phe His Thr Asp Asn Thr Ser Glu His
      20             25             30
Ser Asp Leu Ala Thr Asp Gly Gln Thr Asn Gly Pro Ala Asp Ser Gly
      35             40             45
Thr Gly Thr His Ser Glu Gln Gly Asn Ser Asp Ile Ser Ser Pro Val
      50             55             60
Ser Ser Ser Asp Ala Ala Asn Thr Thr Asp Ser Thr Ala Gly Asn Thr
65             70             75             80
Gly Glu Gly Thr Ala Ala Asn Met Pro Gly Asp Met Ala His Ser Ser
      85             90             95
Thr Ala Thr His Pro Tyr Ala Ser Thr Gly
      100             105

```

<210> 893

<211> 510

<212> DNA

<213> Homo sapiens

<400> 893

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nnggataccta tccctgaatc taagggtggt gacacatgtg tttgggatag caaggtagag
60
aagtcacaga aaaagcctgt ggaaaacagg atgaaggagg acaaaagcag catcagggaa
120
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<210> 894

<211> 170

<212> PRT

<213> Homo sapiens

<400> 894

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Cys Asp Glu Cys Gly Lys Ser Phe Lys Tyr Asn Ser Arg Leu Val Gln
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His Lys Ile Met His Thr Gly Glu Lys Arg Tyr Glu Cys Asp Asp Cys
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His Thr Gly Tyr Gly Glu Lys Thr Thr Arg
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&lt;210&gt; 895

&lt;211&gt; 1119

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 895

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<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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			20					25					30		
Leu	Gln	Leu	Leu	Tyr	Leu	Thr	Asn	Asn	Leu	Leu	Thr	Asp	Gln	Cys	Ile
		35				40						45			
Pro	Val	Leu	Val	Gly	His	Leu	His	Leu	Arg	Ile	Leu	His	Leu	Ala	Asn
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			85					90					95		
Thr	Ile	Ala	Asn	Cys	Lys	Arg	Leu	His	Thr	Leu	Val	Ala	His	Ser	Asn
			100					105					110		
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385	390	395
His Leu Ser Tyr Thr Glu	Ala Val Asn Ala Val Arg	His Val Gln Asp
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Pro Leu Ala Ala Ala Lys	Lys Leu Cys Thr Leu Ala	Gln Ser Tyr Gly
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          645          650          655
Val Pro Leu Glu Asp Ser Leu Asn Leu Ile Glu Val Ala Thr Glu Val
          660          665          670
Pro Lys Arg Lys Thr Gly Tyr Phe Ala Ala Pro Thr Gln Met Glu Pro
          675          680          685
Glu Asp Gln Phe Val Val Pro His Asp Leu Glu Glu Glu Val Lys Glu
          690          695          700
Gln Met Lys Gln His Gln Asp Ser Arg Leu Glu Pro Glu Pro His Glu
705          710          715          720
Glu Asp Arg Thr Glu Pro Pro Glu Glu Phe Asp Thr Ala Leu
          725          730

```

<210> 901  
 <211> 309  
 <212> DNA  
 <213> Homo sapiens

```

<400> 901
tcatgatcca cctgcctcgg cctcccaaag tgctgggatt acatacagat ggcaaacttc
60
atttcctttt tctcttaatg caacaaggtc atcccaagat caggcttcct tcagtttctg
120
tggtaagtag tgatggacac ttatggagtt ttcagagact tatgcattgg gtaacaaggc
180
actgcaagag accccagata gcacagcatc atctcacatt tacaccacat cacatcaaca
240
tcgatgctag gaggtctaaa gctgatgccca ccttcagagc tgcaagtatc caaaagactc
300
cactcatga
309

```

<210> 902  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

```

<400> 902
Met Ile His Leu Pro Arg Pro Pro Lys Val Leu Gly Leu His Thr Asp
1          5          10          15
Gly Lys Leu His Phe Leu Phe Leu Leu Met Gln Gln Gly His Pro Lys
20          25          30
Ile Arg Leu Pro Ser Val Ser Val Val Ser Ser Asp Gly His Leu Trp
35          40          45
Ser Phe Gln Arg Leu Met His Trp Val Thr Arg His Cys Lys Arg Pro
50          55          60
Gln Ile Ala Gln His His Leu Thr Phe Thr Pro His His Ile Asn Ile
65          70          75          80
Asp Ala Arg Arg Ser Lys Ala Asp Ala Thr Phe Arg Ala Ala Ser Ile
85          90          95
Gln Lys Thr Pro Leu Met
100

```

<210> 903  
 <211> 349  
 <212> DNA  
 <213> Homo sapiens

<400> 903  
 agatcttagt gaaaactgga agcaggaaga ataagttagt catggaagcc actttggctc  
 60  
 taagggtctt gatggcctca tgggttgaca ggaacagaag acaaagacta gggcccaccc  
 120  
 aaggtgtgaa gtctaataagg aaaccttttc tccataaggc tacaatgggt ctaccaaaaa  
 180  
 taaaaccatg ccaccccagg gactgcagcc caattttata tcaccatgag gtccaaaaaa  
 240  
 ttccaagctg tgaatttagt ttcaaaggc cttggtctcc agtatcccta gccatgtggc  
 300  
 aaaaacaaac aattctcttt ggaggataca tctttatctt aagacttgn  
 349

<210> 904  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

<400> 904  
 Met Glu Ala Thr Leu Ala Leu Arg Ala Leu Met Ala Ser Trp Val Asp  
 1 5 10 15  
 Arg Asn Arg Arg Gln Arg Leu Gly Pro Thr Gln Gly Val Lys Ser Asn  
 20 25 30  
 Arg Lys Pro Phe Leu His Lys Ala Thr Met Gly Leu Pro Lys Ile Lys  
 35 40 45  
 Pro Cys His Pro Arg Asp Cys Ser Pro Ile Leu Tyr His His Glu Val  
 50 55 60  
 Gln Lys Ile Pro Ser Cys Glu Phe Ser Phe Lys Trp Pro Trp Ser Pro  
 65 70 75 80  
 Val Ser Leu Ala Met Trp Gln Lys Gln Thr Ile Leu Phe Gly Gly Tyr  
 85 90 95  
 Ile Phe Ile Leu Arg Leu  
 100

<210> 905  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<400> 905  
 nntccggaac cggtggtgtg gaccgagcac gattctcacc tagctcacc ggatcagcgt  
 60  
 ctcaacgaag acatcattat cgcggtgac cgggcagacg cggtgattag cgtatcccg  
 120  
 gggctctgcy acaggctggc tggacatggc gtgacctcaa cggtgggtcc caacatcggt  
 180  
 gacgtcgagc tgtttgaccg tcttgatcga cgacatgagg ggacgatcgt cgtcagcgtc  
 240

gccaccctca acccgggaaa gggcatgatt gagttagctc aggctgttga gcgtcttccc  
 300  
 gaggttcagt tgagaatcat cggagatgga ccgcagcggc accaactgga ggccattgcc  
 360  
 gctgataatc cacgcgt  
 377

<210> 906  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 906  
 Xaa Pro Glu Pro Val Val Trp Thr Glu His Asp Ser His Leu Ala His  
 1 5 10 15  
 Pro Asp Gln Arg Leu Asn Glu Asp Ile Ile Ile Ala Gly Asp Arg Ala  
 20 25 30  
 Asp Ala Val Ile Ser Val Ser Gln Gly Leu Cys Asp Arg Leu Ala Gly  
 35 40 45  
 His Gly Val Thr Ser Thr Val Val Pro Asn Ile Val Asp Val Glu Leu  
 50 55 60  
 Phe Asp Arg Pro Asp Arg Arg His Glu Gly Thr Ile Val Val Ser Val  
 65 70 75 80  
 Ala Thr Leu Asn Pro Gly Lys Gly Met Ile Glu Leu Ala Gln Ala Val  
 85 90 95  
 Glu Arg Leu Pro Glu Val Gln Leu Arg Ile Ile Gly Asp Gly Pro Gln  
 100 105 110  
 Arg His Gln Leu Glu Ala Ile Ala Ala Asp Asn Pro Arg  
 115 120 125

<210> 907  
 <211> 332  
 <212> DNA  
 <213> Homo sapiens

<400> 907  
 acgcgtagga tgatgaagtc cgtcactgga tcgttcttgg gtggcaaccg ggaagtcggg  
 60  
 gaccagttct tcaacggcga ggttcaactg aaccttgtgc cgcagggtac attcgccgag  
 120  
 cgcattcgtg ccggcgctgc tggattgca gcattcttca cgcctactgg ctatggtaca  
 180  
 gccgtgcaga agggtagact tgttcttaag tatgaaaaga aggacggtaa ggctgtgcc  
 240  
 gtcattgacgt ccaagccgcg tgaagtgcgc tcgtttgacg gccgtgacta tataatagaa  
 300  
 gaggttatta aggatgaata ggatatggtg aa  
 332

<210> 908  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 908

```

Thr Arg Arg Met Met Lys Ser Val Thr Gly Ser Phe Leu Gly Gly Asn
 1           5           10           15
Arg Glu Val Gly Asp Gln Phe Phe Asn Gly Glu Val Gln Leu Asn Leu
      20           25           30
Val Pro Gln Gly Thr Phe Ala Glu Arg Ile Arg Ala Gly Ala Ala Gly
      35           40           45
Ile Ala Ala Phe Phe Thr Pro Thr Gly Tyr Gly Thr Ala Val Gln Lys
      50           55           60
Gly Glu Leu Val Leu Lys Tyr Glu Lys Lys Asp Gly Lys Ala Val Pro
65           70           75           80
Val Met Thr Ser Lys Pro Arg Glu Val Arg Ser Phe Asp Gly Arg Asp
      85           90           95
Tyr Ile Ile Glu Glu Val Ile Lys Asp Glu
      100           105

```

&lt;210&gt; 909

&lt;211&gt; 318

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 909

```

acgcgctcggg catggcagct gtacagatct atcgcgctcag cagggcctac gcacacatga
60
tgccgcaggg gcaccgacgc tgctgcacatc aaaagagccg cctcgcgccc gcagcgctc
120
ccagggacgg cgactcacgt ggctcgacac gcgcgcgcga gtcgcgtggg tgtgtcacgc
180
ccctttttttt cccaccccaa caccgaaccg gcgggcatg gctgaggatt cgcaccccat
240
tcgctccggc ttgcgcatgc tcaagcgctc ctggagctcg aatgagaatg taccgccgcc
300
acaaagctcg ccgccggc
318

```

&lt;210&gt; 910

&lt;211&gt; 102

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 910

```

Met Ala Ala Val Gln Ile Tyr Arg Val Ser Arg Ala Tyr Ala His Met
 1           5           10           15
Met Pro Gln Gly His Arg Arg Cys Arg His Gln Lys Ser Arg Leu Ala
      20           25           30
Pro Ala Ala Pro Pro Arg Asp Gly Asp Ser Arg Gly Ser Thr Arg Ala
      35           40           45
Arg Glu Ser Arg Gly Cys Val Thr Pro Leu Phe Phe Pro Pro Gln His
      50           55           60
Arg Thr Gly Gly Pro Trp Leu Arg Ile Arg Thr Pro Phe Ala Pro Ala
65           70           75           80
Cys Ala Cys Ser Ser Ala Pro Gly Ala Arg Met Arg Met Tyr Arg Arg
      85           90           95
His Lys Ala Arg Arg Arg

```

100

<210> 911  
 <211> 506  
 <212> DNA  
 <213> Homo sapiens

<400> 911  
 acgcgtgtgc agcactctcc acaagctggc cccaatcact tttgcatcaa attggtacag  
 60  
 caaccttatg aggctggcct tgggggaacc ctgttttagg gatgagctga acttaccggg  
 120  
 aggctgcatg cgaggttggt gtgaaatgca tatctggcct ttagctggt cggtcacct  
 180  
 ctgggggttg cacaggggcg ggggttctgc catggctaga atgcgctaag ggggtgaaac  
 240  
 gaagcctgct gggcccgga accacagagc agcctggcct ttgaaggaga ccctgtggca  
 300  
 cccctgccc accccaagt ccagccattt cacttcctg gagatggtgc aaagcaagaa  
 360  
 aaaaaaaaa atccagtgtt ctcaggtcag ccttcacca gccaggattc atcgtctgat  
 420  
 ctgtttgggg agagagcatg gagggtgga gatgggttg gcccagtggt tttctgatta  
 480  
 actcgagtt cacctgaaac attttg  
 506

<210> 912  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

<400> 912  
 Met Phe Gln Val Asn Cys Glu Leu Ile Arg Lys His Trp Gly Pro Thr  
 1 5 10 15  
 His Leu His His Ser Met Leu Ser Pro Gln Thr Asp Gln Thr Met Asn  
 20 25 30  
 Pro Gly Trp Trp Lys Ala Asp Leu Arg Thr Leu Asp Phe Phe Phe Phe  
 35 40 45  
 Leu Ala Leu His His Leu Gln Gly Ser Glu Met Ala Gly Leu Gly Gly  
 50 55 60  
 Gly Gln Gly Val Pro Gln Gly Leu Leu Gln Arg Pro Gly Cys Ser Val  
 65 70 75 80  
 Val Pro Gly Pro Ser Arg Leu Arg Phe His Pro Leu Ala His Ser Ser  
 85 90 95  
 His Gly Arg Thr Pro Ala Pro Val Pro Thr Pro Glu Val Ser Arg Pro  
 100 105 110  
 Ala Thr Lys Pro Asp Met His Phe Thr Pro Thr Ser His Ala Ala Ser  
 115 120 125  
 Arg

<210> 913  
 <211> 339

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 913

cgcttcatgg cgtgggttcag gcgtacgggt cgggtactg gtgactaccg tggcacgaaa  
 60  
 tttttcgttc gcgagaacgg taaaaccctc gcaacctcga tgttcatggg ttgtgtcgcc  
 120  
 ctggggcgcca cggacctgct ttctgccctc gactcgattc cggcgctccta tggtttcacc  
 180  
 aacgaggggt accttatact taccgctaac gtctttgctc tcatgggctt gcgtcagttg  
 240  
 tatttcctta ttggaagcct gttggaacgt ctggtgtact tgtcgctggg actgggtcgtg  
 300  
 attttgggct ttatcgccct caagctcatt ggccacgag  
 339

&lt;210&gt; 914

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 914

Arg	Phe	Met	Ala	Trp	Phe	Arg	Arg	Thr	Val	Pro	Ala	Thr	Gly	Asp	Tyr
1				5					10					15	
Arg	Gly	Thr	Lys	Phe	Phe	Val	Arg	Glu	Asn	Gly	Lys	Thr	Leu	Ala	Thr
			20					25					30		
Ser	Met	Phe	Met	Val	Cys	Val	Ala	Leu	Gly	Ala	Thr	Asp	Leu	Leu	Phe
			35				40					45			
Ala	Leu	Asp	Ser	Ile	Pro	Ala	Ser	Tyr	Gly	Phe	Thr	Asn	Glu	Gly	Tyr
	50				55						60				
Leu	Ile	Leu	Thr	Ala	Asn	Val	Phe	Ala	Leu	Met	Gly	Leu	Arg	Gln	Leu
65					70				75					80	
Tyr	Phe	Leu	Ile	Gly	Ser	Leu	Leu	Glu	Arg	Leu	Val	Tyr	Leu	Ser	Leu
			85					90					95		
Gly	Leu	Val	Val	Ile	Leu	Gly	Phe	Ile	Ala	Leu	Lys	Leu	Ile	Gly	His
			100					105					110		

Ala

&lt;210&gt; 915

&lt;211&gt; 663

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 915

nnggtacctg tcaatcagta tgtaaacctc actttatgtc gtggttatcc acttcctgat  
 60  
 gacagtgaag atcctgttgt ggacattggt gctgctaccc ctgtcatcaa tggacagtca  
 120  
 ttaaccaagg gagagacttg catgaatcct caggatttta agccaggagc aatggttctg  
 180  
 gagcagaatg gaaaatcggg acacactttg actgggtgatg gtctcaatgg accatcagat  
 240

gcaagtgagc agagagtatc catggcatcg tcaggcagct cccagcctga actagtgact  
 300  
 atccctttga ttaagggccc taaaggggtt gggtttgcaa ttgctgacag ccctactgga  
 360  
 cagaaggtga aaatgatact ggatagtcag tgggtgtcaag gccttcagaa aggagatata  
 420  
 attaaggaaa tataccatca aaatgtgcag aatttaacac atctccaagt ggtagagggtg  
 480  
 ctaaagcagt ttccagtagg tgctgatgta ccattgctta tcttaagagg aggtccccct  
 540  
 tcaccaacca aaagtgccaa aatgaaaaca gataaaaagg aaaatgcagg aagtttggag  
 600  
 gccataaatg agcctattcc tcagcctatg ccttttccac cgagcattat caggtcagga  
 660  
 tcc  
 663

<210> 916

<211> 221

<212> PRT

<213> Homo sapiens

<400> 916

Xaa	Val	Pro	Val	Asn	Gln	Tyr	Val	Asn	Leu	Thr	Leu	Cys	Arg	Gly	Tyr
1				5					10					15	
Pro	Leu	Pro	Asp	Asp	Ser	Glu	Asp	Pro	Val	Val	Asp	Ile	Val	Ala	Ala
			20					25					30		
Thr	Pro	Val	Ile	Asn	Gly	Gln	Ser	Leu	Thr	Lys	Gly	Glu	Thr	Cys	Met
		35				40						45			
Asn	Pro	Gln	Asp	Phe	Lys	Pro	Gly	Ala	Met	Val	Leu	Glu	Gln	Asn	Gly
		50				55					60				
Lys	Ser	Gly	His	Thr	Leu	Thr	Gly	Asp	Gly	Leu	Asn	Gly	Pro	Ser	Asp
65					70					75				80	
Ala	Ser	Glu	Gln	Arg	Val	Ser	Met	Ala	Ser	Ser	Gly	Ser	Ser	Gln	Pro
				85					90					95	
Glu	Leu	Val	Thr	Ile	Pro	Leu	Ile	Lys	Gly	Pro	Lys	Gly	Phe	Gly	Phe
			100					105					110		
Ala	Ile	Ala	Asp	Ser	Pro	Thr	Gly	Gln	Lys	Val	Lys	Met	Ile	Leu	Asp
		115					120					125			
Ser	Gln	Trp	Cys	Gln	Gly	Leu	Gln	Lys	Gly	Asp	Ile	Ile	Lys	Glu	Ile
		130				135					140				
Tyr	His	Gln	Asn	Val	Gln	Asn	Leu	Thr	His	Leu	Gln	Val	Val	Glu	Val
145					150					155				160	
Leu	Lys	Gln	Phe	Pro	Val	Gly	Ala	Asp	Val	Pro	Leu	Leu	Ile	Leu	Arg
			165					170						175	
Gly	Gly	Pro	Pro	Ser	Pro	Thr	Lys	Ser	Ala	Lys	Met	Lys	Thr	Asp	Lys
			180					185					190		
Lys	Glu	Asn	Ala	Gly	Ser	Leu	Glu	Ala	Ile	Asn	Glu	Pro	Ile	Pro	Gln
		195				200						205			
Pro	Met	Pro	Phe	Pro	Pro	Ser	Ile	Ile	Arg	Ser	Gly	Ser			
		210				215						220			

<210> 917

<211> 615



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 917

atcgtggacc agaagttccc tgagtgtggc ttctacggcc tttacgacaa gatcctgctt  
 60  
 ttcaaacatg accccacgtc ggccaacctc ctgcagctgg tgcgctcgtc cggagacatc  
 120  
 caggagggcg acctggtgga ggtggtgctg tcggcctcgg ccaccttcga ggacttccag  
 180  
 atccgcccgc acgccctcac ggtgcactcc tategggcgc ctgccttctg tgatcactgc  
 240  
 ggggagatgc tcttcggcct agtgcgccag ggcctcaagt gcgatggctg cgggctgaac  
 300  
 taccacaagc gctgtgcctt cagcatcccc aacaactgta gtggggcccg caaacggcgc  
 360  
 ctgtcatcca cgtctctggc cagtggccac tcggtgcgcc tcggcacctc cgagtccctg  
 420  
 ccctgcacgg ctgaagagga gccgtagcac caccgaactc ctgcctcgcc gtccccgtca  
 480  
 tcctcttctt cctcttctgc ctcactgtat acggggccgc ccattgagct ggacaagatg  
 540  
 ctgctctcca aggtcaaggt gccgcacacc ttcctcatcc acagctatac acggcccacc  
 600  
 gtttgccagg cttgc  
 615

&lt;210&gt; 918

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 918

Ile Val Asp Gln Lys Phe Pro Glu Cys Gly Phe Tyr Gly Leu Tyr Asp  
 1 5 10 15  
 Lys Ile Leu Leu Phe Lys His Asp Pro Thr Ser Ala Asn Leu Leu Gln  
 20 25 30  
 Leu Val Arg Ser Ser Gly Asp Ile Gln Glu Gly Asp Leu Val Glu Val  
 35 40 45  
 Val Leu Ser Ala Ser Ala Thr Phe Glu Asp Phe Gln Ile Arg Pro His  
 50 55 60  
 Ala Leu Thr Val His Ser Tyr Arg Ala Pro Ala Phe Cys Asp His Cys  
 65 70 75 80  
 Gly Glu Met Leu Phe Gly Leu Val Arg Gln Gly Leu Lys Cys Asp Gly  
 85 90 95  
 Cys Gly Leu Asn Tyr His Lys Arg Cys Ala Phe Ser Ile Pro Asn Asn  
 100 105 110  
 Cys Ser Gly Ala Arg Lys Arg Arg Leu Ser Ser Thr Ser Leu Ala Ser  
 115 120 125  
 Gly His Ser Val Arg Leu Gly Thr Ser Glu Ser Leu Pro Cys Thr Ala  
 130 135 140  
 Glu Glu Glu Pro  
 145

<210> 919  
 <211> 294  
 <212> DNA  
 <213> Homo sapiens

<400> 919  
 accggtatgc gtccgctggc tgtgctcggc gacaacatca ccaccgacca tctatcgccg  
 60  
 acaaatgcga tcctgctcga tagcgacgag ggtgagtacc tcgccaagat gggcccgcgcg  
 120  
 gaagaagact tcatttcgaa cgcgacccat cgtggcgatc acctgaccgc acagcgcgcc  
 180  
 accttcgcca acccgacctt gctcaacgag atggccgtag tcgatggtga agtgaagaaa  
 240  
 ggctcgcttg cccgcgtgga accggaaggc catgtgatgc gcatgtggga agcc  
 294

<210> 920  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 920  
 Thr Gly Met Arg Pro Leu Ala Val Leu Gly Asp Asn Ile Thr Thr Asp  
 1 5 10 15  
 His Leu Ser Pro Thr Asn Ala Ile Leu Leu Asp Ser Ala Ala Gly Glu  
 20 25 30  
 Tyr Leu Ala Lys Met Gly Pro Pro Glu Glu Asp Phe Ile Ser Asn Ala  
 35 40 45  
 Thr His Arg Gly Asp His Leu Thr Ala Gln Arg Ala Thr Phe Ala Asn  
 50 55 60  
 Pro Thr Leu Leu Asn Glu Met Ala Val Val Asp Gly Glu Val Lys Lys  
 65 70 75 80  
 Gly Ser Leu Ala Arg Val Glu Pro Glu Gly His Val Met Arg Met Trp  
 85 90 95  
 Glu Ala

<210> 921  
 <211> 378  
 <212> DNA  
 <213> Homo sapiens

<400> 921  
 acgcgtttgc gcatcgcttt gaccggctctg acgatggctg agtacttccg cgatgttcag  
 60  
 aaccaggacg tgctgttggt catcgacaac atcttccggt tctcccaggc tggttctgag  
 120  
 gtttcaaccc tgctaggtcg tatgccctcg gcggtgggct accagcccaa cttggccgac  
 180  
 gagatgggccc aattgcagga gcgaatcacc tcgaccctg gtcactccat cacctcgatg  
 240  
 caggccgtct acgtccccgc tgacgattac accgaccctg ctccggcgac gaccttcgcc  
 300

cacctggatg ccaccacgga gctttctcgt gagattgcct ctcgtggcct gtaccgggcc  
 360  
 gtggatccgc tggcgctcg  
 378

<210> 922  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 922  
 Thr Arg Leu Arg Ile Ala Leu Thr Gly Leu Thr Met Ala Glu Tyr Phe  
 1 5 10 15  
 Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn Ile Phe  
 20 25 30  
 Arg Phe Ser Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met  
 35 40 45  
 Pro Ser Ala Val Gly Tyr Gln Pro Asn Leu Ala Asp Glu Met Gly Gln  
 50 55 60  
 Leu Gln Glu Arg Ile Thr Ser Thr Arg Gly His Ser Ile Thr Ser Met  
 65 70 75 80  
 Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala  
 85 90 95  
 Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Ser Arg Glu Ile  
 100 105 110  
 Ala Ser Arg Gly Leu Tyr Pro Ala Val Asp Pro Leu Ala Ser  
 115 120 125

<210> 923  
 <211> 571  
 <212> DNA  
 <213> Homo sapiens

<400> 923  
 accggtatcg aactgccgca agacacgggc aagcatgtcg ccgacgaaca actgcaacgc  
 60  
 ctggacaccg cgctggagca cgtgcgcgga gaaatccgca ttaccctgga gcatgcacgc  
 120  
 caacgcaaga atgtcgaaga agaagacatc ttgcgcgccc accttgcgct attggaagac  
 180  
 cccacgctgc tggacgccgc cactgggtgcc atcgaacacg gcagcgccgc caccacgcc  
 240  
 tggcgcgatg caatccaggc gcaatgcgcc gtgttgctgg ccctgggcaa accgctgttt  
 300  
 gccgagcgcg ccaacgacct gcgcgatctg caacagcgag tactgcgtgc gctgttgggg  
 360  
 gaagcctggc acttcgaatt gccggccggg ccgattttca ggnnggccat taacttaccc  
 420  
 ccttcgcct tggtgcaact gagggcccaa aacgccgtgg gtatttgcat ggccgaaggc  
 480  
 ggcgctacgt ctcacgtcgc gattttggcc cgaggcaaag gcttgccgtg cgtgggtcgcg  
 540  
 ctggggcgccg aagtgtcga cgtgccccaa g  
 571

<210> 924  
 <211> 190  
 <212> PRT  
 <213> Homo sapiens

<400> 924  
 Thr Gly Ile Glu Leu Pro Gln Asp Thr Gly Lys His Val Ala Asp Glu  
 1 5 10 15  
 Gln Leu Gln Arg Leu Asp Thr Ala Leu Glu His Val Arg Gly Glu Ile  
 20 25 30  
 Arg Ile Thr Leu Glu His Ala Arg Gln Arg Lys Asn Val Glu Glu Glu  
 35 40 45  
 Asp Ile Phe Ala Ala His Leu Ala Leu Leu Glu Asp Pro Thr Leu Leu  
 50 55 60  
 Asp Ala Ala Thr Gly Ala Ile Glu His Gly Ser Ala Ala Thr His Ala  
 65 70 75 80  
 Trp Arg Asp Ala Ile Gln Ala Gln Cys Ala Val Leu Leu Ala Leu Gly  
 85 90 95  
 Lys Pro Leu Phe Ala Glu Arg Ala Asn Asp Leu Arg Asp Leu Gln Gln  
 100 105 110  
 Arg Val Leu Arg Ala Leu Leu Gly Glu Ala Trp His Phe Glu Leu Pro  
 115 120 125  
 Ala Gly Pro Ile Phe Arg Xaa Ala Ile Asn Leu Pro Pro Ser Ala Leu  
 130 135 140  
 Leu Gln Leu Ser Ala Gln Asn Ala Val Gly Ile Cys Met Ala Glu Gly  
 145 150 155 160  
 Gly Ala Thr Ser His Val Ala Ile Leu Ala Arg Gly Lys Gly Leu Pro  
 165 170 175  
 Cys Val Val Ala Leu Gly Ala Glu Val Leu Asp Val Pro Gln  
 180 185 190

<210> 925  
 <211> 620  
 <212> DNA  
 <213> Homo sapiens

<400> 925  
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg  
 60  
 ncatggtgtg tgcacgtgtg cnactgtgta tgcattggtaa tgtgcacgtg tgcactgtgt  
 120  
 gtggtgtgta tgcattggtg gtgcacgtgt gcactgtgtg tgtgtgtatg catgtgtgtg  
 180  
 cacgtgtgcc tgtgtgtatg catggtaatg tgcgtgtgca ctgtgtggtg tgtatgcatg  
 240  
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 300  
 atggtaatgt gcacgtgtgc actgtgtgtg gtgtgtatga tgggtgtgtgc acgtgtgcac  
 360  
 ggtgtgtggt gtgtatgcat gtgtgtgcac gtgtgcactg tgtggcaggg gtgtttggtg  
 420  
 tgtgtgcatg tatgcatggt gtgtgcatac gtgtgcagca gcacctgggc ccatctccag  
 480

tgcccagcag catcacacgc actttggtgc ttataaatg catggtcagt gaggtgccca  
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<210> 926  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<400> 926  
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys  
 1 5 10 15  
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met  
 20 25 30  
 Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val Cys  
 35 40 45  
 Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Val Cys Leu  
 50 55 60  
 Cys Val Cys Met Val Met Cys Val Cys Thr Val Trp Cys Val Cys Met  
 65 70 75 80  
 Cys Val His Val Cys Thr Val Tyr Ala  
 85

<210> 927  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 927  
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 120  
 tctcaggtct gtgcttctct gggggccacc cagccatect gccaccagc tcagaggcag  
 180  
 ggacaaagcc ctcccaagag gcagcaggca gcaagggta gccagcgcag tggggacagg  
 240  
 caggtacaac ctggaaaccc caaaggaccc cagatggcaa tgtgacacgg cccatccacc  
 300  
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 360

<210> 928  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 928  
 Met Glu Leu Leu Glu Ile Val Arg His Asp Gln Arg Glu Glu Ala Phe  
 1 5 10 15  
 Gly Val Leu Phe Arg Ser Phe Gln Gln Gln Thr Gly His Gly Asp Pro

	20		25		30										
Ile	Ser	Gly	Leu	Cys	Phe	Ser	Gly	Gly	His	Pro	Ala	Ile	Leu	Pro	Thr
	35		40		45										
Ser	Ser	Glu	Ala	Gly	Thr	Lys	Pro	Ser	Gln	Glu	Ala	Ala	Gly	Ser	Lys
	50		55		60										
Gly	Gln	Pro	Ala	Gln	Trp	Gly	Gln	Ala	Gly	Thr	Thr	Trp	Lys	Pro	Gln
65			70		75				80						
Arg	Thr	Pro	Asp	Gly	Asn	Val	Thr	Arg	Pro	Ile	His	Gln	Ala	Pro	Val
			85		90				95						
Met	Pro	Ala	Ser	His	Arg	Gly	Glu	Pro	Asp	Pro	Gly	Thr	Ile	Leu	
	100		105		110										

&lt;210&gt; 929

&lt;211&gt; 2340

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 929

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nnctccccag ggccgagtct tccggagtca gcagagagcc tggatggatc acaggaggat
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120
aacaacagcc ggctcaaggc caagggcgtg ggccagcacg acaacgcca gaactttggt
180
aaccagagct ttgaggagct gcgagcagcc tgtctaagaa agggggagct cttcgaggac
240
cccttattcc ctgctgaacc cagctcactg ggcttcaagg acctgggccc caactccaaa
300
aatgtgcaga acatctctctg gcagcggccc aaggatatca taaacaaccc tctattcacc
360
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420
gctgccatcg gctcccttac cacctgcccc aaactgctat accgcgtggt gcccagagga
480
cagagcttca agaaaaacta tgctggcatc ttccattttc agatttggca gtttggacag
540
tgggtgaacg tgggtgtaga tgaccggctg cccacaaaga atgacaagct ggtgtttgtg
600
cactcaaccg aacgcagtga gttctggagt gccctgctgg agaaggcgta tgccaagctg
660
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720
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780
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840
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900
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960
ggccggattg agtggaatgg agcttgaggt gacagtgccg gggagtggga agaggtggcc
1020
tcagacatcc agatgcagct gctgcacaag acggaggagc gggagttctg gatgtcctac
1080

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caagatttcc tgaacaactt cacgctcctg gagatctgca acctcacgcc tgatacactc  
 1140  
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 1200  
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 1260  
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 1320  
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 1380  
 ctgcagacca ttggctttgt cctctacgcg gtcccaaaag agtttcagaa cattcaggat  
 1440  
 gtccacttga agaaggaatt cttcacgaag tatcaggacc acggcttctc agagatcttc  
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 accaactcac gggaggtgag cagccaactc cggtgcctc cgggggaata tatcattatt  
 1560  
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 1620  
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 1680  
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 1740  
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 1800  
 aaaagcttca agaccaaggg ctttggcctg gatgcttgcc gctgcatgat caacctcatg  
 1860  
 gataaagatg gctctggcaa gctggggctt ctagagttca agatcctgtg gaaaaaactc  
 1920  
 aagaaatgga tggacatctt cagagagtgt gaccaggacc attcaggcac cttgaactcc  
 1980  
 tatgagatgc gcctggttat tgagaaagca ggcataaagc tgaacaacaa ggtaatgcag  
 2040  
 gtctctggtg ccaggatgac agatgatggc ctgatcatag actttgacag cttcatcagc  
 2100  
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 2160  
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 2220  
 tgtaggagcc tggatcatct taccagcagc agcagcagcg aggttctagc ccaggagggg  
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 2340

<210> 930

<211> 702

<212> PRT

<213> Homo sapiens

<400> 930

Met	Val	Ala	His	Ile	Asn	Asn	Ser	Arg	Leu	Lys	Ala	Lys	Gly	Val	Gly
1				5					10					15	
Gln	His	Asp	Asn	Ala	Gln	Asn	Phe	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Leu
			20					25					30		
Arg	Ala	Ala	Cys	Leu	Arg	Lys	Gly	Glu	Leu	Phe	Glu	Asp	Pro	Leu	Phe

```

      35      40      45
Pro Ala Glu Pro Ser Ser Leu Gly Phe Lys Asp Leu Gly Pro Asn Ser
  50      55      60
Lys Asn Val Gln Asn Ile Ser Trp Gln Arg Pro Lys Asp Ile Ile Asn
  65      70      75      80
Asn Pro Leu Phe Ile Met Asp Gly Ile Ser Pro Thr Asp Ile Cys Gln
      85      90      95
Gly Ile Leu Gly Asp Cys Trp Leu Leu Ala Ala Ile Gly Ser Leu Thr
      100      105      110
Thr Cys Pro Lys Leu Leu Tyr Arg Val Val Pro Arg Gly Gln Ser Phe
      115      120      125
Lys Lys Asn Tyr Ala Gly Ile Phe His Phe Gln Ile Trp Gln Phe Gly
      130      135      140
Gln Trp Val Asn Val Val Asp Asp Arg Leu Pro Thr Lys Asn Asp
      145      150      155      160
Lys Leu Val Phe Val His Ser Thr Glu Arg Ser Glu Phe Trp Ser Ala
      165      170      175
Leu Leu Glu Lys Ala Tyr Ala Lys Leu Ser Gly Ser Tyr Glu Ala Leu
      180      185      190
Ser Gly Gly Ser Thr Met Glu Gly Leu Glu Asp Phe Thr Gly Gly Val
      195      200      205
Ala Gln Ser Phe Gln Leu Gln Arg Pro Pro Gln Asn Leu Leu Arg Leu
      210      215      220
Leu Arg Lys Ala Val Glu Arg Ser Ser Leu Met Gly Cys Ser Ile Glu
      225      230      235      240
Val Thr Ser Asp Ser Glu Leu Glu Ser Met Thr Asp Lys Met Leu Val
      245      250      255
Arg Gly His Ala Tyr Ser Val Thr Gly Leu Gln Asp Val His Tyr Arg
      260      265      270
Gly Lys Met Glu Thr Leu Ile Arg Val Arg Asn Pro Trp Gly Arg Ile
      275      280      285
Glu Trp Asn Gly Ala Trp Ser Asp Ser Ala Arg Glu Trp Glu Glu Val
      290      295      300
Ala Ser Asp Ile Gln Met Gln Leu Leu His Lys Thr Glu Asp Gly Glu
      305      310      315      320
Phe Trp Met Ser Tyr Gln Asp Phe Leu Asn Asn Phe Thr Leu Leu Glu
      325      330      335
Ile Cys Asn Leu Thr Pro Asp Thr Leu Ser Gly Asp Tyr Lys Ser Tyr
      340      345      350
Trp His Thr Thr Phe Tyr Glu Gly Ser Trp Arg Arg Gly Ser Ser Ala
      355      360      365
Gly Gly Cys Arg Asn His Pro Gly Thr Phe Trp Thr Asn Pro Gln Phe
      370      375      380
Lys Ile Ser Leu Pro Glu Gly Asp Asp Pro Glu Asp Asp Ala Glu Gly
      385      390      395      400
Asn Val Val Val Cys Thr Cys Leu Val Ala Leu Met Gln Lys Asn Trp
      405      410      415
Arg His Ala Arg Gln Gln Gly Ala Gln Leu Gln Thr Ile Gly Phe Val
      420      425      430
Leu Tyr Ala Val Pro Lys Glu Phe Gln Asn Ile Gln Asp Val His Leu
      435      440      445
Lys Lys Glu Phe Phe Thr Lys Tyr Gln Asp His Gly Phe Ser Glu Ile
      450      455      460
Phe Thr Asn Ser Arg Glu Val Ser Ser Gln Leu Arg Leu Pro Pro Gly

```



```

465          470          475          480
Glu Tyr Ile Ile Ile Pro Ser Thr Phe Glu Pro His Arg Asp Ala Asp
          485          490          495
Phe Leu Leu Arg Val Phe Thr Glu Lys His Ser Glu Ser Trp Glu Leu
          500          505          510
Asp Glu Val Asn Tyr Ala Glu Gln Leu Gln Glu Lys Val Ser Glu
          515          520          525
Asp Asp Met Asp Gln Asp Phe Leu His Leu Phe Lys Ile Val Ala Gly
          530          535          540
Glu Gly Lys Glu Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu Asn Arg
545          550          555          560
Met Ala Ile Lys Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly Leu Asp
          565          570          575
Ala Cys Arg Cys Met Ile Asn Leu Met Asp Lys Asp Gly Ser Gly Lys
          580          585          590
Leu Gly Leu Leu Glu Phe Lys Ile Leu Trp Lys Lys Leu Lys Lys Trp
          595          600          605
Met Asp Ile Phe Arg Glu Cys Asp Gln Asp His Ser Gly Thr Leu Asn
          610          615          620
Ser Tyr Glu Met Arg Leu Val Ile Glu Lys Ala Gly Ile Lys Leu Asn
625          630          635          640
Asn Lys Val Met Gln Val Leu Val Ala Arg Tyr Ala Asp Asp Gly Leu
          645          650          655
Ile Ile Asp Phe Asp Ser Phe Ile Ser Cys Phe Leu Arg Leu Lys Thr
          660          665          670
Met Phe Thr Phe Phe Leu Thr Met Asp Pro Lys Asn Thr Gly His Ile
          675          680          685
Cys Leu Ser Leu Glu Gln Trp Leu Gln Met Thr Met Trp Gly
          690          695          700

```

<210> 931  
 <211> 297  
 <212> DNA  
 <213> Homo sapiens

```

<400> 931
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acgaccgatc acaagacccg ctggtacgcc gagaagcagt acgccgagct cgtgggtgag
120
gatgtcaaga tccgagagtg gctccacaag aatctggagc gcgcgggtct ttcgtccatc
180
gagatcgagc gtcgctccga gcgcgtgacc attttccttt acgccgctcg cccgggcatc
240
gttatcgggc gcaatggccg ggaggccgag cgcgtgcn ntagagctcga aaagctt
297

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<210> 932  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

```

<400> 932
Met Gly Gln Lys Ile Asn Pro His Gly Phe Arg Leu Gly Val Thr Thr

```

```

1           5           10           15
Asp His Lys Thr Arg Trp Tyr Ala Glu Lys Gln Tyr Ala Glu Leu Val
                20           25           30
Gly Glu Asp Val Lys Ile Arg Glu Trp Leu His Lys Asn Leu Glu Arg
                35           40           45
Ala Gly Leu Ser Ser Ile Glu Ile Glu Arg Arg Ser Glu Arg Val Thr
                50           55           60
Ile Phe Leu Tyr Ala Ala Arg Pro Gly Ile Val Ile Gly Arg Asn Gly
65           70           75           80
Arg Glu Ala Glu Arg Val Arg Xaa Glu Leu Glu Lys Leu
                85           90

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<210> 933  
 <211> 305  
 <212> DNA  
 <213> Homo sapiens

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<400> 933
nnacgcgtcg ccaagctggt gatggccgaa tacaaggggc tcaacgtcat cgtcaaaacc
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tccgccgatc cggaagcca agccaatgcc gtgcaggatc tggcgggggc aggcacgcac
120
gcgctggcca tcctgccgac cgacccggat cagctgggtt cggcgatcca gcaggtcaag
180
gacgacggca agttcgtggc gctggtcgac cgtgcgcctt cgtcaacga caacacgatc
240
cgcgatctct acgtggccgg caacaaccgg gcgctcggcg aagtggcggg caaatcatg
300
ggcga
305

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<210> 934  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

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<400> 934
Xaa Arg Val Ala Lys Leu Leu Met Ala Glu Tyr Lys Gly Leu Asn Val
1           5           10           15
Ile Val Lys Thr Ser Ala Asp Pro Ala Ser Gln Ala Asn Ala Val Gln
                20           25           30
Asp Leu Ala Gly Ala Gly Ile Asp Ala Leu Ala Ile Leu Pro Thr Asp
                35           40           45
Pro Asp Gln Leu Val Ser Ala Ile Gln Gln Val Lys Asp Asp Gly Lys
50           55           60
Phe Val Ala Leu Val Asp Arg Ala Pro Ser Val Asn Asp Asn Thr Ile
65           70           75           80
Arg Asp Leu Tyr Val Ala Gly Asn Asn Pro Ala Leu Gly Glu Val Ala
                85           90           95
Gly Lys Phe Met Gly
                100

```

<210> 935  
 <211> 333

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 935

acgcgtgaag ggctgatgag tgctatgaaa aagccagggg cccgaggaca ctgggggtgga  
60  
caggctcccc tggggaagtc ctcttagaac tgagggatca acactggagg agactgcaag  
120  
gggtacggga taaatgttcc tggatgaagga aacagcaggg gcaaaggccc tgcagcagaa  
180  
aggagcagagg ccctttggag taacagaaag accatgggtga caggagctca gaaagaccac  
240  
tggtgttaag actataagcc agtggaggcc agattgggga atgggatggg aggggtgctt  
300  
gaagaccatg gtgaggctct cttggtcttt act  
333

&lt;210&gt; 936

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 936

Met	Val	Phe	Lys	His	Pro	Ser	His	Pro	Ile	Pro	Gln	Ser	Gly	Leu	His
1			5					10						15	
Trp	Leu	Ile	Val	Leu	Thr	Pro	Val	Val	Phe	Leu	Ser	Ser	Cys	His	His
			20					25					30		
Gly	Leu	Ser	Val	Thr	Pro	Lys	Gly	Leu	Ala	Pro	Phe	Cys	Cys	Arg	Ala
			35				40					45			
Phe	Ala	Pro	Ala	Val	Ser	Phe	Thr	Arg	Asn	Ile	Tyr	Pro	Val	Pro	Leu
	50					55					60				
Ala	Val	Ser	Ser	Ser	Val	Asp	Pro	Ser	Val	Leu	Arg	Gly	Leu	Pro	Gln
65					70					75				80	
Gly	Ser	Leu	Ser	Thr	Pro	Val	Ser	Ser	Gly	Pro	Trp	Leu	Phe	His	Ser
			85					90						95	
Thr	His	Gln	Pro	Phe	Thr	Arg									
			100												

&lt;210&gt; 937

&lt;211&gt; 464

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 937

nnnttatctg cggaggggggt ggccaccctg cccacactca tgctgcaggc ctccaccgac  
60  
ccggcggagc acgagctcaa ggatctgttg acggccgacc tcatggacca gcacaacctc  
120  
gaccgtgccc tggcagggtt gcgtgccagt cactcatcgc acgaagctcg cgccgagggtg  
180  
cagcggcgtg ccgatctcgc ccgtggccat ctgcgccatcc ttcccgcagg cgatgcccgt  
240  
acggcgttgg agaccctgtg cgacgagggtg ggttccccggg cggcctgaac cccgaccctg  
300

ccagntcgcg tcccatctcc tggccgggac cgtccagcg tctgctctct gacagctcat  
 360  
 cgttcttccg acaccaagga gtttctcgtg gcccgctcatc tcgatctcat cggcattggg  
 420  
 cccggcaacc cggactggat caccctggct gccgtcaagg ccan  
 464

<210> 938  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 938  
 Xaa Leu Ser Ala Glu Gly Val Ala Thr Leu Pro Thr Leu Met Leu Gln  
 1 5 10 15  
 Ala Ser Thr Asp Pro Ala Asp Asp Glu Leu Lys Asp Leu Leu Thr Ala  
 20 25 30  
 Asp Leu Met Asp Gln His Asn Leu Asp Arg Ala Leu Ala Gly Leu Arg  
 35 40 45  
 Ala Ser His Val Ile Asp Glu Ala Arg Ala Glu Val Gln Arg Arg Ala  
 50 55 60  
 Asp Leu Ala Arg Gly His Leu Ala Ile Leu Pro Ala Gly Asp Ala Arg  
 65 70 75 80  
 Thr Ala Leu Glu Thr Leu Cys Asp Glu Val Gly Ser Arg Ala Ala  
 85 90 95

<210> 939  
 <211> 385  
 <212> DNA  
 <213> Homo sapiens

<400> 939  
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 ggactgctgc cggctcgaggt ggacttcgcc gccacgaaga cccttgccctt gtcgcacggg  
 120  
 acatggcggg ggatcgaggt tgggtggctat gaaatccatc acgggctct gtcgttcgct  
 180  
 gaggacgctg aagccttcct cgacggcgta cacgtcggtc cggatatggg gacgatgtgg  
 240  
 cacggggcat tcgagcacga cgaattccgt cgcacgtggc tggctgacgc ggcccgtcac  
 300  
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 360  
 atgatcgaaa ccctcgccga cgcgt  
 385

<210> 940  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 940  
 Xaa Thr Ile Leu Asp Pro Asp Gly Gln Glu Thr Thr Pro Gly Ser Val

```

      1           5           10           15
Ile Glu Gly Leu Gly Leu Leu Pro Val Glu Val Asp Phe Ala Ala Thr
      20           25           30
Lys Thr Leu Ala Leu Ser His Gly Thr Trp Arg Gly Ile Glu Val Gly
      35           40           45
Gly Tyr Glu Ile His His Gly Arg Leu Ser Phe Ala Glu Asp Ala Glu
      50           55           60
Ala Phe Leu Asp Gly Val His Val Gly Pro Val Trp Gly Thr Met Trp
      65           70           75           80
His Gly Ala Phe Glu His Asp Glu Phe Arg Arg Thr Trp Leu Ala Asp
      85           90           95
Ala Ala Arg His Ala Gly Ser Ser Trp Arg Pro His Ser Asp Glu Leu
      100          105          110
Gly Tyr Gln Ala Arg Arg Glu Ala Met Ile Glu Thr Leu Ala Asp Ala
      115          120          125

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<210> 941  
 <211> 348  
 <212> DNA  
 <213> Homo sapiens

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<400> 941
atcttctggt cggcggtgat cacgctggtg accatcggcc tgctgtttgc cggcaacttc
60
gaagccatgc aaaccatggt cgtgctggcc gggctgccgt tctcgggtgt gctgattttc
120
ttcatgttcg gtttgcacaa ggcgatgcgc caggacgtgg ccatggagca ggagcaggca
180
caattggctg aacgtggtcg ccgtggtttc agcgagcgcc tgaccgcgct ggacctgcaa
240
ccgagccagg gcaccgtgca acgctttatg gacaaacatg tgacgccggc gttggaacaa
300
gcggcgactg cgttgctga tcaagggctg gaagtgcaga ccctgctt
348

```

<210> 942  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

```

<400> 942
Ile Phe Trp Ser Ala Val Ile Thr Leu Val Thr Ile Gly Leu Leu Phe
1           5           10           15
Ala Gly Asn Phe Glu Ala Met Gln Thr Met Val Val Leu Ala Gly Leu
      20           25           30
Pro Phe Ser Val Val Leu Ile Phe Met Phe Gly Leu His Lys Ala
      35           40           45
Met Arg Gln Asp Val Ala Met Glu Gln Glu Ala Gln Leu Ala Glu
      50           55           60
Arg Gly Arg Arg Gly Phe Ser Glu Arg Leu Thr Ala Leu Asp Leu Gln
      65           70           75           80
Pro Ser Gln Gly Thr Val Gln Arg Phe Met Asp Lys His Val Thr Pro
      85           90           95
Ala Leu Glu Gln Ala Ala Thr Ala Leu Arg Asp Gln Gly Leu Glu Val

```

100  
Gln Thr Leu Leu  
115

105

110

<210> 943  
<211> 439  
<212> DNA  
<213> Homo sapiens

<400> 943  
ccatggcagg agcagagcag atagagcagg acctcgtctc cttctctttg cattttgtgc  
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ctcctctaata gcatcctggg ctctgtctaa ccctgtggga aacaccgtct cttctctcct  
120  
ttgccctctt ctgtgatcac atcctcactt ctgagcctat ctgcccattc agtcaatccc  
180  
ccttggttct gggatgctat ttccctggcc gcctccctct aggagtgttt agaaccctca  
240  
ctgtgggcag aagggaggga agatggctga ggtacctgga aagggacgtg tggatccccg  
300  
ggcatggaag gaaggaggca ggagagctag aaaaagggat gagatctaata gttccctaag  
360  
gaacctggct tagtgctggc ccttcacata ctgagacatg gaatccttac tactgttctc  
420  
tgaggaaaga ggctgttcc  
439

<210> 944  
<211> 118  
<212> PRT  
<213> Homo sapiens

<400> 944  
Met Ala Gly Ala Glu Gln Ile Glu Gln Asp Leu Val Ser Phe Ser Leu  
1 5 10 15  
His Phe Val Pro Pro Leu Met His Pro Gly Leu Leu Leu Thr Leu Trp  
20 25 30  
Glu Thr Pro Ser Leu Leu Ser Phe Ala Leu Phe Cys Asp His Ile Leu  
35 40 45  
Thr Ser Glu Pro Ile Cys Pro Ser Ser Gln Ser Pro Leu Val Leu Gly  
50 55 60  
Cys Tyr Phe Pro Gly Arg Leu Pro Leu Gly Val Phe Arg Thr Leu Thr  
65 70 75 80  
Val Gly Arg Arg Glu Gly Arg Trp Leu Arg Tyr Leu Glu Arg Asp Val  
85 90 95  
Trp Ile Pro Gly His Gly Arg Lys Glu Ala Gly Glu Leu Glu Lys Gly  
100 105 110  
Met Arg Ser Asn Val Pro  
115

<210> 945  
<211> 339  
<212> DNA  
<213> Homo sapiens

<400> 945  
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 120  
 tatatatata gcgtgtacaa caaaacatgc actgtttact cagcaccgccg tgtttgtctc  
 180  
 agcaatagct tttctaaaga actgctacta tttgaaatgg agggggagggg gggtcctgga  
 240  
 cagagtattg tgcaagttga aagtctctgg atggggctat gtatataccta ccagccaatt  
 300  
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 339

<210> 946  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 946  
 Xaa Ile Arg Glu Ala Phe His Ile Phe Phe Leu Leu Ile Ile Ser Ile  
 1 5 10 15  
 Ala Leu Tyr Val Glu Met Val Ile Tyr Ile Tyr Thr His Thr His Ile  
 20 25 30  
 Tyr Val Cys Val Cys Ile Tyr Val Tyr Ile Tyr Ser Val Tyr Asn Lys  
 35 40 45  
 Thr Cys Thr Val Tyr Ser Ala Pro Arg Val Cys Leu Ser Asn Ser Phe  
 50 55 60  
 Ser Lys Glu Leu Leu Leu Phe Glu Met Glu Gly Glu Gly Gly Pro Gly  
 65 70 75 80  
 Gln Ser Ile Val Gln Val Glu Ser Leu Trp Met Gly Leu Cys Ile Ser  
 85 90 95  
 Tyr Gln Pro Ile Trp Val Gln Ile Gly Phe Glu Gly Leu Pro Leu Ser  
 100 105 110  
 Thr

<210> 947  
 <211> 648  
 <212> DNA  
 <213> Homo sapiens

<400> 947  
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 120  
 agtagtgctg ccggctcaag cgatgcctca gcctttctgc tgtgtgcgaa gctttgcaga  
 180  
 ggagatgatg cttcaaagtt gtccctgttg gggatgagca gccaggcctt tataactgga  
 240  
 gacagtcagt catggatacg tggatactct ggaaaccctc atccctggag gtctgagccc  
 300

ctggatacca tggccttctt aggcctggagt tgctgccctt gtccatttac cataaaaatt  
 360  
 ggacaagaga ataccaggac acacctgagt ttctcatcgt atgctaaacc tgttcttcca  
 420  
 cgtacatccc caatgtgtac agccctactt tttctgctg atcaagttca attacttctg  
 480  
 ctaagatggg gactattctt gcctgctggg ccttggatgc aaggacccca atgttcaggc  
 540  
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 648

<210> 948

<211> 154

<212> PRT

<213> Homo sapiens

<400> 948

Met	Glu	Met	Ser	Gly	Gln	Gln	Val	Tyr	Gly	Val	Leu	Val	Ala	Ser	His
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Leu	Cys	Thr	Gly	Val	Gly	Lys	Glu	Trp	Thr	Gly	Val	Asp	Lys	Ser	Ser
			20					25					30		
Ser	Ala	Ala	Gly	Ser	Ser	Asp	Ala	Ser	Ala	Phe	Leu	Leu	Cys	Ala	Lys
		35					40					45			
Leu	Cys	Arg	Gly	Asp	Asp	Ala	Ser	Lys	Leu	Ser	Leu	Leu	Gly	Met	Ser
		50				55					60				
Ser	Gln	Ala	Phe	Ile	His	Trp	Asp	Ser	Gln	Ser	Trp	Ile	Arg	Gly	Tyr
65					70					75				80	
Ser	Gly	Asn	Pro	His	Pro	Trp	Arg	Ser	Glu	Pro	Leu	Asp	Thr	Met	Pro
			85						90					95	
Phe	Leu	Gly	Trp	Ser	Cys	Cys	Pro	Cys	Pro	Phe	Thr	Ile	Lys	Ile	Gly
			100					105						110	
Gln	Glu	Asn	Thr	Arg	Thr	His	Leu	Ser	Phe	Ser	Ser	Tyr	Ala	Lys	Pro
		115					120					125			
Val	Leu	Pro	Arg	Thr	Ser	Pro	Met	Cys	Thr	Ala	Leu	Leu	Phe	Ser	Ala
		130					135					140			
Asp	Gln	Val	Gln	Leu	Leu	Leu	Leu	Arg	Trp						
145							150								

<210> 949

<211> 661

<212> DNA

<213> Homo sapiens

<400> 949

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 120  
 atatgctgta acgtttctta acctaggaca gattcaagaa catggctcat cttatattcg  
 180  
 aggctgtgct tttcaccatg gcttctctcc agcaattggg gtatttggga cagatggatt  
 240



ggacatagat gacaacatca ttcactttac agtgggggaa ggcataagaa tatgggggaa  
 300  
 tgccaaccga gtccgaggga atttgattgc actttcggtt tggccaggaa cctatcagaa  
 360  
 cagaaaagat ttaagttcaa ctctctggca tgcagcaatt gagataaata gagggaccaa  
 420  
 tacagtttta cagaataatg tagtggctgg atttgggaaga gcaggatacc gcattgatgg  
 480  
 tgaaccttgc ccaggccagt ttaatcctgt ggaaaagtgg tttgacaatg aagcccatgg  
 540  
 aggtttatat gggatctata tgaaccaaga tggccttcct ggatgttctc ttatacaagg  
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 661

<210> 950  
 <211> 210  
 <212> PRT  
 <213> Homo sapiens

<400> 950  
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 His Ser Gly Gln Glu Gly Phe Arg Asp Ser Thr Asp Pro Arg Tyr Ala  
 20 25 30  
 Val Thr Phe Leu Asn Leu Gly Gln Ile Gln Glu His Gly Ser Ser Tyr  
 35 40 45  
 Ile Arg Gly Cys Ala Phe His His Gly Phe Ser Pro Ala Ile Gly Val  
 50 55 60  
 Phe Gly Thr Asp Gly Leu Asp Ile Asp Asp Asn Ile Ile His Phe Thr  
 65 70 75 80  
 Val Gly Glu Gly Ile Arg Ile Trp Gly Asn Ala Asn Arg Val Arg Gly  
 85 90 95  
 Asn Leu Ile Ala Leu Ser Val Trp Pro Gly Thr Tyr Gln Asn Arg Lys  
 100 105 110  
 Asp Leu Ser Ser Thr Leu Trp His Ala Ala Ile Glu Ile Asn Arg Gly  
 115 120 125  
 Thr Asn Thr Val Leu Gln Asn Asn Val Val Ala Gly Phe Gly Arg Ala  
 130 135 140  
 Gly Tyr Arg Ile Asp Gly Glu Pro Cys Pro Gly Gln Phe Asn Pro Val  
 145 150 155 160  
 Glu Lys Trp Phe Asp Asn Glu Ala His Gly Gly Leu Tyr Gly Ile Tyr  
 165 170 175  
 Met Asn Gln Asp Gly Leu Pro Gly Cys Ser Leu Ile Gln Gly Phe Thr  
 180 185 190  
 Ile Trp Thr Cys Trp Asp Tyr Gly Ile Tyr Phe Gln Thr Thr Glu Ser  
 195 200 205  
 Val His  
 210

<210> 951  
 <211> 2615

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 951

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120  
agcttcagcc tgactcgggt ggattgtagc ggctggggcc ccacatcat gccggtgccc  
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300  
ctcaccagca tctcaccac tgccttctcc cgccttcgct acctggagtc gcttgacctc  
360  
agccacaatg gcctgacagc cctgccagcc gagagcttca ccagctcacc cctgagcgac  
420  
gtgaacctta gccacaacca gctccgggag gtctcagtgt ctgccttcac gacgcacagt  
480  
cagggccggg cactacacgt ggacctctcc cacaacctct caccgcctcg tgccccaccc  
540  
cacgagggcc ggctgcctg cgcaccat tcagagcctg aacctggcct ggaaccggct  
600  
ccatgcctg cccaacctcg agacttgccc ctgcgctacc tgagcctgga tgggaacctt  
660  
ctagctgtca ttggtccggg tgccttcgcg gggctgggag gccttacaca cctgtctctg  
720  
gccagcctgc agaggctccc tgagctggcg ccagtggt tccgtgagct accgggcctg  
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840  
ggcctgagct cctgcagga gctggacctt tcgggcacca acctggtgcc cctgcctgag  
900  
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960  
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1020  
ctgcactgcy tagacacccg ggaatctgct gccaggggccc ccaccatctt gtgacaaatg  
1080  
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1320  
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1380  
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1440  
caggtccact gggctgagtg tccccttggg cccatggccc agtcactcag gggcgagttt  
1500

cttttctaac atagcccttt ctttgccatg aggccatgag gcccgttca tccttttcta  
 1560  
 tttccctaga accttaatgg tagaaggaat tgcaaagaat caagtccacc cttctcatgt  
 1620  
 gacagatggg gaaactgagg ccttgagaag gaaaaaggct aatctaagtt cctgcgggca  
 1680  
 gtggcatgac tggagcacag cctcctgcct ccagcccg acccaatgca ctttcttgtc  
 1740  
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 1800  
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 1860  
 tctgaccagc tgtgcggcat gggctaagtc actctgccct tcggagcctc tggaagctta  
 1920  
 gggcacattg gttccagcct agccagtttc tcaccctggg ttgggggtccc ccagcatcca  
 1980  
 gactggaaac ctaccattt tccctgagc atcctctaga tgctgcccc aggagtgtgt  
 2040  
 gcagttctgg agcctcatct ggctgggatc tccaaggggc ctcttggtt cagtccccac  
 2100  
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 2160  
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 2220  
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 2280  
 accggcctcc cctacccttg ctggccgggg atggagacat gtcatttgta aaagcagaaa  
 2340  
 aaggttgcat ttgttcactt ttgtaatat gtcttgggcc tgtgttgggg tgttggggga  
 2400  
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 2460  
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 2520  
 aataaacact ataaaatgaa gactaaggaa acagcccagg gttcgggaag tgagatgcta  
 2580  
 ccctgggggt agagcataga catgggtcgg gcaga  
 2615

&lt;210&gt; 952

&lt;211&gt; 357

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 952

Xaa	Pro	Ala	Pro	Thr	Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Ala	Val
1				5				10					15	
Ser	Gly	Ala	Gln	Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys
			20				25				30			Glu
Val	Glu	Thr	Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val
		35				40					45			Asp
Cys	Ser	Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu
	50				55				60					Asp
Thr	Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn
														Glu

65	70								75								80	
Ser Val Leu Ala Gly	Pro Gly Tyr Thr	Thr Leu Ala Gly	Leu Asp Leu															
85		90		95														
Ser His Asn Leu Leu	Thr Ser Ile Ser	Pro Thr Ala Phe	Ser Arg Leu															
100		105		110														
Arg Tyr Leu Glu Ser	Leu Asp Leu Ser	His Asn Gly Leu	Thr Ala Leu															
115		120		125														
Pro Ala Glu Ser Phe	Thr Ser Ser Pro	Leu Ser Asp Val	Asn Leu Ser															
130		135		140														
His Asn Gln Leu Arg	Glu Val Ser Val	Ser Ala Phe Thr	Thr His Ser															
145		150		155														
Gln Gly Arg Ala Leu	His Val Asp Leu	Ser His Asn Leu	Ser Pro Pro															
165		170		175														
Arg Ala Pro Pro His	Glu Gly Arg Pro	Ala Cys Ala His	His Ser Glu															
180		185		190														
Pro Glu Pro Gly Leu	Glu Pro Ala Pro	Cys Arg Ala Gln	Pro Arg Asp															
195		200		205														
Leu Pro Leu Arg Tyr	Leu Ser Leu Asp	Gly Asn Pro Leu	Ala Val Ile															
210		215		220														
Gly Pro Gly Ala Phe	Ala Gly Leu Gly	Gly Leu Thr His	Leu Ser Leu															
225		230		235														
Ala Ser Leu Gln Arg	Leu Pro Glu Leu	Ala Pro Ser Gly	Phe Arg Glu															
245		250		255														
Leu Pro Gly Leu Gln	Val Leu Asp Leu	Ser Gly Asn Pro	Lys Leu Asn															
260		265		270														
Trp Ala Gly Ala Glu	Val Phe Ser Gly	Leu Ser Ser Leu	Gln Glu Leu															
275		280		285														
Asp Leu Ser Gly Thr	Asn Leu Val Pro	Leu Pro Glu Ala	Leu Leu Leu															
290		295		300														
His Leu Pro Ala Leu	Gln Ser Val Ser	Val Gly Gln Asp	Val Arg Cys															
305		310		315														
Arg Arg Leu Val Arg	Glu Gly Thr Tyr	Pro Arg Arg Pro	Gly Ser Ser															
325		330		335														
Pro Lys Val Ala Leu	His Cys Val Asp	Thr Arg Glu Ser	Ala Ala Arg															
340		345		350														
Gly Pro Thr Ile Leu																		
355																		

<210> 953

<211> 347

<212> DNA

<213> Homo sapiens

<400> 953

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120
tgttgtacct ggcggctctg cggagtaacc gctgcggaaca cacagtagga cgggagggag
180
aagccattgc gtttcaccct ttcattggccc ttcctttccc cttccaagtg agctctttga
240
ggtgagtcac ggagggcagt gtccctctgc atcctgtctg gggttgtcaa atatggccaa
300

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gtgggctcca tcggggcagc ggggtggggtg ggggggtgtct gtcagag  
347

<210> 954

<211> 103

<212> PRT

<213> Homo sapiens

<400> 954

Met	Glu	Pro	Thr	Trp	Pro	Tyr	Leu	Thr	Thr	Pro	Asp	Arg	Met	Gln	Arg
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Asp	Thr	Ala	Leu	His	Asp	Ser	Pro	Gln	Arg	Ala	His	Leu	Glu	Gly	Glu
		20						25				30			
Arg	Lys	Gly	His	Glu	Arg	Val	Lys	Arg	Asn	Gly	Phe	Ser	Leu	Pro	Ser
	35						40				45				
Tyr	Cys	Val	Ser	Ala	Ala	Val	Thr	Pro	Gln	Ser	Arg	Gln	Val	Gln	Gln
	50					55				60					
Ser	Arg	His	Gly	Lys	Thr	Ser	Thr	Pro	Asn	Asp	Gly	Ser	Arg	Asp	Gly
65				70					75					80	
Glu	Ser	Val	Val	His	Thr	Leu	Arg	Gly	Asp	Pro	Arg	Glu	Thr	Gly	Leu
				85				90						95	
Arg	Thr	Gly	Met	Ala	Ser	Arg									
				100											

<210> 955

<211> 634

<212> DNA

<213> Homo sapiens

<400> 955

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120  
agggtctctgc aggtgaacgg ttctgcaggt gagcggctct gcaggtgagc ggctctgcat  
180  
gtgagtgcct ctgtgactgg ctgcgaagca gcatttgtgc acacttgact ggccacaaca  
240  
gaatgttctt ctctgttgtc agcactgagg aggaagctcc tgcctaagcg accacagcca  
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360  
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420  
agaggcctcc gttgcacaaa tcacacacct actgtgcctg acgtggctgg gcctccagca  
480  
ggaccegtct ctgagaacac acgggtgcta gtccaagtcc acagcacggc tcaagtcact  
540  
cccacaaacc tctctataca aacacacaaa gctctgggag gctaccctgc atccaagagt  
600  
caccatctca cacctggaac aagggttacg gccg  
634

<210> 956

<211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 956  
 Met Glu Ser Gly Glu Ser Asn Val Ser Met Glu Arg Val Pro Gly Cys  
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 Gly Arg Leu Gly Arg Ser Phe Leu Leu Ser Ala Asp Asn Arg Glu Glu  
 20 25 30  
 His Ser Val Val Ala Ser Gln Val Cys Thr Asn Ala Ala Cys Glu Pro  
 35 40 45  
 Val Thr Glu Ala Leu Thr Cys Arg Ala Ala His Leu Gln Ser Arg Ser  
 50 55 60  
 Pro Ala Glu Pro Phe Thr Cys Arg Ala Leu His Leu Gln Asn Arg Ser  
 65 70 75 80  
 Pro Ala Glu Pro Phe Thr Cys Arg Thr Ile His Leu Gln Ser Arg Ser  
 85 90 95  
 Pro Ala Glu Pro Phe Thr Cys Arg Ala Ala His Leu Gln Ser Pro Ser  
 100 105 110  
 Arg

<210> 957  
 <211> 823  
 <212> DNA  
 <213> Homo sapiens

<400> 957  
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 120  
 gtacctcctg gccaccagc actgcgcagc cgtggtgtcc agcctcctgg gcagcccctt  
 180  
 gcccttggaac aggtaccag ctcagactcc aggcttaggg gtccctctgg aatgatgctc  
 240  
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 300  
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 360  
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 420  
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 720  
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823

<210> 958  
<211> 105  
<212> PRT  
<213> Homo sapiens

<400> 958  
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Val Ser Gln Val Pro Thr Gly Thr Ser Pro Leu Gln Ala Phe Trp Asp  
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Pro His Trp Leu Arg Trp Ala Leu His Ser Thr Pro Thr Gly Lys Leu  
35 40 45  
Leu Phe Leu Pro Ser Ser Lys Val Pro Lys Leu Pro Gly Cys Ser Val  
50 55 60  
Gly Pro Arg Leu Gln His Thr Leu Glu Ala Ala Pro His Pro Val Ser  
65 70 75 80  
Trp Phe Arg Leu Leu Gln Ala Leu Ser Ser Ala Gly His Pro Leu Leu  
85 90 95  
Pro Val Ser Arg Pro Leu Gly Thr Ala  
100 105

<210> 959  
<211> 586  
<212> DNA  
<213> Homo sapiens

<400> 959  
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acagtggtag gcctgatcac cgacaacgat gaggcagcct atagggagga ggtagagac  
120  
ctggcagtgt ggtgccagga taacaacctc tccctcaacg tgatcaagac cacgaagatg  
180  
atcgtggact acaggaaaag gagggtcgag cagccccca ttctcattga tggggctgta  
240  
tgggagccag ttgagagctt caagttcctt ggtgtccaca tcaccatcga actatcatgg  
300  
tccaaacaca ccaagacagt agtgaagagg gtgcgacaat gcctattcca cctcggtaga  
360  
caaaaaagat ttggaatgga tcctcagacc ctcaaaaagt ttgacatcta caccatcgag  
420  
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480  
gcactacaga gggtagtgcg tacggcccag tacatcactg gggctaagct tcctgccatc  
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586

<210> 960  
<211> 195  
<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 960

Xaa His Asp Cys Met Ala Lys His Asp Ser Asn Thr Ile Ile Lys Phe  
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 20 25 30  
 Ala Tyr Arg Glu Glu Val Arg Asp Leu Ala Val Trp Cys Gln Asp Asn  
 35 40 45  
 Asn Leu Ser Leu Asn Val Ile Lys Thr Thr Lys Met Ile Val Asp Tyr  
 50 55 60  
 Arg Lys Arg Arg Val Glu His Ala Pro Ile Leu Ile Asp Gly Ala Val  
 65 70 75 80  
 Trp Glu Pro Val Glu Ser Phe Lys Phe Leu Gly Val His Ile Thr Ile  
 85 90 95  
 Glu Leu Ser Trp Ser Lys His Thr Lys Thr Val Val Lys Arg Val Arg  
 100 105 110  
 Gln Cys Leu Phe His Leu Gly Arg Gln Lys Arg Phe Gly Met Asp Pro  
 115 120 125  
 Gln Thr Leu Lys Lys Phe Asp Ile Tyr Thr Ile Glu Ser Ile Met Thr  
 130 135 140  
 Gly Cys Ile Thr Ala Trp Tyr Gly Asn Cys Ser Ala Ser Asp Arg Lys  
 145 150 155 160  
 Ala Leu Gln Arg Val Val Arg Thr Ala Gln Tyr Ile Thr Gly Ala Lys  
 165 170 175  
 Leu Pro Ala Ile Gln Asp Leu Tyr Thr Arg Arg Cys Gln Arg Lys Thr  
 180 185 190  
 Leu Thr Ile  
 195

&lt;210&gt; 961

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 961

acgcgttgtc gtctctccgt agaccattca gtttggaaca acttccactg gagtctgtgc  
 60  
 atgactggat ggtctctttg acagccctgt caaggaatac caacagaata ttgattctcc  
 120  
 taaactgtat agtaacctgc taaccagtcg gaaagagcta ccaccaatg gagatactaa  
 180  
 atccatggta atggaccatc gagggcaacc tccagagttg gctgctcttc ccactcctga  
 240  
 gtctacacc gtgcttcacc agaagacct gcaggccatg aagagccact cagaaaaggc  
 300  
 ccatggccat ggagcttcaa ggaaagaaac cctcagttt tttccgteta gtccgccacc  
 360  
 tcattcccca ataagtcag ggcatatccc cagtgccatt gttcttccaa atgctaccca  
 420  
 tgactacaac acgtctttct caaactccaa tgctcacaaa gctgaaaaga agcttcaaaa  
 480  
 cattgatcac ccttcacgc gt  
 502



<210> 962  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 962  
 Met Val Met Asp His Arg Gly Gln Pro Pro Glu Leu Ala Ala Leu Pro  
 1 5 10 15  
 Thr Pro Glu Ser Thr Pro Val Leu His Gln Lys Thr Leu Gln Ala Met  
 20 25 30  
 Lys Ser His Ser Glu Lys Ala His Gly His Gly Ala Ser Arg Lys Glu  
 35 40 45  
 Thr Pro Gln Phe Phe Pro Ser Ser Pro Pro Pro His Ser Pro Ile Ser  
 50 55 60  
 His Gly His Ile Pro Ser Ala Ile Val Leu Pro Asn Ala Thr His Asp  
 65 70 75 80  
 Tyr Asn Thr Ser Phe Ser Asn Ser Asn Ala His Lys Ala Glu Lys Lys  
 85 90 95  
 Leu Gln Asn Ile Asp His Pro Phe Thr Arg  
 100 105

<210> 963  
 <211> 1298  
 <212> DNA  
 <213> Homo sapiens

<400> 963  
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 120  
 acgccaccca gggccagtcg ggtctgctca cagcccagag aggccgcgtg tccagccgcg  
 180  
 ggcaagagac agagcaggtc cctgtgtatc caagtcctg agcccgtag accggcccca  
 240  
 ggccctgtag agagccagca gccaccatgg cgaaggagga agatgaggag aagaaagcca  
 300  
 agaaagggaa gaaggggaag aaggcaccgg acccgagaa gcccaaacgg agcctgaagg  
 360  
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 420  
 agttccgcag cgcctcgcc ttcttctggg gcctccacac cggccccac aagaccaagc  
 480  
 gcacgaggaa ggccgcacc gtgctcgggt acacgtcaga gcttatgacg cacatgcgca  
 540  
 tgggcaagaa gaagcgggag atgaagggca agaagccgtc cttcatgggtg atccgcttcc  
 600  
 caggccgcgc tggctacggc cgcctgcggc cgcgcgccc gtcactcagc aaagcgtcca  
 660  
 cggccatcaa ctggctcaca aaaaagttcc tcctcaagaa ggccgaggag tcgggcagcg  
 720  
 aacaggccac agtggacgcc tggctgcagc gctcgagctc ccgcatgggc tcccgcaaac  
 780

tccccctccc gtcgggtgcc gagatcctgc ggcctggggg ccggctccgg aggttcccc  
 840  
 gcagccgcag catctacgcg tcaggcgagc cctgggctt cctgcccttc gaggacgagg  
 900  
 cccattcca tcaactcggc tcccgaagt cgctgtacgg gcttgagggc ttccaggacc  
 960  
 tgggcgagta ttatgactat caccgcgacg gcgacgacta ctacgaccgg cagtactcc  
 1020  
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 1080  
 caccctacgg cgaccactac tacgggtacc cgcccaggga tccctacgac tactaccacc  
 1140  
 ccgactatta cgggtggcccc gttgatccgg ggtacaccta cggctacggc tacgacgatt  
 1200  
 acgaaccccc atatgcgcc ccgtcggggg actcgtctcc ttacagctac cacgatgggt  
 1260  
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 1298

<210> 964

<211> 235

<212> PRT

<213> Homo sapiens

<400> 964

Ser	Ala	Ser	Gln	Ala	Ala	Val	Ala	Thr	Ala	Ala	Cys	Gly	Arg	Ala	Pro
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Gly	His	Ser	Ala	Lys	Arg	Pro	Arg	Pro	Ser	Thr	Gly	Ser	Gln	Lys	Ser
			20					25					30		
Ser	Ser	Ser	Arg	Arg	Pro	Arg	Ser	Arg	Ala	Ala	Asn	Arg	Pro	Gln	Trp
		35					40					45			
Thr	Pro	Gly	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Trp	Ala	Pro	Ala	Asn	Ser
	50					55					60				
Pro	Ser	Arg	Arg	Val	Pro	Arg	Ser	Cys	Gly	Leu	Gly	Ala	Gly	Ser	Gly
65				70					75					80	
Gly	Ser	Pro	Ala	Ala	Ala	Ala	Ser	Thr	Arg	Gln	Ala	Ser	Pro	Trp	Ala
			85						90					95	
Ser	Cys	Pro	Ser	Arg	Thr	Arg	Pro	His	Ser	Ile	Thr	Arg	Ala	Pro	Ala
		100						105					110		
Ser	Arg	Cys	Thr	Gly	Leu	Arg	Ala	Ser	Arg	Thr	Trp	Ala	Ser	Ile	Met
		115					120					125			
Thr	Ile	Thr	Ala	Thr	Ala	Thr	Thr	Thr	Thr	Gly	Ser	His	Ser	Thr	
	130					135					140				
Ala	Thr	Arg	Ser	Arg	Asn	Pro	Thr	Trp	Arg	Ala	Ser	Ala	Pro	Thr	Ala
145					150				155					160	
Arg	Pro	Gly	His	Pro	Thr	Ala	Thr	Thr	Thr	Thr	Gly	Thr	Arg	Pro	Arg
			165						170					175	
Ile	Pro	Thr	Thr	Thr	Thr	Thr	Pro	Thr	Ile	Thr	Val	Ala	Pro	Leu	Ile
		180						185				190			
Arg	Gly	Thr	Pro	Thr	Ala	Thr	Ala	Thr	Thr	Ile	Thr	Asn	Pro	His	Met
	195					200						205			
Arg	Pro	Arg	Arg	Gly	Thr	Arg	Leu	Leu	Thr	Ala	Thr	Thr	Met	Gly	Thr
	210					215					220				
Arg	Ala	Arg	Arg	Thr	Leu	Met	Ala	Thr	Thr	Trp					

225

230

235

&lt;210&gt; 965

&lt;211&gt; 336

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 965

nnngtgacca ttatgggtgg tgcccgtaacc cgtgaagtgg aaggcgttga ttttgttggc  
 60  
 cgggtcagcg atgccgaaaa ggctgaaatc ctgcggccgcg ccgatgtgta tgtcgccccc  
 120  
 aataccggcg gtgagagctt tggcattgtc ttggtggaag ccattggcggc aggcgcagcc  
 180  
 gttgttgctt cagacttgga ggccttcgc gcagtgtgca acgccgattc cgatgatgtt  
 240  
 gccggcgcgc tatatcgcaa tgaggatagt aatgaccttg ctctgtgtact caacgaggtg  
 300  
 ctgcaggatc ctgagtatcg tgcccgctta gtgcac  
 336

&lt;210&gt; 966

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 966

Xaa	Val	Thr	Ile	Met	Gly	Gly	Ala	Arg	Thr	Arg	Glu	Val	Glu	Gly	Val
1				5				10					15		
Asp	Phe	Val	Gly	Arg	Val	Ser	Asp	Ala	Glu	Lys	Ala	Glu	Ile	Leu	Gly
		20					25					30			
Arg	Ala	Asp	Val	Tyr	Val	Ala	Pro	Asn	Thr	Gly	Gly	Glu	Ser	Phe	Gly
		35				40					45				
Ile	Val	Leu	Val	Glu	Ala	Met	Ala	Ala	Gly	Ala	Ala	Val	Val	Ala	Ser
	50				55				60						
Asp	Leu	Glu	Ala	Phe	Arg	Ala	Val	Cys	Asn	Ala	Asp	Ser	Asp	Asp	Val
65				70				75				80			
Ala	Gly	Ala	Leu	Tyr	Arg	Asn	Glu	Asp	Ser	Asn	Asp	Leu	Ala	Arg	Val
		85				90						95			
Leu	Asn	Glu	Val	Leu	Glu	Asp	Pro	Glu	Tyr	Arg	Ala	Arg	Leu	Val	His
	100					105						110			

&lt;210&gt; 967

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 967

ncaaattggca attcatagcc cgccagatcg gacacggagc tgggtggtatc cacggattcg  
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 ggcgcggagg cgtcgggctc aagctccgct tcggcaccgg tcggcactga ggaatctccg  
 120  
 tcggcctccg ctteggccgc agcctgggct gcgccagact ctgcgggagg caccttctcc  
 180

cgggttcgcc agccaaatgg cgttgcaggc tccagcatcc agtccggtgc cttcggcacc  
 240  
 cccgcactgc gcagagaggc cgccagaaac gatggcaccg gcggcgcggg aggtgatata  
 300  
 ggcgcttcgg ccggagcgct cacggactcc ggcactacag gtgcagcttg cgcttctg  
 360  
 ggcggagcaa cagggtcact tcgaggcggg gat  
 393

<210> 968  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 968  
 Pro Ala Arg Ser Asp Thr Glu Leu Val Val Ser Thr Asp Ser Gly Ala  
 1 5 10 15  
 Glu Ala Ser Gly Ser Ser Ser Ala Ser Ala Pro Val Gly Thr Glu Glu  
 20 25 30  
 Ser Pro Ser Ala Ser Ala Ser Ala Ala Ala Trp Ala Ala Pro Asp Ser  
 35 40 45  
 Ala Gly Gly Thr Phe Ser Arg Val Arg Gln Pro Asn Gly Val Ala Gly  
 50 55 60  
 Ser Ser Ile Gln Ser Gly Ala Phe Gly Thr Pro Ala Leu Arg Arg Glu  
 65 70 75 80  
 Ala Ala Arg Asn Asp Gly Thr Gly Gly Ala Gly Gly Asp Thr Gly Ala  
 85 90 95  
 Ser Ala Gly Ala Leu Thr Asp Ser Gly Thr Thr Gly Ala Ala Cys Ala  
 100 105 110  
 Ser Cys Gly Gly Ala Thr Gly Ser Leu Arg Gly Gly Asp  
 115 120 125

<210> 969  
 <211> 880  
 <212> DNA  
 <213> Homo sapiens

<400> 969  
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 ttatccttac atgtattgca gaggatcaat atgaccatgc atttttgcac gatgatcaac  
 120  
 atgaattttc gagtaaaactt acatagaatg cctatgagac acaggaagaa ggcagcagac  
 180  
 aagaatctta ccctgccgtc tttagtatgt gaagtactgg acctgatggt agagtttatt  
 240  
 gtaacacaca tgatgaagga gtttcctatg gatctctata tacgctgcat ccaggtagta  
 300  
 cacaaactgc tctgctacca gaagaagtgt cgggtacgcc tgcattacac ctggcgaggag  
 360  
 ctctggtcag ccttgataaa tttgctgaag ttccttatgt caaatgagac tgtacttttg  
 420  
 gccaaacaca acattttttac attagccctt atgattgtga acctatttaa tatgtttatc  
 480

acatatggcg acacatttct gccaaacccc agcagctatg atgaacttta ctatgagatt  
 540  
 atccgcatgc accagagctt tgacaacctc tactccatgg tcctgaggct ttctaccaat  
 600  
 gcaggccagt ggaaggaagc agctagcaag gtgacccatg cattgggtaa tatcagagcc  
 660  
 atcatcaacc actttaaccc caaaattgag tcctacgctg ctgtgaatca catatcccaa  
 720  
 ctgtcagagg agcaggtgct ggaggtggtg agagccaact atgacacgct cacgctgaag  
 780  
 ctgcaggatg gcctggacca gtatgagcgc tactcagagc agcacaagga agctgccttc  
 840  
 ttcaaagagc tggttcgatc cattagcacc aacgtccgga  
 880

<210> 970

<211> 263

<212> PRT

<213> Homo sapiens

<400> 970

Met	Thr	Met	His	Phe	Cys	Met	Met	Ile	Asn	Met	Asn	Phe	Arg	Val	Asn	1	5	10	15
Leu	His	Arg	Met	Pro	Met	Arg	His	Arg	Lys	Lys	Ala	Ala	Asp	Lys	Asn	20	25	30	
Leu	Thr	Leu	Pro	Ser	Leu	Val	Cys	Glu	Val	Leu	Asp	Leu	Met	Val	Glu	35	40	45	
Phe	Ile	Val	Thr	His	Met	Met	Lys	Glu	Phe	Pro	Met	Asp	Leu	Tyr	Ile	50	55	60	
Arg	Cys	Ile	Gln	Val	Val	His	Lys	Leu	Leu	Cys	Tyr	Gln	Lys	Lys	Cys	65	70	75	80
Arg	Val	Arg	Leu	His	Tyr	Thr	Trp	Arg	Glu	Leu	Trp	Ser	Ala	Leu	Ile	85	90	95	
Asn	Leu	Leu	Lys	Phe	Leu	Met	Ser	Asn	Glu	Thr	Val	Leu	Leu	Ala	Lys	100	105	110	
His	Asn	Ile	Phe	Thr	Leu	Ala	Leu	Met	Ile	Val	Asn	Leu	Phe	Asn	Met	115	120	125	
Phe	Ile	Thr	Tyr	Gly	Asp	Thr	Phe	Leu	Pro	Thr	Pro	Ser	Ser	Tyr	Asp	130	135	140	
Glu	Leu	Tyr	Tyr	Glu	Ile	Ile	Arg	Met	His	Gln	Ser	Phe	Asp	Asn	Leu	145	150	155	160
Tyr	Ser	Met	Val	Leu	Arg	Leu	Ser	Thr	Asn	Ala	Gly	Gln	Trp	Lys	Glu	165	170	175	
Ala	Ala	Ser	Lys	Val	Thr	His	Ala	Leu	Val	Asn	Ile	Arg	Ala	Ile	Ile	180	185	190	
Asn	His	Phe	Asn	Pro	Lys	Ile	Glu	Ser	Tyr	Ala	Ala	Val	Asn	His	Ile	195	200	205	
Ser	Gln	Leu	Ser	Glu	Glu	Gln	Val	Leu	Glu	Val	Val	Arg	Ala	Asn	Tyr	210	215	220	
Asp	Thr	Leu	Thr	Leu	Lys	Leu	Gln	Asp	Gly	Leu	Asp	Gln	Tyr	Glu	Arg	225	230	235	240
Tyr	Ser	Glu	Gln	His	Lys	Glu	Ala	Ala	Phe	Phe	Lys	Glu	Leu	Val	Arg	245	250	255	
Ser	Ile	Ser	Thr	Asn	Val	Arg													

260

<210> 971  
 <211> 337  
 <212> DNA  
 <213> Homo sapiens

<400> 971  
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 120  
 aatcccaacc ccaaatacct ggttgtaac ggagacgaat ccgaaccg cactgcaag  
 180  
 gacatgccgc tcattatggc aagccgcac acgcttgctg aaggtgctct tatctccgc  
 240  
 tacgctttcg gatccgagca ggctttcatc tacctccgtg gagaagttgt tcaggtagcc  
 300  
 cggcgccttg aagaaaaaa aaaaatgcga nnnnnnn  
 337

<210> 972  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<400> 972  
 Ser Arg Gly Leu Thr Met Glu Pro Ser Glu Val Leu Asn Leu Ile Lys  
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 Asp Ser Gly Leu Arg Gly Arg Gly Gly Ala Gly Phe Pro Thr Gly Val  
 20 25 30  
 Lys Trp Ser Phe Val Pro Gln Asn Asn Pro Asn Pro Lys Tyr Leu Val  
 35 40 45  
 Val Asn Gly Asp Glu Ser Glu Pro Gly Thr Cys Lys Asp Met Pro Leu  
 50 55 60  
 Ile Met Ala Ser Pro His Thr Leu Val Glu Gly Ala Leu Ile Ser Arg  
 65 70 75 80  
 Tyr Ala Phe Gly Ser Glu Gln Ala Phe Ile Tyr Leu Arg Gly Glu Val  
 85 90 95  
 Val Gln Val Ala Arg Arg Leu Glu Glu Lys Lys Lys Met Arg Xaa Xaa  
 100 105 110

<210> 973  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 973  
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 ccagcagggc ggcacagcca aggaaatggc atggtcctgc tgcattggtc tcagtgggt  
 120  
 ccgggacctt ctgtataggc atcacttagg aaccagtcag accatcagat tctcaggacc  
 180

cactggatca actgagtcag gaactcaggg ttttcaacac atcctccggg gggattccag  
 240  
 tggctgtgta actttgagga ccactggcaa agtggctctg gggtcagaga tccgagttca  
 300  
 tattctgggt ctgcctctga ctgactgcaa cggtagggcaa gtcacttgcc gtgcccagcc  
 360

<210> 974  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 974  
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 1 5 10 15  
 Tyr Arg His His Leu Gly Thr Ser Gln Thr Ile Arg Phe Ser Gly Pro  
 20 25 30  
 Thr Gly Ser Thr Glu Ser Gly Thr Gln Gly Phe Gln His Ile Leu Arg  
 35 40 45  
 Gly Asp Ser Ser Gly Cys Val Thr Leu Arg Thr Thr Gly Lys Val Ala  
 50 55 60  
 Leu Gly Ser Glu Ile Arg Val His Ile Leu Gly Leu Pro Leu Thr Asp  
 65 70 75 80  
 Cys Asn Gly Gly Gln Val Thr Cys Arg Ala Gln  
 85 90

<210> 975  
 <211> 2604  
 <212> DNA  
 <213> Homo sapiens

<400> 975  
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 120  
 ccttgataa gtggtttctg attttgagag gacagcagag ggctgtatca cacaagacat  
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 240  
 tgaccagcca cgatgcaggt tgaagaagcc accggtcagg ctgcgggccc tcgtcgggga  
 300  
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 360  
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 420  
 ctggctgagc tggaagacgg agccctgctg ctgcagaccc tgcagctttc aaaaatttcc  
 480  
 tttccaattg gccaacgact tctgggatcc aaaaggaaga tgagtctcaa tccgattgag  
 540  
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 600  
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720  
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780  
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960  
cgtatgactt ccactaactt ggccctgggtg tttggatctg ctctcctgaa aaaaggaaag  
1020  
tttggcaaga gagagtccag gaaaacaaag ctggggattg atcactatgt tgcttctgtc  
1080  
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1140  
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1200  
cgcaggaact tgaggaagat ccagagtgc cgcataaaga tggaaagagga tgcactactt  
1260  
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1320  
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1380  
gatgaggaag gagcgggtaa ccctccatt ccggagcaag accgcccatt gtcctgtgtg  
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1500  
ctataagggtg ccagacaggg gaaaagggtg ggggtacatc tgggatgtca caggaaacat  
1560  
taaggagaga gttgaaggta aagatctgaa ggtaagaagg agttccacct gatgctcggg  
1620  
tcaggatgag aattccaaac aactgccag ccccttccact ggggatgctt ggtctcttct  
1680  
gctggtaaaa gcagagatgt ttctgtgtca tgcccaagct ccccggtgct accttgctt  
1740  
tctcttttac ccctgatctt ggctttctct ctctctctgc agactttcct ttaattgatg  
1800  
tgacatttgt ggtaaacacc tttcccaggg aacctcaca atcttgagat gctttccctt  
1860  
ccccaaatgg gattgcatga tttccctgac tttcctaccc tcctccagag agctcagttg  
1920  
gaaaggccct caagaggcat gctagaacgt taggtcagcc tactgacagc tgacaaacaa  
1980  
ttaatgcgaa atcatgtcac accaaccat agcctgttcc acgcagcaac tccaccacct  
2040  
taggatttcc ccctccaaat tattcagacc aatggcttgc caaatggcct ctcccaaat  
2100  
tctgtacagt tttgctcagg tcacgccaac agggaaacct caagtgtagg tctaatttag  
2160  
gtttctggga tccaaagtta gaggaaaatt tagattttat tgcttgatc tgctttaaag  
2220  
acaattggtg ttacaccct cttgtcagca aaacagctag ttaggtaagg acatatagtt  
2280



ccaagtaggt aaagtcactt gattacaaat gttcttaact atcgtctctg taattccttt  
 2340  
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 2460  
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 2604

<210> 976

<211> 411

<212> PRT

<213> Homo sapiens

<400> 976

Met	Gln	Val	Glu	Glu	Ala	Thr	Gly	Gln	Ala	Ala	Gly	Arg	Arg	Arg	Gly
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Asn	Val	Val	Arg	Arg	Val	Phe	Gly	Arg	Ile	Arg	Arg	Phe	Phe	Ser	Arg
			20					25					30		
Arg	Arg	Asn	Glu	Pro	Thr	Leu	Pro	Arg	Glu	Phe	Thr	Arg	Arg	Gly	Arg
		35					40					45			
Arg	Gly	Ala	Val	Ser	Val	Asp	Ser	Leu	Ala	Glu	Leu	Glu	Asp	Gly	Ala
	50					55				60					
Leu	Leu	Leu	Gln	Thr	Leu	Gln	Leu	Ser	Lys	Ile	Ser	Phe	Pro	Ile	Gly
65				70					75					80	
Gln	Arg	Leu	Leu	Gly	Ser	Lys	Arg	Lys	Met	Ser	Leu	Asn	Pro	Ile	Ala
			85				90						95		
Lys	Gln	Ile	Pro	Gln	Val	Val	Glu	Ala	Cys	Cys	Gln	Phe	Ile	Glu	Lys
			100				105						110		
His	Gly	Leu	Ser	Ala	Val	Gly	Ile	Phe	Thr	Leu	Glu	Tyr	Ser	Val	Gln
	115					120					125				
Arg	Val	Arg	Gln	Leu	Arg	Glu	Phe	Asp	Gln	Gly	Leu	Asp	Val	Val	
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Ser	Phe	Leu	Leu	Thr	Ala	Thr	Leu	Lys	Pro	Gln	Asp	Gln	Leu	Ser	Ala
			180				185						190		
Leu	Gln	Leu	Leu	Val	Tyr	Leu	Thr	Pro	Pro	Cys	His	Ser	Asp	Thr	Leu
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Glu	Arg	Leu	Leu	Lys	Ala	Leu	His	Lys	Ile	Thr	Glu	Asn	Cys	Glu	Asp
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Ser	Ile	Gly	Ile	Asp	Gly	Gln	Leu	Val	Pro	Gly	Asn	Arg	Met	Thr	Ser
225				230						235				240	
Thr	Asn	Leu	Ala	Leu	Val	Phe	Gly	Ser	Ala	Leu	Leu	Lys	Lys	Gly	Lys
			245				250						255		
Phe	Gly	Lys	Arg	Glu	Ser	Arg	Lys	Thr	Lys	Leu	Gly	Ile	Asp	His	Tyr
			260				265					270			
Val	Ala	Ser	Val	Asn	Val	Val	Arg	Ala	Met	Ile	Asp	Asn	Trp	Asp	Val

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      275              280              285
Leu Phe Gln Val Pro Pro His Ile Gln Arg Gln Val Ala Lys Arg Val
      290              295              300
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      305              310              315              320
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      325              330              335
Ser Asp Pro Val Glu Thr Ser Ala Glu Ala Arg Ala Ala Val Leu Ala
      340              345              350
Gln Ser Lys Pro Ser Asp Glu Gly Ser Ser Glu Glu Pro Ala Val Pro
      355              360              365
Ser Gly Thr Ala Arg Ser His Asp Asp Glu Glu Gly Ala Gly Asn Pro
      370              375              380
Pro Ile Pro Glu Gln Asp Arg Pro Leu Leu Arg Val Pro Arg Glu Lys
      385              390              395              400
Glu Ala Lys Thr Gly Val Ser Tyr Phe Phe Pro
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&lt;210&gt; 977

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 977

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&lt;210&gt; 978

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 978

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Glu Met Pro Ser Arg Thr Leu Arg Gln Ala Ser His Glu Ser Ile Glu
20         25         30
Asp Ser Met Asn Ser Tyr Gly Ser Glu Gly Asn Leu Asn Tyr Gly Gly
35         40         45
Val Cys Leu Ala Ser Asp Ala Gln Phe Ser Asp Phe Leu Gly Ser Met
50         55         60
Gly Pro Ala Gln Phe Val Gly Arg Gln Thr Leu Ala Thr Thr Pro Met

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		85		90		95									
Asp	Ile	Ile	Gln	Ala	Arg	Gly	Leu	Thr	Ala	Lys	Pro	Gly	Ser	Lys	Thr
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&lt;210&gt; 980

&lt;211&gt; 73

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 980

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		20						25				30			
Cys	Phe	Gln	Val	Leu	Thr	Ala	Ser	Gly	Trp	Ser	Leu	Glu	Ala	Thr	Glu
		35					40					45			
Glu	Arg	Asn	Ala	Trp	Leu	Arg	Ala	Ala	Glu	His	Ser	Glu	Ala	Ser	Arg
	50					55					60				
Glu	Asp	Ser	Arg	Pro	Ala	Arg	Ala	Pro							
65					70										

&lt;210&gt; 981

&lt;211&gt; 404

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 981

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 35 40 45  
 Leu Phe Pro Lys Arg Ala Arg Tyr Pro Ser Phe Ser Gly Pro Leu Tyr  
 50 55 60  
 Leu Phe Phe Ser Leu Pro Glu Thr Pro Phe Leu Leu Asn Asn Leu Met  
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Ala Asn Phe Lys Ala His Asp Leu Lys Leu Val Thr Glu Ile Asn His			
35	40	45	
Leu Asp Asn Gln Ile Phe Ile Asp Tyr Ala Lys Leu Ile Lys Glu Ser			
50	55	60	
Asp Ala Leu Pro Val Asp Gln Gln Val Ala Phe Phe Leu Asn Asn Met			
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Gln Ser Ile Ile Asp Gly Lys Pro Glu Leu Asn Ile Thr Glu Leu Ser			
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Gly Phe			

&lt;210&gt; 987

&lt;211&gt; 4224

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 987

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3660  
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3720  
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3780  
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3840  
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3900  
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3960  
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4020  
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4080  
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4200  
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4224

<210> 988  
 <211> 873  
 <212> PRT  
 <213> Homo sapiens

<400> 988

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Ala His Lys Tyr Leu Pro Ala Leu Asp Glu Phe Pro His Pro Pro Lys
 1           5           10           15
Arg Leu Arg Ser Asp Pro Asp Ala Cys Pro Thr Met Pro Leu Leu Ala
      20           25           30
Met Leu Leu Arg Gly Leu Thr Gln Ile Gln Ser Arg Ile Leu Gly Pro
      35           40           45
Gly Arg Lys Cys Cys Ala Leu Ala Asn Leu Ala Asp Met Leu Thr Val
 50           55           60
Phe Ala Leu Thr Glu Asp Asp Pro Gln Glu Val Ser Ala Thr Val Tyr
65           70           75           80
Leu Asp Lys Leu Ala Thr Val Ile Ser Val Trp Asn Ser Asp Thr Gln
      85           90           95
Asn Pro Tyr His Gln Gln Ala Leu Ala Glu Lys Val Lys Glu Ala Glu
      100           105           110
Arg Asp Val Ser Leu Thr Ser Leu Ala Lys Leu Pro Ser Glu Thr Ile
      115           120           125
Phe Val Gly Cys Glu Phe Leu His His Leu Leu Arg Glu Trp Gly Glu
      130           135           140
Glu Leu Gln Ala Val Leu Arg Ser Ser Gln Gly Thr Ser Tyr Asp Ser
145           150           155           160
Tyr Arg Leu Cys Asp Ser Leu Thr Ser Phe Ser Gln Asn Ala Thr Leu
      165           170           175
Tyr Leu Asn Arg Thr Ser Leu Ser Lys Glu Asp Arg Gln Val Val Ser
      180           185           190
Glu Leu Ala Glu Cys Val Arg Asp Phe Leu Arg Lys Thr Ser Thr Val
      195           200           205
Leu Lys Asn Arg Ala Leu Glu Asp Ile Thr Ala Ser Ile Ala Met Ala
      210           215           220
Val Ile Gln Gln Lys Met Asp Arg His Met Glu Val Cys Tyr Ile Phe
225           230           235           240
Ala Ser Glu Lys Lys Trp Ala Phe Ser Asp Glu Trp Val Ala Cys Leu
      245           250           255
Gly Ser Asn Arg Ala Leu Phe Arg Glu Pro Asp Leu Val Leu Arg Leu
      260           265           270
Leu Glu Thr Val Ile Asp Val Ser Thr Ala Asp Arg Ala Ile Pro Glu
      275           280           285
Ser Gln Ile Arg Gln Val Ile His Leu Ile Leu Glu Cys Tyr Ala Asp
      290           295           300
Leu Ser Leu Pro Gly Lys Asn Lys Val Leu Ala Gly Ile Leu Arg Ser
305           310           315           320
Trp Gly Arg Lys Gly Leu Ser Glu Lys Leu Leu Ala Tyr Val Glu Gly
      325           330           335
Phe Gln Glu Asp Leu Asn Thr Thr Phe Asn Gln Leu Thr Gln Ser Ala
      340           345           350
Ser Glu Gln Gly Leu Ala Lys Ala Val Ala Ser Val Ala Arg Leu Val
      355           360           365
Ile Val His Pro Glu Val Thr Val Lys Lys Met Cys Ser Leu Ala Val

```

	370					375					380					
Val 385	Asn	Leu	Gly	Thr	His 390	Lys	Phe	Leu	Ala	Gln 395	Ile	Leu	Thr	Ala	Phe 400	
Pro	Ala	Leu	Arg	Phe	Val	Glu	Val	Gln	Gly	Pro	Asn	Ser	Ser	Ala	Thr	
				405					410					415		
Phe	Met	Val	Ser	Cys	Leu	Lys	Glu	Thr	Val	Trp	Met	Lys	Phe	Ser	Thr	
			420					425					430			
Pro	Lys	Glu	Gly	Lys	Gln	Phe	Leu	Glu	Leu	Leu	Asn	Cys	Leu	Met	Ser	
		435					440					445				
Pro	Val	Lys	Pro	Gln	Gly	Ile	Pro	Val	Ala	Ala	Leu	Glu	Pro	Asp		
	450					455					460					
Glu 465	Val	Leu	Lys	Glu	Phe	Val	Leu	Pro	Phe	Leu	Arg	Leu	Asp	Val	Glu	
				470						475				480		
Glu	Val	Asp	Leu	Ser	Leu	Arg	Ile	Phe	Ile	Gln	Thr	Leu	Glu	Ala	Asn	
				485					490					495		
Ala	Cys	Arg	Glu	Glu	Tyr	Trp	Leu	Gln	Thr	Cys	Ser	Pro	Phe	Pro	Leu	
			500					505					510			
Leu	Phe	Ser	Leu	Cys	Gln	Leu	Leu	Asp	Arg	Phe	Ser	Lys	Tyr	Trp	Gln	
		515					520					525				
Leu	Pro	Lys	Glu	Lys	Arg	Cys	Leu	Ser	Leu	Asp	Arg	Lys	Asp	Leu	Ala	
	530					535					540					
Ile 545	His	Ile	Leu	Glu	Leu	Leu	Cys	Glu	Ile	Val	Ser	Ala	Asn	Ala	Glu	
				550						555				560		
Thr	Phe	Ser	Pro	Asp	Val	Trp	Ile	Lys	Ser	Leu	Ser	Trp	Leu	His	Arg	
				565					570					575		
Lys	Leu	Glu	Gln	Leu	Asp	Trp	Thr	Val	Gly	Leu	Arg	Leu	Lys	Ser	Phe	
			580					585					590			
Phe	Glu	Gly	His	Phe	Lys	Cys	Glu	Val	Pro	Ala	Thr	Leu	Phe	Glu	Ile	
		595					600					605				
Cys	Lys	Leu	Ser	Glu	Asp	Glu	Trp	Thr	Ser	Gln	Ala	His	Pro	Gly	Tyr	
	610					615					620					
Gly 625	Ala	Gly	Thr	Gly	Leu	Leu	Ala	Trp	Met	Glu	Cys	Cys	Cys	Val	Ser	
				630						635				640		
Ser	Gly	Ile	Ser	Glu	Arg	Met	Leu	Ser	Leu	Leu	Val	Val	Asp	Val	Gly	
				645					650					655		
Asn	Pro	Glu	Glu	Val	Arg	Leu	Phe	Ser	Lys	Gly	Phe	Leu	Val	Ala	Leu	
			660					665					670			
Val	Gln	Val	Met	Pro	Trp	Cys	Ser	Pro	Gln	Glu	Trp	Gln	Arg	Leu	His	
		675					680					685				
Gln	Leu	Thr	Arg	Arg	Leu	Leu	Glu	Lys	Gln	Leu	Leu	His	Val	Pro	Tyr	
	690					695					700					
Ser 705	Leu	Glu	Tyr	Ile	Gln	Phe	Val	Pro	Leu	Leu	Asn	Leu	Lys	Pro	Phe	
				710						715				720		
Ala	Gln	Glu	Leu	Gln	Leu	Ser	Val	Leu	Phe	Leu	Arg	Thr	Phe	Gln	Phe	
				725					730					735		
Leu	Cys	Ser	His	Ser	C											

```

      805              810              815
Tyr Val Leu Ala Leu Glu Thr Leu Thr Cys Tyr Glu Thr Leu Ser Lys
      820              825              830
Thr Asn Pro Ser Val Ser Ser Leu Leu Gln Arg Ala His Glu Gln Cys
      835              840              845
Phe Leu Lys Ser Ile Ala Glu Gly Ile Gly Pro Glu Glu Arg Arg Gln
      850              855              860
Thr Leu Leu Gln Lys Met Ser Ser Phe
865              870

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<210> 989  
 <211> 402  
 <212> DNA  
 <213> Homo sapiens

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<400> 989
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60
gacacccttg ttgacgtctt gtcaggcggt gagcggcgtc gtgtcgcgt atgcaagctg
120
ttgatcgagc agcctgacct gctgcttctc gatgagccca ccaaccacct ggatgctgag
180
tctgtcaact gggttgaggg acacctcaag tcctatccgg gagctgtgct agccgtcact
240
cacgaccgct atttccttga tcacgtcgcc gactggatct gtgaggtcga tcgcggccag
300
ttgcaccctt acgagggcaa ctactcgacg tacctggaca ccaagcgcaa gcgtctccag
360
atcgaaggca agaaagacgc taaacgcgcc aagatcctcg ag
402

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<210> 990  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

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<400> 990
Ala Trp Asp Ile Asp Thr Arg Leu Glu Gln Ala Met Asp Ala Leu Gln
1      5      10      15
Cys Pro Pro Gly Asp Thr Pro Val Asp Val Leu Ser Gly Gly Glu Arg
20     25     30
Arg Arg Val Ala Leu Cys Lys Leu Leu Ile Glu Gln Pro Asp Leu Leu
35     40     45
Leu Leu Asp Glu Pro Thr Asn His Leu Asp Ala Glu Ser Val Asn Trp
50     55     60
Leu Glu Gly His Leu Lys Ser Tyr Pro Gly Ala Val Leu Ala Val Thr
65     70     75     80
His Asp Arg Tyr Phe Leu Asp His Val Ala Glu Trp Ile Cys Glu Val
85     90     95
Asp Arg Gly Gln Leu His Pro Tyr Glu Gly Asn Tyr Ser Thr Tyr Leu
100    105    110
Asp Thr Lys Arg Lys Arg Leu Gln Ile Glu Gly Lys Lys Asp Ala Lys
115    120    125
Arg Ala Lys Ile Leu Glu

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130

<210> 991  
 <211> 359  
 <212> DNA  
 <213> Homo sapiens

<400> 991  
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 60  
 cccgcctatc aggcctttaga gtcagggaaa aatttaaaat ctgcatttct tcctttaatt  
 120  
 gcccaatttt taggagtaga tggttattgg ttaacgacgg ggaatactga agattctttt  
 180  
 agagaaagtg atgtatttag cccgactgta gtgagtgcag aatctactga tcagtatgtt  
 240  
 tggattgaag ttgtagaagc taacttttct tgcgggacag gtgaatctat tgaatttcac  
 300  
 tttgatgcta ttaatggaaa aattccattc cctgcttcat tctttaaaga aaaacgcgt  
 359

<210> 992  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 992  
 Ser Arg Ile Lys Ala Lys Lys Thr Gln Ala Glu Val Ala Glu Ala Val  
 1 5 10 15  
 Lys Met Ser Gln Pro Ala Tyr Gln Ala Leu Glu Ser Gly Lys Asn Leu  
 20 25 30  
 Lys Ser Ala Phe Leu Pro Leu Ile Ala Gln Phe Leu Gly Val Asp Gly  
 35 40 45  
 Tyr Trp Leu Thr Thr Gly Asn Thr Glu Asp Ser Phe Arg Glu Ser Asp  
 50 55 60  
 Val Phe Ser Pro Thr Val Val Ser Ala Glu Ser Thr Asp Gln Tyr Val  
 65 70 75 80  
 Trp Ile Glu Val Val Glu Ala Asn Phe Ser Cys Gly Thr Gly Glu Ser  
 85 90 95  
 Ile Glu Phe His Phe Asp Ala Ile Asn Gly Lys Ile Pro Phe Pro Ala  
 100 105 110  
 Ser Phe Phe Lys Glu Lys Arg  
 115

<210> 993  
 <211> 450  
 <212> DNA  
 <213> Homo sapiens

<400> 993  
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 60  
 tcgcgggtccg gatccgcgat gatggccgcg tggcctgaag caatggggta ggtgcccggtg  
 120

atgcgctcgct ttggcgcacg aggtttacgc cgtggggagt tcataaggga aataccagca  
 180  
 cagggtcgga ccagttgtta cgatcgctgc atgatctact tgcgcagga ttatatcggt  
 240  
 gagctaccca agcaacatat ctcgctggga aagtttgatc ccgacaatat tctcgcgga  
 300  
 ccgaacgaac tgtttgccac gtggtttaaa gaagccgttg agaacgaagt cggcgaccct  
 360  
 actgcggtca ccgtggccac ggtggacgac aacggtcagc ccgatgcgcg agtcgctgac  
 420  
 cttctgtacc tcaactccga cggcttccac  
 450

<210> 994

<211> 110

<212> PRT

<213> Homo sapiens

<400> 994

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1				5				10					15		
Glu	Ile	Pro	Ala	Gln	Gly	Arg	Thr	Ser	Cys	Tyr	Asp	Arg	Cys	Met	Ile
		20					25					30			
Tyr	Leu	Ser	Gln	Asp	Tyr	Ile	Gly	Glu	Leu	Pro	Lys	Gln	His	Ile	Ser
	35					40					45				
Leu	Gly	Lys	Phe	Asp	Pro	Asp	Asn	Ile	Pro	Ala	Asp	Pro	Asn	Glu	Leu
	50					55				60					
Phe	Ala	Thr	Trp	Phe	Lys	Glu	Ala	Val	Glu	Asn	Glu	Val	Gly	Asp	Pro
65					70					75				80	
Thr	Ala	Val	Thr	Val	Ala	Thr	Val	Asp	Asp	Asn	Gly	Gln	Pro	Asp	Ala
			85					90					95		
Arg	Val	Val	Asp	Leu	Leu	Tyr	Leu	Asn	Ser	Asp	Gly	Phe	His		
			100					105					110		

<210> 995

<211> 924

<212> DNA

<213> Homo sapiens

<400> 995

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 120  
 aactacgaca tgctcatcgg cgtcaaccag ggagagggcc tcaagtctgt ggaggactct  
 180  
 gcagagagcg aggacggtgt gtctgccagc gcctttgact tctgtctc caactttgtg  
 240  
 gacaacctgt atggctaccc ggaaggcaag gatgtgcttc gggagaccat caagtttatg  
 300  
 tacacagact gggccgaccg ggacaatggc gaaatgcgcc gcaaaaccct gctggcgctc  
 360  
 ttactgacc accaatgggt ggcaccagct gtggccactg ccaagctgca cgccgactac  
 420

cagtctcccg tctactttta caccttctac caccactgcc aggcggaggg ccggcctgag  
 480  
 tgggcagatg cggcgacagg ggatgaactg ccctatgtct ttggcgtgcc catggtgggt  
 540  
 gccaccgacc tcttccccctg taacttctcc aagaatgacg tcatgctcag tgccgtggtc  
 600  
 atgacctact ggaccaactt cgccaagact ggggacccca accagccggt gccgcaggat  
 660  
 accaagttca tccacaccaa gcccaatcgc ttcgaggagg tgggtgtggag caaattcaac  
 720  
 agcaaggaga agcagtatct gcacataggg ctgaagccac gcgtgctga caactaccgc  
 780  
 gccacaagg tggccttctg gctggagctc gtgccccacc tgcacaacct gcacacggag  
 840  
 ctcttcacca ccaccacggc cctgcctccc tacgccacgc gctggccgcc tcgtcccccc  
 900  
 gctggcgccc cgggcacacg ccgg  
 924

<210> 996

<211> 308

<212> PRT

<213> Homo sapiens

<400> 996

Arg	Glu	Leu	Val	Asp	Gln	Asp	Val	Gln	Pro	Ala	Arg	Tyr	His	Ile	Ala
1				5				10						15	
Phe	Gly	Pro	Val	Val	Asp	Gly	Asp	Val	Val	Pro	Asp	Asp	Pro	Glu	Ile
		20						25					30		
Leu	Met	Gln	Gln	Gly	Glu	Phe	Leu	Asn	Tyr	Asp	Met	Leu	Ile	Gly	Val
		35					40					45			
Asn	Gln	Gly	Glu	Gly	Leu	Lys	Phe	Val	Glu	Asp	Ser	Ala	Glu	Ser	Glu
	50					55					60				
Asp	Gly	Val	Ser	Ala	Ser	Ala	Phe	Asp	Phe	Thr	Val	Ser	Asn	Phe	Val
65					70					75				80	
Asp	Asn	Leu	Tyr	Gly	Tyr	Pro	Glu	Gly	Lys	Asp	Val	Leu	Arg	Glu	Thr
			85						90					95	
Ile	Lys	Phe	Met	Tyr	Thr	Asp	Trp	Ala	Asp	Arg	Asp	Asn	Gly	Glu	Met
		100						105					110		
Arg	Arg	Lys	Thr	Leu	Leu	Ala	Leu	Phe	Thr	Asp	His	Gln	Trp	Val	Ala
		115					120					125			
Pro	Ala	Val	Ala	Thr	Ala	Lys	Leu	His	Ala	Asp	Tyr	Gln	Ser	Pro	Val
	130					135						140			
Tyr	Phe	Tyr	Thr	Phe	Tyr	His	His	Cys	Gln	Ala	Glu	Gly	Arg	Pro	Glu
145					150					155				160	
Trp	Ala	Asp	Ala	Ala	His	Gly	Asp	Glu	Leu	Pro	Tyr	Val	Phe	Gly	Val
			165					170					175		
Pro	Met	Val	Gly	Ala	Thr	Asp	Leu	Phe	Pro	Cys	Asn	Phe	Ser	Lys	Asn
		180					185					190			
Asp	Val	Met	Leu	Ser	Ala	Val	Val	Met	Thr	Tyr	Trp	Thr	Asn	Phe	Ala
		195					200					205			
Lys	Thr	Gly	Asp	Pro	Asn	Gln	Pro	Val	Pro	Gln	Asp	Thr	Lys	Phe	Ile
	210					215					220				
His	Thr	Lys	Pro	Asn	Arg	Phe	Glu	Glu	Val	Val	Trp	Ser	Lys	Phe	Asn



```

225          230          235          240
Ser Lys Glu Lys Gln Tyr Leu His Ile Gly Leu Lys Pro Arg Val Arg
          245          250          255
Asp Asn Tyr Arg Ala Asn Lys Val Ala Phe Trp Leu Glu Leu Val Pro
          260          265          270
His Leu His Asn Leu His Thr Glu Leu Phe Thr Thr Thr Thr Arg Leu
          275          280          285
Pro Pro Tyr Ala Thr Arg Trp Pro Pro Arg Pro Pro Ala Gly Ala Pro
          290          295          300
Gly Thr Arg Arg
305

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&lt;210&gt; 997

&lt;211&gt; 320

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 997

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aaatttaata ccatagcctt ctcttggttg atccttctag gcatgagtta tggcattaaa
60
acgggcatcc atcttggtgt cgatatcgta cttaatgccg tgcctaaacg agtatcaaga
120
gccttgctctt tggtcgggtgc ctttgccgct attatgtacg gtctcattct acttgattct
180
acctggttag ccttactcgg tategatgta cgagggtggtg ccatcgaata ttgggcgaag
240
atgttcaaaa taggtattgg tactgaagag cttcggttacc ctatctttat gcaagatatg
300
tttgatttgc gcccacgcgt
320

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&lt;210&gt; 998

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 998

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Lys Phe Asn Thr Ile Ala Phe Ser Trp Leu Ile Leu Leu Gly Met Ser
1          5          10          15
Tyr Gly Ile Lys Thr Gly Ile His Leu Gly Val Asp Ile Val Leu Asn
          20          25          30
Ala Val Pro Lys Arg Val Ser Arg Ala Leu Ser Leu Phe Gly Ala Phe
          35          40          45
Ala Ala Ile Met Tyr Gly Leu Ile Leu Leu Asp Ser Thr Trp Leu Ala
50          55          60
Leu Leu Gly Ile Asp Val Arg Gly Gly Ala Ile Glu Tyr Trp Ala Lys
65          70          75          80
Met Phe Lys Ile Gly Ile Gly Thr Glu Glu Leu Arg Tyr Pro Ile Phe
          85          90          95
Met Gln Asp Met Phe Asp Leu Arg Pro Arg
          100          105

```

&lt;210&gt; 999

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 999

acgcgttcag gcggttaaca atcgcgctaa gaagctgacc aaggaaaatg tcggcatggt  
 60  
 acatctgagc aagagcttca tcggtgttta tctctactca gaaggcaagt ttgtgaccag  
 120  
 caactatctc aatcgtggct acaaggacat tctgagctat gcagacgatg ctagtctttt  
 180  
 gcaaaagcct ccagcagtgg cttcagatga tctggataca ggtctcttga agagggcctt  
 240  
 ggatgagtggt gtggctgatg ctaagaacca cattctcaat actgaaaact tcttttagcgg  
 300  
 gtcaaccgggt ctcaacattg acagtttcta cgtctttgggt gaccaagaca tctgctggca  
 360  
 gttggcagct attctgaagc agagcatgaa tcgggaattg t  
 401

&lt;210&gt; 1000

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1000

Met	Val	His	Leu	Ser	Lys	Ser	Phe	Ile	Gly	Val	Tyr	Leu	Tyr	Ser	Glu
1				5					10					15	
Gly	Lys	Phe	Val	Thr	Ser	Asn	Tyr	Leu	Asn	Arg	Gly	Tyr	Lys	Asp	Ile
			20					25					30		
Leu	Ser	Tyr	Ala	Asp	Asp	Ala	Ser	Leu	Leu	Gln	Lys	Pro	Pro	Ala	Val
		35					40				45				
Ala	Ser	Asp	Asp	Leu	Asp	Thr	Gly	Leu	Leu	Lys	Arg	Ala	Leu	Asp	Glu
	50					55				60					
Trp	Val	Ala	Asp	Ala	Lys	Asn	His	Ile	Leu	Asn	Thr	Glu	Asn	Phe	Phe
65					70				75					80	
Ser	Gly	Ser	Thr	Gly	Leu	Asn	Ile	Asp	Ser	Phe	Tyr	Val	Phe	Gly	Asp
			85					90					95		
Gln	Asp	Ile	Cys	Trp	Gln	Leu	Ala	Ala	Ile	Leu	Lys	Gln	Ser	Met	Asn
			100					105					110		
Arg	Glu	Leu													
			115												

&lt;210&gt; 1001

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1001

cgcggtattg caatgcgcct ggtgccgaat gctaaacctg ctcttgattg cccggtactg  
 60  
 ttcccttatg cccctaattgc ggtgattggt ggcttcctgg ccactaccgt tggttcaatt  
 120  
 atcgggatga ttgtcttccc gctgtttggt ctggcgatga tccttcggg tctgctaact  
 180

aaacttcttcg ctggtgggtgc cgctggagtc tttggcaacg cgatgggagg acgtaaaggg  
 240  
 gcaattattg gcggcgtagt gcacgggctg tttatcaccc tgttaccagc gatgctaate  
 300  
 cccttactgg aaaccttcgg cttcaaaggc gtcacáttca gtgattccga t  
 351

<210> 1002

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1002

Arg	Gly	Ile	Ala	Met	Arg	Leu	Val	Pro	Asn	Ala	Lys	Pro	Ala	Leu	Asp
1				5				10					15		
Cys	Pro	Val	Leu	Phe	Pro	Tyr	Ala	Pro	Asn	Ala	Val	Ile	Val	Gly	Phe
		20					25				30				
Leu	Ala	Thr	Thr	Val	Gly	Ser	Ile	Ile	Gly	Met	Ile	Val	Phe	Pro	Leu
		35				40					45				
Phe	Gly	Leu	Ala	Met	Ile	Leu	Pro	Gly	Leu	Leu	Thr	Asn	Phe	Phe	Ala
	50				55						60				
Gly	Gly	Ala	Ala	Gly	Val	Phe	Gly	Asn	Ala	Met	Gly	Gly	Arg	Lys	Gly
65				70				75					80		
Ala	Ile	Ile	Gly	Gly	Val	Val	His	Gly	Leu	Phe	Ile	Thr	Leu	Leu	Pro
			85					90					95		
Ala	Met	Leu	Ile	Pro	Leu	Leu	Glu	Thr	Phe	Gly	Phe	Lys	Gly	Val	Thr
		100						105					110		
Phe	Ser	Asp	Ser	Asp											
		115													

<210> 1003

<211> 444

<212> DNA

<213> Homo sapiens

<400> 1003

acgcgtcctc ctttagtcga tcgcgaatat gataggcgaa gcgacgtgat ggtgtgacgc  
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 120  
 acccccgcat ggggcacact ctccggccta aagtcctcgt tcgctgacgg gccacataaa  
 180  
 ctgcgcggtt tgttcgacgc cgaccctcac cgcgctgagc gctacacctt tgacgtcgcg  
 240  
 gatttgcacg tcgatttata gaagaacctc cttaccgacg agattcgtga cgctctcttc  
 300  
 gaactggctg cgcagatgcg cgtcaccgag cgtcgtgacg cgatgtatgc cggtagacac  
 360  
 atcaacgtca ccgaggaccg cgccgtcctc cataccgcgc tgtgtcgtcc ccgcactgac  
 420  
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 444

<210> 1004

<211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 1004  
 Met Gln Thr Pro Ile Asp Ala Thr Ser Thr Pro Ala Trp Gly Thr Leu  
 1 5 10 15  
 Ser Gly Leu Lys Ser Arg Phe Ala Asp Gly Pro His Lys Leu Arg Arg  
 20 25 30  
 Leu Phe Asp Ala Asp Pro His Arg Ala Glu Arg Tyr Thr Phe Asp Val  
 35 40 45  
 Ala Asp Leu His Val Asp Leu Ser Lys Asn Leu Leu Thr Asp Glu Ile  
 50 55 60  
 Arg Asp Ala Leu Leu Glu Leu Ala Ala Gln Met Arg Val Thr Glu Arg  
 65 70 75 80  
 Arg Asp Ala Met Tyr Ala Gly Glu His Ile Asn Val Thr Glu Asp Arg  
 85 90 95  
 Ala Val Leu His Thr Ala Leu Cys Arg Pro Arg Thr Asp Glu Leu His  
 100 105 110  
 Val Asp Gly Gln Asp  
 115

<210> 1005  
 <211> 299  
 <212> DNA  
 <213> Homo sapiens

<400> 1005  
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 120  
 tatctatctg ccttagccac tcgtgtctga cgagcacctc acacctccag aggctcctca  
 180  
 tttcttccca tgctgtcttc tcccacactc ctccctctca catgagggca acttcatcct  
 240  
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 299

<210> 1006  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 1006  
 Met Ala Ile Pro Leu Val Thr Ala Ser Ser Pro Met Asp Leu Asn Thr  
 1 5 10 15  
 Pro Asn Val Leu Val Thr Pro Lys Phe Thr Pro Pro Ala Arg Ala Ser  
 20 25 30  
 Leu Leu Gly Leu His Thr His Leu Ser Ile Cys Leu Ser His Ser Cys  
 35 40 45  
 Leu Thr Ser Thr Ser His Leu Gln Arg Leu Leu Ile Ser Ser His Ala  
 50 55 60  
 Cys Phe Ser His Thr Pro Pro Ser His Met Arg Ala Thr Ser Ser Ser



ngccttcatg gctgntatgc ctggcctcat ccccatccct ggcacccgtg acgatagcca  
 60  
 cattccactg gtgtttcccc aggaaagcca accctacctg catctcagca gagcttccac  
 120  
 ggagttggaa ccccgctccg agaggggtgtg ggctcagggg ccaggggtca cacaaactcc  
 180  
 agaaggagga cgtagttggt ttgcaaggct gtcctttgcc ctggttgaat aaccttcggt  
 240  
 ctgccccgag aggaacgtgg gcattaggct gcacccgcag gaagccatgt attttctgag  
 300  
 aaacttgccc catggtgcag atct  
 324

<210> 1010

<211> 104

<212> PRT

<213> Homo sapiens

<400> 1010

Met	Gly	Gln	Val	Ser	Gln	Lys	Ile	His	Gly	Phe	Leu	Arg	Val	Gln	Pro
1				5					10					15	
Asn	Ala	His	Val	Pro	Leu	Gly	Ala	Asp	Arg	Arg	Leu	Phe	Asn	Gln	Gly
		20						25					30		
Lys	Gly	Gln	Pro	Cys	Lys	Pro	Thr	Thr	Ser	Ser	Phe	Trp	Ser	Leu	Cys
		35					40					45			
Asp	Pro	Trp	Pro	Leu	Ser	Pro	His	Pro	Leu	Gly	Ala	Gly	Phe	Gln	Leu
	50					55					60				
Arg	Gly	Ser	Ser	Ala	Glu	Met	Gln	Val	Gly	Leu	Ala	Phe	Leu	Gly	Lys
65					70					75				80	
His	Gln	Trp	Asn	Val	Ala	Ile	Val	Thr	Gly	Ala	Arg	Asp	Gly	Asp	Glu
			85						90					95	
Ala	Arg	His	Xaa	Ser	His	Glu	Gly								
															100

<210> 1011

<211> 330

<212> DNA

<213> Homo sapiens

<400> 1011

ctgcagaaaa ggaggggggtt cccatgccaa ggcagaactg tctgggacag acgctgcccc  
 60  
 gatccctgcg gctgcctgca ctctggacca cgagctctga gagcagcagg ttgagggccg  
 120  
 gtgggcagca gctcggaggc tccgcgaggt gcaggagacg caggcatggc cggtgagctg  
 180  
 actcctgagg aggaggccca gtacaaaaag gctttctccg cggttgacac ggatggaaac  
 240  
 ggcaccatca atgccaggga gctgggcgcg gcgctgaagg ccacgggcaa gaacctctcg  
 300  
 gaggcccagc taaagaaact catctccgag  
 330

<210> 1012

<211> 55  
 <212> PRT  
 <213> Homo sapiens

<400> 1012  
 Met Ala Gly Glu Leu Thr Pro Glu Glu Glu Ala Gln Tyr Lys Lys Ala  
 1 5 10 15  
 Phe Ser Ala Val Asp Thr Asp Gly Asn Gly Thr Ile Asn Ala Gln Glu  
 20 25 30  
 Leu Gly Ala Ala Leu Lys Ala Thr Gly Lys Asn Leu Ser Glu Ala Gln  
 35 40 45  
 Leu Lys Lys Leu Ile Ser Glu  
 50 55

<210> 1013  
 <211> 432  
 <212> DNA  
 <213> Homo sapiens

<400> 1013  
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 60  
 tgggggcgctc tcctcgctgc cgggagcggc gaggaaggat taacgatgac cagcgacgctc  
 120  
 cccgggattg gctcgaacgc cgccactttg gcgcgttccc aggctcgcag tgacaaggctc  
 180  
 gaggctgatt tggcgggtcca tcccgcacaag tggcgcattc tgggggggga ccgtcctact  
 240  
 ggcagcctgc acatcggtca ctacttcggg tcgctggcga atcggttacg cgtgcagaac  
 300  
 aagggcattg agtctttcct tgcgctcgt gactaccagg ttatctatga ccgcgggggg  
 360  
 ggtggtgacc tgcaggccaa tggtatgtcg aatgtcgccg attacctggc aatcggcatt  
 420  
 gacccaacgc gt  
 432

<210> 1014  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 1014  
 Met Thr Ser Asp Val Pro Gly Ile Gly Ser Asn Ala Ala Thr Leu Ala  
 1 5 10 15  
 Arg Ser Gln Ala Arg Ser Asp Lys Val Glu Ala Asp Leu Ala Val His  
 20 25 30  
 Pro Asp Lys Trp Arg Ile Leu Gly Asp Arg Pro Thr Gly Ser Leu  
 35 40 45  
 His Ile Gly His Tyr Phe Gly Ser Leu Ala Asn Arg Val Arg Val Gln  
 50 55 60  
 Asn Lys Gly Ile Glu Ser Phe Leu Val Val Ala Asp Tyr Gln Val Ile  
 65 70 75 80  
 Tyr Asp Arg Gly Gly Gly Gly Asp Leu Gln Ala Asn Val Met Ser Asn

85 90 95  
 Val Ala Asp Tyr Leu Ala Ile Gly Ile Asp Pro Thr Arg  
 100 105

<210> 1015

<211> 467

<212> DNA

<213> Homo sapiens

<400> 1015

nngaattcga tggctgtgaa aggtcgagct cttaagtgtt ttcatatccc ctgtgtgggt  
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 gaaaacttcc cgatgaaagc gcgcacgggt gaagagctga aagaattgga aagagtttta  
 120  
 cagcaaaaga agattgaagc agagtgtctt aaactacgga aggaaattgt agaggctcag  
 180  
 tctggagtta agttgattaa acagcgatcat gaagaggatg atgaagaaga ggaagaggaa  
 240  
 gacaagacag taaaatatag caatttgccc aattacctgc ttggtagtct gagtactgat  
 300  
 tttggggtag atacctcttt attgtcaagc caattggagc ttcattccag agaagagaaa  
 360  
 atcaaccaa ttatattatt gaaagatatc atttacaagg taaaaactgt tttcaataat  
 420  
 gagtttgacg ctgcatataa acaaaaagag ttgaaattg cagcggt  
 467

<210> 1016

<211> 155

<212> PRT

<213> Homo sapiens

<400> 1016

Xaa Asn Ser Met Ala Val Lys Gly Arg Ala Leu Lys Cys Phe His Ile  
 1 5 10 15  
 Pro Cys Val Val Glu Asn Phe Pro Met Lys Ala Arg Thr Val Glu Glu  
 20 25 30  
 Leu Lys Glu Leu Glu Arg Val Leu Gln Gln Lys Lys Ile Glu Ala Glu  
 35 40 45  
 Cys Leu Lys Leu Arg Lys Glu Ile Val Glu Ala Gln Ser Gly Val Lys  
 50 55 60  
 Leu Ile Lys Gln Arg His Glu Glu Asp Asp Glu Glu Glu Glu Glu  
 65 70 75 80  
 Asp Lys Thr Val Lys Tyr Ser Asn Leu Pro Asn Tyr Leu Leu Gly Ser  
 85 90 95  
 Leu Ser Thr Asp Phe Gly Val Asp Thr Ser Leu Leu Ser Ser Gln Leu  
 100 105 110  
 Glu Leu His Ser Arg Glu Glu Lys Ile Asn Gln Ile Ile Leu Leu Lys  
 115 120 125  
 Asp Ile Ile Tyr Lys Val Lys Thr Val Phe Asn Asn Glu Phe Asp Ala  
 130 135 140  
 Ala Tyr Lys Gln Lys Glu Phe Glu Ile Ala Arg  
 145 150 155



<210> 1017  
 <211> 335  
 <212> DNA  
 <213> Homo sapiens

<400> 1017  
 acgcgtggct ggttgggtat gtggaaccat gtgcgcgcta atgagaagga tgcgaagggg  
 60  
 aacattaaag tgggtcgccc cggctacttt gcgagggtca tggatttcta tgcgcattat  
 120  
 ctgaaggggtg cggttaccog tttccgtccg aattttattg tgcaggataa tacggggccgt  
 180  
 tggcgtgttc agtcgtcgtg gccgcagccg aatcgactg ttacttttgc gggaccccg  
 240  
 ggcattgtcc gctacgttac gacgttggcg gccgcacgc atgggaatgg tcaggctatt  
 300  
 ccgcaggcgg atgcacagtc tcttaaccgc gagaa  
 335

<210> 1018  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 1018  
 Met Trp Asn His Val Arg Ala Asn Glu Lys Asp Ala Lys Gly Asn Ile  
 1 5 10 15  
 Lys Val Gly Arg Pro Gly Tyr Phe Ala Glu Val Met Asp Phe Tyr Ala  
 20 25 30  
 His Tyr Leu Lys Gly Ala Val Thr Arg Phe Arg Pro Asn Phe Ile Val  
 35 40 45  
 Gln Asp Asn Thr Gly Arg Trp Arg Val Gln Ser Ser Trp Pro Gln Pro  
 50 55 60  
 Asn Arg Thr Val Thr Phe Ala Gly Pro Arg Gly Ile Val Arg Tyr Gly  
 65 70 75 80  
 Thr Thr Leu Ala Ala Arg Thr His Gly Asn Gly Gln Ala Ile Pro Gln  
 85 90 95  
 Ala Asp Ala Gln Ser Leu Asn Arg Glu  
 100 105

<210> 1019  
 <211> 454  
 <212> DNA  
 <213> Homo sapiens

<400> 1019  
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 60  
 ctctggagcc tctctctcaa tggcgttgcc catggtgcct ggcttgggtg atgaggcggg  
 120  
 tgaagggcgt ggggccaggt ggtgcgggat gaagtcagcc tcgttgaaga gctcgtggct  
 180  
 ggaggagccg ctgcctgagc cttcagggcc cagtgtgccc agggggccacc gacagagtgg  
 240

cagagagcag gtgacttcct ggcaactgagg agcgaggacc cggagaagta cttcctcaat  
 300  
 ggtggctgga ccatccagtg gaacggggac taccaggtgg cagggaccac cttcacatac  
 360  
 gcacgcaggg gcaactggga gaacctcacg tccccgggtc ccaccaagga gcctgtcttg  
 420  
 atccagctgc tgttccagga gagcaaccct gggg  
 454

<210> 1020

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1020

Met	Ala	Leu	Pro	Met	Val	Pro	Gly	Leu	Gly	Asp	Glu	Ala	Gly	Glu	Gly
1			5					10					15		
Arg	Gly	Ala	Arg	Trp	Cys	Gly	Met	Lys	Ser	Ala	Ser	Leu	Lys	Ser	Ser
		20					25					30			
Trp	Leu	Glu	Glu	Pro	Leu	Pro	Glu	Pro	Ser	Gly	Pro	Ser	Val	Pro	Arg
	35					40					45				
Gly	His	Arg	Gln	Ser	Gly	Arg	Glu	Gln	Val	Thr	Ser	Trp	His	Cys	Gly
	50				55				60						
Ala	Arg	Thr	Arg	Arg	Ser	Thr	Ser	Ser	Met	Val	Ala	Gly	Pro	Ser	Ser
65				70					75					80	
Gly	Thr	Gly	Thr	Thr	Arg	Trp	Gln	Gly	Pro	Pro	Ser	His	Thr	His	Ala
			85				90					95			
Gly	Ala	Thr	Gly	Arg	Thr	Ser	Arg	Pro	Arg	Val	Pro	Pro	Arg	Ser	Leu
		100					105					110			
Ser	Gly	Ser	Ser	Cys	Cys	Ser	Arg	Arg	Ala	Thr	Leu	Gly			
	115						120					125			

<210> 1021

<211> 366

<212> DNA

<213> Homo sapiens

<400> 1021

cagctgtgtc gtgacctcct gtagaccaga gagaggtaga gcatgaaaaa tgctcattga  
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 gccgagatta tctgacagga ccaaagcata taaagttgac tgaagcagga gcaaacacgc  
 120  
 tgggttgaggg tcaagtgtg gggcagcagc aacaacaaac caaaaaaag ccctttgaac  
 180  
 tcccttaatg ttgcccaaag gttctggtag agaacaagtc acatgcctaa gaaggtcttt  
 240  
 taaagggcac tcttgagtt tcagcatttg gtccggggaa ttgcacaagg ctctgcttaa  
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 atgcagagct ctttctagca tcttcatatt caaggcggaa aaactgagct tggcgaggaa  
 360  
 ccctgt  
 366

<210> 1022

<211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 1022  
 Met Lys Met Leu Glu Arg Ala Leu His Leu Ser Arg Ala Leu Cys Asn  
 1 5 10 15  
 Ser Pro Asp Gln Met Leu Lys Leu Gln Glu Cys Pro Leu Lys Asp Leu  
 20 25 30  
 Leu Arg His Val Thr Cys Ser Leu Pro Glu Pro Leu Gly Asn Ile Lys  
 35 40 45  
 Gly Val Gln Arg Ala Phe Phe Trp Phe Val Val Ala Ala Ala Pro Ala  
 50 55 60  
 Leu Asp Pro Gln Pro Ala Cys Leu Leu Leu Leu Gln Ser Thr Leu Tyr  
 65 70 75 80  
 Ala Leu Val Leu Ser Asp Asn Leu Gly Ser Met Ser Ile Phe His Ala  
 85 90 95  
 Leu Pro Leu Ser Gly Leu Gln Glu Val Thr Thr Gln Leu  
 100 105

<210> 1023  
 <211> 426  
 <212> DNA  
 <213> Homo sapiens

<400> 1023  
 gccgggcttc ggggtctctga agcgatcaac ctggccgact cggatgcaga tctggacggc  
 60  
 ggcatcctga ccatacagca gaccaagttt ggcaagtccc gcatgggtgcc gctacacccc  
 120  
 agcgtgatcg gtccgatggc agcctaccgg gccttgcgcc gccagtacgt gcctgcgaag  
 180  
 ccgcagatga cattcttcgt gggctcgcgt ggcgtgcacc ggggtgaacc gctgggagat  
 240  
 aggcaggtgc atcgagtgtt ctgtcagctg cgcgagcaat tgggttgat cgatcgcggc  
 300  
 ggccatggcc gaccgcgggt gcatgacctg cgccatagct tcgccgtgag acggatgatc  
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 ctgtggcacc agcagggagc gaaccttgac caacgaatgc tggccctgtc cacgtacatg  
 420  
 ggccac  
 426

<210> 1024  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

<400> 1024  
 Ala Gly Leu Arg Val Ser Glu Ala Ile Asn Leu Ala Asp Ser Asp Ala  
 1 5 10 15  
 Asp Leu Asp Gly Gly Ile Leu Thr Ile Gln Gln Thr Lys Phe Gly Lys  
 20 25 30  
 Ser Arg Met Val Pro Leu His Pro Ser Val Ile Gly Pro Met Ala Ala

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          35          40          45
Tyr Arg Ala Leu Arg Arg Gln Tyr Val Pro Ala Lys Pro Gln Met Thr
   50          55          60
Phe Phe Val Gly Ser Arg Gly Val His Arg Gly Glu Pro Leu Gly Asp
65          70          75          80
Arg Gln Val His Arg Val Phe Cys Gln Leu Arg Glu Gln Leu Gly Trp
          85          90          95
Ile Asp Arg Gly Gly His Gly Arg Pro Arg Val His Asp Leu Arg His
   100          105          110
Ser Phe Ala Val Arg Arg Met Ile Leu Trp His Gln Gln Gly Ala Asn
   115          120          125
Leu Asp Gln Arg Met Leu Ala Leu Ser Thr Tyr Met Gly His
   130          135          140

```

&lt;210&gt; 1025

&lt;211&gt; 518

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1025

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nacgcgtggt gcgcgcaggt ggcgccgcgg tccctttgct ccctgcgcaa gccggagggg
60
tgcccagaag gctaccacta gcctcagcga aggggtgcgcc ctgagagccg ggtagcctcg
120
gatagcggcg ctgcgtacgc gatgatggat gagccgtggt gggaaggcg cgtcgcctcg
180
gacgtccact gcaccctgcg cgagaaggaa ctgaagctgc ccaccttccg agccactcc
240
ccactcctga agagccgccg gttcttcgtg gacatcctga ccctgctgag cagccactgc
300
cagctctgcc ctgcagcccg gcacctggcc gtctacctgc tggaccactt catggatcgc
360
tacaacgtca ccacctcaa gcagctctac accgtggccg tctcctgcct cctgcttgca
420
agtaagtctg aggatcggga agaccacgtc cccaagttgg agcaaataaa cagcacgagg
480
atcctgagca gccagaactt caccctcacc aagaagga
518

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&lt;210&gt; 1026

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1026

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Met Met Asp Glu Pro Trp Trp Glu Gly Arg Val Ala Ser Asp Val His
  1          5          10          15
Cys Thr Leu Arg Glu Lys Glu Leu Lys Leu Pro Thr Phe Arg Ala His
          20          25          30
Ser Pro Leu Leu Lys Ser Arg Arg Phe Phe Val Asp Ile Leu Thr Leu
          35          40          45
Leu Ser Ser His Cys Gln Leu Cys Pro Ala Ala Arg His Leu Ala Val
          50          55          60
Tyr Leu Leu Asp His Phe Met Asp Arg Tyr Asn Val Thr Thr Ser Lys

```

65		70		75		80									
Gln	Leu	Tyr	Thr	Val	Ala	Val	Ser	Cys	Leu	Leu	Leu	Ala	Ser	Lys	Phe
		85		90		95									
Glu	Asp	Arg	Glu	Asp	His	Val	Pro	Lys	Leu	Glu	Gln	Ile	Asn	Ser	Thr
		100		105		110									
Arg	Ile	Leu	Ser	Ser	Gln	Asn	Phe	Thr	Leu	Thr	Lys	Lys			
		115		120		125									

&lt;210&gt; 1027

&lt;211&gt; 465

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1027

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ggcccaaaag tcataaaaga aaagctgaca caggagctga aggaccacaa cgccaccagc
60
atcctgcagc agctgccgct gctcaaggcc atgcgggaaa agccagccgg aggcattccct
120
gtgctgggca gcctgggtgaa caccngtcct gaagcacatc atnnctggct gaaggtcatc
180
acagctaaca tcctccagct gcaggtgaag ccctcggcca atgaccagga gctgctagtc
240
aagatcccc tggacatggt ggctggattc aacacgcccc tggtaagac catcgtggag
300
ttccacatga cgactgaggc ccaagccacc atccgcatgg acaccagtgc aagtggcccc
360
accgcctgg tcctcagtga ctgtgccacc agccatggga gcctgcgcat ccaactgctg
420
cataagctct ccttcaagct gaacgcctca gctaagcagg tcatg
465

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&lt;210&gt; 1028

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1028

Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys	Asp	His
1				5				10					15		
Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Lys	Ala	Met	Arg
		20				25						30			
Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser	Leu	Val	Asn	Thr
	35					40					45				
Xaa	Pro	Glu	Ala	His	His	Xaa	Trp	Leu	Lys	Val	Ile	Thr	Ala	Asn	Ile
	50				55					60					
Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp	Gln	Glu	Leu	Leu	Val
65				70				75					80		
Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe	Asn	Thr	Pro	Leu	Val	Lys
		85				90				95					
Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr	Glu	Ala	Gln	Ala	Thr	Ile	Arg
		100				105					110				
Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro	Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys
	115					120				125					
Ala	Thr	Ser	His	Gly	Ser	Leu	Arg	Ile	Gln	Leu	Leu	His	Lys	Leu	Ser

130 135 140  
 Phe Lys Leu Asn Ala Ser Ala Lys Gln Val Met  
 145 150 155

<210> 1029  
 <211> 479  
 <212> DNA  
 <213> Homo sapiens

<400> 1029  
 acgcgtgaag ggaaactgtc ctcacagatg agtgtgaggg ttcaaaaaga tactgcctgc  
 60  
 caagcactgg ccacaaatgc ctggcagaac aactgctcat aagtgtgtag ttgttgttat  
 120  
 tattactaac caagtgagga aaattatccc tagcaggtcc agatgaccgt gtgcatgaat  
 180  
 cacagggaga ccctaaagga tttcctcctg taaagctctt tccccaccta tttgctactg  
 240  
 cctgaaattg ctttagcagg aaacagaatc tctcatgcca caagtgagca taaagtttaa  
 300  
 aatgtaaatg ctctaggaaa aggcaactca tctcttaa at tctctccaag gttcaaatcc  
 360  
 tttccaaaga ggaggctttt gtataagtca gaaggcccag tccctgaagg tcatggaaaa  
 420  
 ggtcatgaca cacggagggg gtgtcaaagg gagactggga aactgaagat gaagctagc  
 479

<210> 1030  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 1030  
 Met Ser Cys Leu Phe Leu Glu His Leu His Phe Lys Leu Tyr Ala His  
 1 5 10 15  
 Leu Trp His Glu Arg Phe Cys Phe Leu Leu Lys Gln Phe Gln Ala Val  
 20 25 30  
 Ala Asn Arg Trp Gly Lys Ser Phe Thr Gly Gly Asn Pro Leu Gly Ser  
 35 40 45  
 Pro Cys Asp Ser Cys Thr Arg Ser Ser Gly Pro Ala Arg Asp Asn Phe  
 50 55 60  
 Pro His Leu Val Ser Asn Asn Asn Asn Asn Tyr Thr Leu Met Ser Ser  
 65 70 75 80  
 Cys Ser Ala Arg His Leu Trp Pro Val Leu Gly Arg Gln Tyr Leu Phe  
 85 90 95  
 Glu Pro Ser His Ser Ser Val Arg Thr Val Ser Leu His Ala  
 100 105 110

<210> 1031  
 <211> 322  
 <212> DNA  
 <213> Homo sapiens

<400> 1031

nacgcgtttt atgtcagcgt tgaattggaa gacggcaagt ctatcgccat gctgccccag  
 60  
 gcagatggct gggttgaagt ggaggtgaag tgcccggcgg gcactcacta ccgtataac  
 120  
 atcgacggcg aaaccgatgt acccgacccg gcatccaggg cgcaagccaa cgatgtgcat  
 180  
 ggggtggagcg tcgtcgtcga cccgctcgcc tatcaatggc gacaccctaa ctggcaaggc  
 240  
 cgcccctggc atgagggcgt gatttacgag ctgcacgttg gcgtactggg cgggtacgcc  
 300  
 gctgttgaac agcaactgcc gc  
 322

<210> 1032

<211> 107

<212> PRT

<213> Homo sapiens

<400> 1032

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Arg	Pro	Trp	His	Glu	Ala	Val	Ile	Tyr	Glu	Leu	His	Val	Gly	Val	Leu
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<210> 1033

<211> 579

<212> DNA

<213> Homo sapiens

<400> 1033

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 Ile Gly Ile Lys Gly Ala His Val Ile Lys Asp Gly Lys Ala Asp Arg  
 50 55 60  
 Gly Ile Phe Phe Cys Gly Thr Gly Met Gly Met Ala Ile Thr Ala Asn  
 65 70 75 80  
 Lys Val Pro Gly Ile Arg Ala Cys Thr Ala His Asp Ser Phe Ser Val  
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&lt;213&gt; Homo sapiens

&lt;400&gt; 1036

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 Val Cys Val Xaa Glu Ala Val Cys Ile Cys Xaa Cys Leu Cys Ala Cys  
 35 40 45  
 Thr Xaa Met Cys Ala Cys Met Glu Cys Ile Cys Val Cys Val Trp Thr  
 50 55 60  
 Val Cys Val Ile Met Gln Tyr Val Arg Val Cys Val Trp Ser Val Ser  
 65 70 75 80  
 Val Trp His Val Cys Val Tyr Leu Leu Cys Val Ser Val Cys Val Xaa  
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 Thr Cys Ile Cys Ile Glu Ser Val Cys Ala Val Cys Met Cys Val Ser  
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&lt;210&gt; 1037

&lt;211&gt; 5832

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1037

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<210> 1038

<211> 1485

<212> PRT

<213> Homo sapiens

<400> 1038

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Asn Arg Met Ser Pro Ser Lys Ser Pro Phe Leu Pro Ser Met Lys Met
      805              810              815
Gln Lys Val Met Pro Thr Val Pro Thr Ser Gln Val Thr Gly Pro Pro
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Pro Gln Pro Pro Pro Ile Arg Arg Glu Ile Thr Phe Pro Pro Gly Ser
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Val Glu Ala Ser Gln Pro Val Leu Lys Gln Arg Arg Lys Ile Thr Ser
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Lys Asp Ile Val Thr Pro Glu Ala Trp Arg Val Met Met Ser Leu Lys
  865              870              875              880
Ser Gly Leu Leu Ala Glu Ser Thr Trp Ala Leu Asp Thr Ile Asn Ile
      885              890              895
Leu Leu Tyr Asp Asp Ser Thr Val Ala Thr Phe Asn Leu Ser Gln Leu
      900              905              910
Ser Gly Phe Leu Glu Leu Leu Val Glu Tyr Phe Arg Lys Cys Leu Ile
      915              920              925
Asp Ile Phe Gly Ile Leu Met Glu Tyr Glu Val Gly Asp Pro Ser Gln
      930              935              940
Lys Ala Leu Asp His Asn Ala Ala Arg Lys Asp Asp Ser Gln Ser Leu
  945              950              955              960
Ala Asp Asp Ser Gly Lys Glu Glu Glu Asp Ala Glu Cys Ile Asp Asp
      965              970              975
Asp Glu Glu Asp Glu Glu Asp Glu Glu Asp Ser Glu Lys Thr Glu
      980              985              990
Ser Asp Glu Lys Ser Ser Ile Ala Leu Thr Ala Pro Asp Ala Ala Ala
      995              1000              1005
Asp Pro Lys Glu Lys Pro Lys Gln Ala Ser Lys Phe Asp Lys Leu Pro
  1010              1015              1020
Ile Lys Ile Val Lys Lys Asn Asn Leu Phe Val Val Asp Arg Ser Asp
  1025              1030              1035              1040
Lys Leu Gly Arg Val Gln Glu Phe Asn Ser Gly Leu Leu His Trp Gln
      1045              1050              1055
Leu Gly Gly Gly Asp Thr Thr Glu His Ile Gln Thr His Phe Glu Ser
      1060              1065              1070
Lys Met Glu Ile Pro Pro Arg Arg Pro Pro Pro Pro Leu Ser Ser
      1075              1080              1085
Ala Gly Lys Lys Lys Glu Leu Ala Gly Lys Gly Asp Ser Glu Glu Gln
      1090              1095              1100
Gln Glu Lys Ser Ile Ile Ala Thr Ile Asp Asp Val Leu Ser Ala Arg
  1105              1110              1115              1120
Pro Gly Ala Leu Pro Glu Asp Ala Asn Pro Gly Pro Gln Thr Glu Ser
      1125              1130              1135
Ser Lys Phe Pro Phe Gly Ile Gln Gln Ala Lys Ser His Arg Asn Ile
      1140              1145              1150
Lys Leu Leu Glu Asp Glu Pro Arg Ser Arg Asp Glu Thr Pro Leu Cys
      1155              1160              1165
Thr Ile Ala His Trp Gln Asp Ser Leu Ala Lys Arg Cys Ile Cys Val
      1170              1175              1180
Ser Asn Ile Val Arg Ser Leu Ser Phe Val Pro Gly Asn Asp Ala Glu

```

1185                      1190                      1195                      1200  
 Met Ser Lys His Pro Gly Leu Val Leu Ile Leu Gly Lys Leu Ile Leu  
                                  1205                      1210                      1215  
 Leu His His Glu His Pro Glu Arg Lys Arg Ala Pro Gln Thr Tyr Glu  
                                  1220                      1225                      1230  
 Lys Glu Glu Asp Glu Asp Lys Gly Val Ala Cys Ser Lys Asp Glu Trp  
                                  1235                      1240                      1245  
 Trp Trp Asp Cys Leu Glu Val Leu Arg Asp Asn Thr Leu Val Thr Leu  
                                  1250                      1255                      1260  
 Ala Asn Ile Ser Gly Gln Leu Asp Leu Ser Ala Tyr Thr Glu Ser Ile  
 1265                      1270                      1275                      1280  
 Cys Leu Pro Ile Leu Asp Gly Leu Leu His Trp Met Val Cys Pro Ser  
                                  1285                      1290                      1295  
 Ala Glu Ala Gln Asp Pro Phe Pro Thr Val Gly Pro Asn Ser Val Pro  
                                  1300                      1305                      1310  
 Ser Pro Gln Arg Leu Val Leu Glu Thr Leu Cys Lys Leu Ser Ile Gln  
                                  1315                      1320                      1325  
 Asp Asn Asn Val Asp Leu Ile Leu Ala Thr Pro Pro Phe Ser Arg Gln  
                                  1330                      1335                      1340  
 Glu Lys Phe Tyr Ala Thr Leu Val Arg Tyr Val Gly Asp Arg Lys Asn  
 1345                      1350                      1355                      1360  
 Pro Val Cys Arg Glu Met Ser Met Ala Leu Leu Ser Asn Leu Ala Gln  
                                  1365                      1370                      1375  
 Gly Asp Ala Leu Ala Ala Arg Ala Ile Ala Val Gln Lys Gly Ser Ile  
                                  1380                      1385                      1390  
 Gly Asn Leu Ile Ser Phe Leu Glu Asp Gly Val Thr Met Ala Gln Tyr  
                                  1395                      1400                      1405  
 Gln Gln Ser Gln His Asn Leu Met His Met Gln Pro Pro Pro Leu Glu  
                                  1410                      1415                      1420  
 Pro Pro Ser Val Asp Met Met Cys Arg Ala Ala Lys Ala Leu Leu Ala  
 1425                      1430                      1435                      1440  
 Met Ala Arg Val Asp Glu Asn Arg Ser Glu Phe Leu Leu His Glu Gly  
                                  1445                      1450                      1455  
 Arg Leu Leu Asp Ile Ser Ile Ser Ala Val Leu Asn Ser Leu Val Ala  
                                  1460                      1465                      1470  
 Ser Val Ile Cys Asp Val Leu Phe Gln Ile Gly Gln Leu  
                                  1475                      1480                      1485

&lt;210&gt; 1039

&lt;211&gt; 379

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1039

gcaggagcca gggatgctgc tgaacatccc gcagtgcacg agacaggcct ccaccacacg  
60

gaattacctt ggcctgaggt gttacgagag cacagagaga aaccaggtac agacgcgggg  
120

cagaggggag agagggagag agtgtgagag ctaagggtttc gggagaagac tttgtggaaa  
180

aagtcttttg ctgggtcctg caacatagcc aggattcagt gacaggtgag gaccactcca  
240

gattttgtat gtattgaagg ccctgaatac ttttttgaaa gagaatgaca tgagtacacc  
300



tggtcagcca cacgtgagag ggggtggagg agggaagtac cagaggcagg gagaccaggt  
 360  
 agaaagacct cgccatagt  
 379

<210> 1040  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 1040  
 Met Ala Arg Ser Phe Tyr Leu Val Ser Leu Pro Leu Val Leu Pro Ser  
 1 5 10 15  
 Ser Asn Pro Ser His Val Trp Leu Thr Arg Cys Thr His Val Ile Leu  
 20 25 30  
 Phe Gln Lys Ser Ile Gln Gly Leu Gln Tyr Ile Gln Asn Leu Glu Trp  
 35 40 45  
 Ser Ser Pro Val Thr Glu Ser Trp Leu Cys Cys Arg Thr Gln Pro Lys  
 50 55 60  
 Thr Phe Ser Thr Lys Ser Ser Pro Glu Thr Leu Ala Leu Thr Leu Ser  
 65 70 75 80  
 Pro Ser Leu Pro Ser Ala Pro Arg Leu Tyr Leu Val Ser Leu Cys Ala  
 85 90 95  
 Leu Val Thr Pro Gln Ala Lys Val Ile Pro Cys Gly Gly Gly Leu Ser  
 100 105 110  
 Arg Ala Leu Arg Asp Val Gln Gln His Pro Trp Leu Leu  
 115 120 125

<210> 1041  
 <211> 388  
 <212> DNA  
 <213> Homo sapiens

<400> 1041  
 ttagtggccg tggaggccat cggctacatc gcgagtattg acaaggccga tatgtcaatc  
 60  
 gaaacggcgt acctgccgcg gctgttggtt tccctggccc tgaccatccc ggtgctcgcc  
 120  
 ttgtcgatga tcccgccct gcacttcccg cattggccgt tgtgggcgtt ggcgcttacc  
 180  
 accccggtgg tggtctgggg tgccctggccg ctgcaccacg ccgcgtggac caacctgcgg  
 240  
 caccggcgcg ccatcatgga caccctggtg tcgctcggcg tcctcacttc gtacctctgg  
 300  
 tcggtatgga tgctgaccac aggcggcgag cacctctacc tggaggtagc cgtccaccgt  
 360  
 cagcagctg atcctggccg gcaaattt  
 388

<210> 1042  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 1042

Leu Val Ala Val Glu Ala Ile Gly Tyr Ile Ala Ser Ile Asp Lys Ala  
 1 5 10 15  
 Asp Met Ser Ile Glu Thr Ala Tyr Leu Pro Arg Leu Leu Val Ser Leu  
 20 25 30  
 Ala Leu Thr Ile Pro Val Leu Ala Leu Ser Met Ile Pro Ala Leu His  
 35 40 45  
 Phe Pro His Trp Pro Leu Trp Ala Leu Ala Leu Thr Thr Pro Val Val  
 50 55 60  
 Phe Trp Gly Ala Trp Pro Leu His His Ala Ala Trp Thr Asn Leu Arg  
 65 70 75 80  
 His Gly Ala Ala Ile Met Asp Thr Leu Val Ser Leu Gly Val Leu Thr  
 85 90 95  
 Ser Tyr Leu Trp Ser Val Trp Met Leu Thr Thr Gly Gly Glu His Leu  
 100 105 110  
 Tyr Leu Glu Val Ala Val His Arg His Asp Ala Asp Pro Gly Arg Gln  
 115 120 125  
 Ile

&lt;210&gt; 1043

&lt;211&gt; 555

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1043

accggtgaaa cctgatcgg ccaatcgttt tccaccgttc ccggcggcaa gggcgcaaac  
 60  
 caggcggctcg cttcgggcgcg tcttggggcc gaagtcgcga tggtcggttg cgtgggtacc  
 120  
 gatgcctacg gcgcgcaatt acgcgacgca ttgttggtgg aaggcatcga ttgccaggcc  
 180  
 gtcagcaccg tcgacgggttc cagcgggtgtg gcgctgatcg tggatgatga cagcagccag  
 240  
 aatgcgatcg ttatcgtcgc cggtagcaat ggcgagctga ctccggccaa gttacagacc  
 300  
 tttgacagcg tgctgcaggc tgccgacgtg attgtctgcc agcttgagac gccgatggag  
 360  
 actgtcggcc atgcgcctaa gcgcgggtcgc gaactgggca agacggtgat cctcaatccg  
 420  
 gcgcgggcca gcggcccgcgt gcctgaggat tggtagcccg ccatcgatta cctgattccc  
 480  
 aacgaaagcg aagcctcggc cttgagtggc gtgggtggtgg attcactgga cagcgccaag  
 540  
 gtcgctgcta cgcgt  
 555

&lt;210&gt; 1044

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1044

Thr Gly Glu Thr Leu Ile Gly Gln Ser Phe Ser Thr Val Pro Gly Gly

```

      1           5           10           15
Lys Gly Ala Asn Gln Ala Val Ala Ser Ala Arg Leu Gly Ala Glu Val
      20           25           30
Ala Met Val Gly Cys Val Gly Thr Asp Ala Tyr Gly Ala Gln Leu Arg
      35           40           45
Asp Ala Leu Leu Val Glu Gly Ile Asp Cys Gln Ala Val Ser Thr Val
      50           55           60
Asp Gly Ser Ser Gly Val Ala Leu Ile Val Val Asp Asp Ser Ser Gln
      65           70           75           80
Asn Ala Ile Val Ile Val Ala Gly Ser Asn Gly Glu Leu Thr Pro Ala
      85           90           95
Lys Leu Gln Thr Phe Asp Ser Val Leu Gln Ala Ala Asp Val Ile Val
      100          105          110
Cys Gln Leu Glu Thr Pro Met Asp Thr Val Gly His Ala Pro Lys Arg
      115          120          125
Gly Arg Glu Leu Gly Lys Thr Val Ile Leu Asn Pro Ala Pro Ala Ser
      130          135          140
Gly Pro Leu Pro Glu Asp Trp Tyr Ala Ala Ile Asp Tyr Leu Ile Pro
      145          150          155          160
Asn Glu Ser Glu Ala Ser Ala Leu Ser Gly Val Val Val Asp Ser Leu
      165          170          175
Asp Ser Ala Lys Val Ala Ala Thr Arg
      180          185

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&lt;210&gt; 1045

&lt;211&gt; 371

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1045

```

ctattgccat actaccgccg cggcaaccta caggacatga tcaacgccaa cctcttcaat
60
cactccaaat tccccgagac gcaccttatg aatctatttc tcggcgtctg caaggccctg
120
cgcgccatgc acgattacca cgcacccgccg gcagagcgca tgccaattgg gcaccgaagg
180
cagaccacca cccaggtgca aagcaacagt ggtagagcgg tcgctcatcg acgaaacgta
240
cggaagaaga cgaagagacg gagcaggaaa gacctgttat ggaatcacag aaccacatcg
300
ggcagggcgg cgagcacaaa accatatgcg catcgcgaca ttaaaccagg tacgtgctgc
360
aagctcctcg g
371

```

&lt;210&gt; 1046

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1046

```

Leu Leu Pro Tyr Tyr Arg Arg Gly Asn Leu Gln Asp Met Ile Asn Ala
1           5           10           15
Asn Leu Phe Asn His Ser Lys Phe Pro Glu Thr His Leu Met Asn Leu

```

			20					25					30			
Phe	Leu	Gly	Val	Cys	Lys	Ala	Leu	Arg	Ala	Met	His	Asp	Tyr	His	Ala	
		35					40					45				
Pro	Pro	Ala	Glu	Arg	Met	Pro	Ile	Gly	His	Arg	Arg	Gln	Thr	Thr	Thr	
	50					55					60					
Gln	Val	Gln	Ser	Asn	Ser	Gly	Arg	Ala	Val	Ala	His	Arg	Arg	Asn	Val	
65					70					75					80	
Arg	Lys	Lys	Thr	Lys	Arg	Arg	Ser	Arg	Lys	Asp	Leu	Leu	Trp	Asn	His	
			85						90					95		
Arg	Thr	Thr	Ser	Gly	Arg	Ala	Ala	Ser	Thr	Lys	Pro	Tyr	Ala	His	Arg	
			100					105					110			
Asp	Ile	Lys	Pro	Gly	Thr	Cys	Cys	Lys	Leu	Leu						
		115					120									

```
<210> 1047
<211> 754
<212> DNA
<213> Homo sapiens
```

```

<400> 1047
natgcccgaga aggcacctgga cgaggcggttgc ccagccctgg atgcggctct gccagcccta
60
cgcaacctca acaagaacga agtgaccag gtacgtgcca tgcagcggcc acccccgggt
120
gtgaaactgg tcatagaagc tgtgtgcatt atgaaaggca tcaagcccaa gaagggtgctt
180
ggagaaaaagc caggcaccaa ggtggatgac tactgggagc ctggcaaggg gctgctgcag
240
gacccggggcc acttccttga gagcctcttc aagtttgaca aggacaacat tggagatgtg
300
gtgatcaaag ccattccagc gtacatcgat aatgaagagt tccagccagc caccattgcc
360
aagggtgtcca aggggtgccc cttcatttgg ccgtgggggg gggcaatgcc caagtacccc
420
tttgtggcca aggccgtgga gcccgaagcg caagccctgc tggaggccca ggatgacctg
480
ggggtgacac agaggatcct ggatgaggca aaacagcgcc ttcgtgaggt ggaggacggc
540
atcgccacaa tgcaggctaa gtaccgggaa tgcattacca agaaggagga gctggagctg
600
aagtgtgagc agtgtgagca gcggtgggc cacgctggca aggtgcgcac cctcctcctg
660
caaggcctgc aagcggggcc ggcccagaca ggggcccagaa aggaccaggg cgccggtggg
720
tcctggggtg gctgtccaac cccctcctg gcaa
754

```

```
<210> 1048
<211> 251
<212> PRT
<213> Homo sapiens
```

<400> 1048  
Xaa Ala Gln Lys Asp Leu Asp Glu Ala Leu Pro Ala Leu Asp Ala Ala

1	5	10	15
Leu Ala Ser	Leu Arg Asn	Leu Asn Lys	Glu Val Thr Gln Val Arg
20	25	30	
Ala Met Gln	Arg Pro Pro	Gly Val Lys	Leu Val Ile Glu Ala Val
35	40	45	
Cys Ile Met	Lys Gly Ile	Lys Pro Lys	Lys Val Pro Gly Glu Lys Pro
50	55	60	
Gly Thr Lys	Val Asp Asp	Tyr Trp Glu	Pro Gly Lys Gly Leu Leu Gln
65	70	75	80
Asp Pro Gly	His Phe Leu	Glu Ser Leu	Phe Lys Phe Asp Lys Asp Asn
85	90	95	
Ile Gly Asp	Val Val Ile	Lys Ala Ile	Gln Pro Tyr Ile Asp Asn Glu
100	105	110	
Glu Phe Gln	Pro Ala Thr	Ile Ala Lys	Val Ser Lys Gly Cys Pro Phe
115	120	125	
Ile Trp Pro	Trp Gly Gly	Ala Met Pro	Lys Tyr Pro Phe Val Ala Lys
130	135	140	
Ala Val Glu	Pro Lys Arg	Gln Ala Leu	Leu Glu Ala Gln Asp Asp Leu
145	150	155	160
Gly Val Thr	Gln Arg Ile	Leu Asp Glu	Ala Lys Gln Arg Leu Arg Glu
165	170	175	
Val Glu Asp	Gly Ile Ala	Thr Met Gln	Ala Lys Tyr Arg Glu Cys Ile
180	185	190	
Thr Lys Lys	Glu Glu Leu	Glu Leu Lys	Cys Glu Gln Cys Glu Gln Arg
195	200	205	
Leu Gly His	Ala Gly Lys	Val Arg Thr	Leu Leu Leu Gln Gly Leu Gln
210	215	220	
Ala Gly Pro	Ala Gln Thr	Gly Ala Arg	Lys Asp Gln Gly Ala Gly Gly
225	230	235	240
Ser Trp Gly	Gly Cys Pro	Thr Pro Ser	Leu Ala
245	250		

&lt;210&gt; 1049

&lt;211&gt; 558

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1049

cgcagcaata gctgcacttg accagactgg gctttgcaat aagcgcatte cccgggctga  
 60  
 atgctgcaga tccttacagg ctgactgcag ggtgtttcag attctcctgg agtcacacgt  
 120  
 gccagcttga tttcaagaaa caactagaat aacagttttc tgataagaag tctatagcac  
 180  
 tttatggctt acataatcca gagatagatg ggctgggcat gattcccatt ttctgttggg  
 240  
 gaaaccgact cacagagaag ttaagggaca agtataaagt gatgaaactg tgtactgaac  
 300  
 ctcatgtctc ccagactccc ggggtccccg gctttttctc gggggggccc cattcacatt  
 360  
 gcaattcatg gccggggcaa atgtcacccc acagagatat taagcactcc aacactccat  
 420  
 ccaccagggt gcagccaaag gattcagaag acaatgatca ttccatcagc atgcactatg  
 480

cagctaaaga aaggttttgg catgctctgc tttattgttt cacagaagat aagaaaataa  
 540  
 actgcaaagt aacttaag  
 558

<210> 1050  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<400> 1050  
 Met Ile Pro Ile Phe Cys Trp Gly Asn Arg Leu Thr Glu Lys Leu Arg  
 1 5 10 15  
 Asp Lys Tyr Lys Val Met Lys Leu Cys Thr Glu Pro His Val Ser Gln  
 20 25 30  
 Thr Pro Gly Ser Pro Gly Phe Phe Ser Gly Arg Pro His Ser His Cys  
 35 40 45  
 Asn Ser Trp Pro Gly Gln Met Leu Thr His Arg Asp Ile Lys His Ser  
 50 55 60  
 Asn Thr Pro Ser Thr Arg Leu Gln Pro Lys Asp Ser Glu Asp Asn Asp  
 65 70 75 80  
 His Ser Ile Ser Met His Tyr Ala Ala Lys Glu Arg Phe Trp His Ala  
 85 90 95  
 Leu Leu Tyr Cys Phe Thr Glu Asp Lys Lys Ile Asn Cys Lys Val Thr  
 100 105 110

<210> 1051  
 <211> 317  
 <212> DNA  
 <213> Homo sapiens

<400> 1051  
 gcgttgagtc gggatgtcgc attcatgccc ggcgaacctt tttttgccga accggagcgt  
 60  
 aatccgggta atcttcgtct caatttcagt cacatcgcac cggagcgtct ggacgaaggc  
 120  
 ctcaagcgcc tggctgctgt catccgtcac gcacaggctg cacaagcggc ttaaggggag  
 180  
 ggccatgtac aaggtttatg gcgattacca gtcgggcaat tgctacaaga tcaagctgat  
 240  
 gctgcacctg ctggggcagg aatatcgctg gcacccgggg gacatcctca aggtgacacc  
 300  
 gagaccccg aattttt  
 317

<210> 1052  
 <211> 57  
 <212> PRT  
 <213> Homo sapiens

<400> 1052  
 Ala Leu Ser Arg Asp Val Ala Phe Met Pro Gly Glu Pro Phe Phe Ala  
 1 5 10 15  
 Glu Pro Glu Arg Asn Pro Gly Asn Leu Arg Leu Asn Phe Ser His Ile

20 25 30  
 Ala Pro Glu Arg Leu Asp Glu Gly Leu Lys Arg Leu Ala Ala Val Ile  
 35 40 45  
 Arg His Ala Gln Ala Ala Gln Ala Ala  
 50 55

<210> 1053  
 <211> 318  
 <212> DNA  
 <213> Homo sapiens

<400> 1053  
 caattggcta cgcgatccga acgggcgcac gggctctctat gactggcaag ccgtcgctcg  
 60  
 cggggagtgg gccctcgact atgcctacgc gatgtcggtg aacctgacca ccgagaaccg  
 120  
 gcgtgcctgg gaacgcgacc tgctcgagcg ttatctgtgg cgcctcgccg aagaggggtg  
 180  
 cgccaacccg cctcgttcg agcaagcgtg gctacgctac cggcaacagc cgttccacgt  
 240  
 cgggatcttc tcactcttga ccatcggcgc cggacgcttt caaccggcca tgcaaccggc  
 300  
 ggactcnnnn cccncnc  
 318

<210> 1054  
 <211> 96  
 <212> PRT  
 <213> Homo sapiens

<400> 1054  
 Met Gly Leu Tyr Asp Trp Gln Ala Val Ala Arg Gly Glu Trp Ala Leu  
 1 5 10 15  
 Asp Tyr Ala Tyr Ala Met Ser Val Asn Leu Thr Thr Glu Asn Arg Arg  
 20 25 30  
 Ala Trp Glu Arg Asp Leu Leu Glu Arg Tyr Leu Trp Arg Leu Ala Glu  
 35 40 45  
 Glu Gly Val Ala Asn Pro Pro Ser Phe Glu Gln Ala Trp Leu Arg Tyr  
 50 55 60  
 Arg Gln Gln Pro Phe His Val Gly Ile Phe Ser Leu Leu Thr Ile Gly  
 65 70 75 80  
 Ala Gly Arg Phe Gln Pro Ala Met Gln Pro Ala Asp Ser Xaa Pro Xaa  
 85 90 95

<210> 1055  
 <211> 391  
 <212> DNA  
 <213> Homo sapiens

<400> 1055  
 tacaatgtat catcaaccag aaatacaatg agaaccacct gccagtctcc caaatactat  
 60  
 ctgcagccac tcatttaact ctctggcta gctccacgtg ggccgtctga actctcttag  
 120

aagaatcatc tctctgctca ggcaccggga gcaaggggca tctgtcgctc tgcagaacgg  
 180  
 aggggaccag gcctgatgaa caccatcctg ggcccagaaa cctgggaggg taaagagaac  
 240  
 tgccaggggt gaagtccaag gatgggaaaa aggcctccgg ggcagagtcc tgaaatgtca  
 300  
 gaagtacacc aaagaggaaa cagcatcacg ttattgctga ggcagggcct cattctgttg  
 360  
 ccaaggctgc agtgcagtgg tgacaccatg g  
 391

<210> 1056

<211> 83

<212> PRT

<213> Homo sapiens

<400> 1056

Met	Val	Ser	Pro	Leu	His	Cys	Ser	Leu	Gly	Asn	Arg	Met	Arg	Pro	Cys
1				5					10					15	
Leu	Ser	Asn	Asn	Val	Met	Leu	Phe	Pro	Leu	Trp	Cys	Thr	Ser	Asp	Ile
		20						25				30			
Ser	Gly	Leu	Cys	Pro	Gly	Gly	Leu	Phe	Pro	Ile	Leu	Gly	Leu	His	Pro
		35				40					45				
Trp	Gln	Phe	Ser	Leu	Pro	Ser	Gln	Val	Ser	Gly	Pro	Arg	Met	Val	Phe
	50					55				60					
Ile	Arg	Pro	Gly	Pro	Leu	Arg	Ser	Ala	Glu	Arg	Gln	Met	Pro	Leu	Ala
65					70					75				80	
Pro	Gly	Ala													

<210> 1057

<211> 341

<212> DNA

<213> Homo sapiens

<400> 1057

gaattccctg cgcggtgtgac gccgggtcgcc gagcaactcg gcgtgtcgct gacgctgcat  
 60  
 cccgatgata cgccgcgtcc gctgttcggg ttgccgcgca ttgcgtccag cgccgaggac  
 120  
 tatcaggcgc tgttcgatgc ggtaccgtcc aaggcgaacg gcattctgcct gtgcacgggt  
 180  
 tcgctcggcg tgcgcgcgga gaacgatctg cctgaaatgg ccgaacgttt cgccccgcgt  
 240  
 atcgcccttg cgcattctgcg cgcgaccaag cgcgacgccg atggcctgtc gtttcatgaa  
 300  
 tccgaccatc tcgacggcga tgcgacatg gtcgcgtgct c  
 341

<210> 1058

<211> 113

<212> PRT

<213> Homo sapiens



&lt;400&gt; 1058

Glu Phe Pro Ala Arg Val Thr Pro Val Ala Glu Gln Leu Gly Val Ser  
 1 5 10 15  
 Leu Thr Leu His Pro Asp Asp Pro Pro Arg Pro Leu Phe Gly Leu Pro  
 20 25 30  
 Arg Ile Ala Ser Ser Ala Glu Asp Tyr Gln Ala Leu Phe Asp Ala Val  
 35 40 45  
 Pro Ser Lys Ala Asn Gly Ile Cys Leu Cys Thr Gly Ser Leu Gly Val  
 50 55 60  
 Arg Ala Glu Asn Asp Leu Pro Glu Met Ala Glu Arg Phe Gly Pro Arg  
 65 70 75 80  
 Ile Ala Phe Ala His Leu Arg Ala Thr Lys Arg Asp Ala Asp Gly Leu  
 85 90 95  
 Ser Phe His Glu Ser Asp His Leu Asp Gly Asp Val Asp Met Val Ala  
 100 105 110  
 Cys

&lt;210&gt; 1059

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1059

nagctgaccg gctggcagat caacatcatg acgccggaag aaagcgtgaa ccgccgggaa  
 60  
 gtcgagcggtt cgggcctgcg caccacgttc atgaacaagc tggacgtcga tgaggaagtc  
 120  
 gccgacatcc tgatcgacga aggtttcacc ggtatcgagg aaatcgcccta cgtccccatg  
 180  
 caggaactgc tggagatcga ggcgttcgac gaagacacca tcaacgagtt gcgcgcccgt  
 240  
 gcccgcaatg cgctgctgac cgaggccatc gcccggaag agcgccttga gaccgcgcag  
 300  
 gatctgcttg aactcgaagg cgtgacgccg gaactggctg ccaagctggc cgagcgtcaa  
 360  
 gtgcgtacgc gt  
 372

&lt;210&gt; 1060

&lt;211&gt; 124

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1060

Xaa Leu Thr Gly Trp Gln Ile Asn Ile Met Thr Pro Glu Glu Ser Val  
 1 5 10 15  
 Asn Arg Arg Glu Val Glu Arg Ser Gly Leu Arg Thr Thr Phe Met Asn  
 20 25 30  
 Lys Leu Asp Val Asp Glu Glu Val Ala Asp Ile Leu Ile Asp Glu Gly  
 35 40 45  
 Phe Thr Gly Ile Glu Glu Ile Ala Tyr Val Pro Met Gln Glu Leu Leu  
 50 55 60  
 Glu Ile Glu Ala Phe Asp Glu Asp Thr Ile Asn Glu Leu Arg Ala Arg

```

65              70              75              80
Ala Arg Asn Ala Leu Leu Thr Glu Ala Ile Ala Gln Glu Glu Arg Leu
              85              90              95
Glu Thr Ala Gln Asp Leu Leu Glu Leu Glu Gly Val Thr Pro Glu Leu
              100              105              110
Ala Ala Lys Leu Ala Glu Arg Gln Val Arg Thr Arg
              115              120

```

&lt;210&gt; 1061

&lt;211&gt; 456

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1061

```

tctagactcc atggcaccgg gctgagcggg taagtaagaa agataaaaag tgccttttgc
60
cccttcgagg aaaccctttt gcaggccaag caagggctgc aagtgtttgg gagctgagag
120
gagaaggagg attctggagc attgtatttg gcagccggag cgggcagtgg gcgggggggtt
180
gggacacgaa gggctcttcg gaccctgtg cctcttctgc cccaagggcg agaagacggg
240
cttcgcagcg accctcgggg gtccatggag cgcctgcct tcgccccctc gctcttccca
300
ggtctgaacc tggatgggga gaagaaattg aagtgccttg gagacggggg ggcttaaaac
360
actagggagc ctcacgcgcc agccttgggc ccactttcct ttcgatcgtg aggattccgc
420
accccgaagc cgtcttctcg gggctcgggg gcgcgc
456

```

&lt;210&gt; 1062

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1062

```

Met Arg Leu Pro Ser Val Leu Ser Pro Pro Val Ser Lys Ala Leu Gln
1              5              10              15
Phe Leu Leu Pro Ile Gln Val Gln Thr Trp Glu Glu Arg Gly Gly Glu
              20              25              30
Gly Arg Arg Leu His Gly Pro Pro Arg Val Ala Ala Lys Pro Val Phe
              35              40              45
Ser Pro Leu Gly Gln Lys Arg His Arg Gly Pro Lys Ser Pro Ser Cys
50              55              60
Pro Asn Pro Pro Pro Thr Ala Arg Ser Gly Cys Gln Ile Gln Cys Ser
65              70              75              80
Arg Ile Leu Leu Leu Leu Ser Ala Pro Lys His Leu Gln Pro Leu Leu
              85              90              95
Gly Leu Gln Lys Gly Phe Leu Glu Gly Ala Lys Gly Thr Phe Tyr Leu
              100              105              110
Ser Tyr Leu Pro Ala Gln Pro Gly Ala Met Glu Ser Arg
              115              120              125

```

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